```
400211
Seq. No.
                  LIB3431-031-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417260
                  372
BLAST score
                  1.0e-35
E value
                  121
Match length
% identity
                   64
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir__S33632
NCBI Description
                  lir1 protein - rice >gi_20263_emb_CAA\overline{4}8706 \overline{(X68807)}
                  light-regulated gene [Oryza sativa]
                   400212
Seq. No.
                  LIB3431-031-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3914466
BLAST score
                   258
E value
                   6.0e-24
Match length
                   60
% identity
                   92
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
                   subunit precursor [Zea mays]
Seq. No.
                   400213
Seq. ID
                   LIB3431-031-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q3913018
BLAST score
                   579
E value
                   6.0e-60
Match length
                   117
% identity
                   100
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                   aldolase [Oryza sativa]
Seq. No.
                   400214
                   LIB3431-031-P1-K1-F10
Seq. ID
Method
                   BLASTX
                   q2688824
NCBI GI
BLAST score
                   146
                   3.0e-09
E value
Match length
                   76
                   47
% identity
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniaca]
                   400215
Seq. No.
                   LIB3431-031-P1-K1-F11
Seq. ID
                   BLASTX
Method
                   g2944178
NCBI GI
BLAST score
                   346
                   1.0e-32
E value
Match length
                   116
% identity
                  (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
                   thaliana]
```

```
400216
Seq. No.
Seq. ID
                  LIB3431-031-P1-K1-F12
Method
                  BLASTX
                  g132105
NCBI GI
BLAST score
                  559
                  1.0e-57
E value
                  122
Match length
% identity
                  86
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400217
                  LIB3431-031-P1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20369
BLAST score
                  335
                  0.0e + 00
E value
Match length
                  351
% identity
                  99
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
                  400218
Seq. No.
                  LIB3431-031-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1661160
BLAST score
                  178
E value
                  3.0e-13
Match length
                  59
% identity
                  71
NCBI Description
                  (U74295) chlorophyll a/b binding protein [Oryza sativa]
                  400219
Seq. No.
Seq. ID
                  LIB3431-031-P1-K1-F8
Method
                  BLASTX
                  g4507223
NCBI GI
BLAST score
                   460
E value
                  5.0e-46
Match length
                  135
% identity
                  71
NCBI Description
                  signal recognition particle receptor ('docking protein')
                  >gi_134892_sp_P08240_SRPR_HUMAN_SIGNAL_RECOGNITION_PARTICLE
                  RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA)
                   (DP-ALPHA) >gi_88607_pir__A29440 signal recognition
```

docking protein [Homo sapiens]

particle receptor - human >gi 30866 emb CAA29608 (X06272)



```
400220
Seq. No.
                  LIB3431-031-P1-K1-F9
Seq. ID
Method
                  BLASTX
                  g82080
NCBI GI
BLAST score
                  333
                  4.0e-31
E value
                  104
Match length
% identity
                  64
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  400221
Seq. No.
                  LIB3431-031-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  600
                  2.0e-62
E value
                  129
Match length
% identity
                  88
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400222
                  LIB3431-031-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130127
BLAST score
                  397
                  1.0e-38
E value
Match length
                  92
                  84
% identity
                  ferritin 1 precursor - maize >gi 1103628 emb CAA58146
NCBI Description
                  (X83076) ferritin [Zea mays]
Seq. No.
                  400223
                  LIB3431-031-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  614
E value
                  5.0e-64
```

Match length 137 89 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 400224

Seq. ID LIB3431-031-P1-K1-H11

NCBI GI

g538430

```
Method
                  BLASTX
NCBI GI
                  a217909
BLAST score
                  353
                  2.0e-33
E value
Match length
                  105
                  69
% identity
NCBI Description (D14044) glycolate oxidase [Cucurbita sp.]
                  400225
Seq. No.
                  LIB3431-031-P1-N1-A3
Seq. ID
Method
                  BLASTX
NCBI ĠI
                  g3914466
BLAST score
                  472
E value
                  2.0e-47
Match length
                  90
                  96
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  400226
                  LIB3431-031-P1-N1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  338
E value
                  2.0e-31
Match length
                  115
% identity
                  62
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  400227
Seq. ID
                  LIB3431-031-P1-N1-A5
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  227
                  2.0e-18
E value
Match length
                  45
% identity
                  96
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  constructl
Seq. No.
                  400228
                  LIB3431-031-P1-N1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4914452
BLAST score
                  274
E value
                  6.0e-24
Match length
                  75
% identity
                  68
NCBI Description
                  (AL050398) putative protein [Arabidopsis thaliana]
Seq. No.
                  400229
Seq. ID
                  LIB3431-031-P1-N1-A7
Method
                  BLASTX
```

```
BLAST score
                  279
                  1.0e-24
E value
Match length
                  55
% identity
                  98
NCBI Description
                  (L36320) superoxide dismutase [Oryza sativa]
                  400230
Seq. No.
                  LIB3431-031-P1-N1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  632
E value
                  6.0e-66
Match length
                  121
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >qi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  400231
                  LIB3431-031-P1-N1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218171
BLAST score
                  80
E value
                  3.0e-37
Match length
                  168
% identity
                  88
NCBI Description
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
                  a/b binding protein of photosystem II (LHCPII), complete
                  cds
                  400232
Seq. No.
                  LIB3431-031-P1-N1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  33
E value
                  3.0e-09
Match length
                  41
% identity
                  95
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  400233
                  LIB3431-031-P1-N1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5734790
BLAST score
                  335
E value
                  2.0e-31
Match length
                  76
                  86
% identity
NCBI Description
                  (AC007980) ATP-dependent metalloprotease [Arabidopsis
                  thaliana]
Seq. No.
                  400234
Seq. ID
                  LIB3431-031-P1-N1-B9
Method
                  BLASTX
NCBI GI
                  g4138290
```

```
BLAST score
                  398
E value
                  1.0e-38
Match length
                  77
% identity
                  100
NCBI Description
                  (AJ005841) thioredoxin M [Oryza sativa]
                  400235
Seq. No.
                  LIB3431-031-P1-N1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570515
BLAST score
                  196
                  5.0e-15
E value
Match length
                  41
                  93
% identity
NCBI Description
                  (AF022740) glycolate oxidase [Oryza sativa]
Seq. No.
                  400236
Seq. ID
                  LIB3431-031-P1-N1-C10
Method
                  BLASTX
NCBI GI
                  q131397
BLAST score
                  158
E value
                  2.0e-10
Match length
                  147
% identity
                  28
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >qi 81480 pir S00008 photosystem II oxygen-evolving
                  complex protein 3 precursor - spinach
                  >gi 755802 emb CAA29056 (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                  oleracea] >gi 225597 prf 1307179B luminal protein 16kD
                  [Spinacia oleracea]
                  400237
Seq. No.
                  LIB3431-031-P1-N1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  327
E value
                  0.0e + 00
Match length
                  399
% identity
                  95
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  400238
Seq. No.
Seq. ID
                  LIB3431-031-P1-N1-C2
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  432
E value
                  1.0e-42
Match length
                  82
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
```

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)



[Oryza sativa]

Seq. No. 400239

Seq. ID LIB3431-031-P1-N1-C3

Method BLASTN
NCBI GI g2072554
BLAST score 389
E value 0.0e+00
Match length 389
% identity 100

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 400240

Seq. ID LIB3431-031-P1-N1-C4

Method BLASTX
NCBI GI g132105
BLAST score 653
E value 2.0e-68
Match length 124
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400241

Seq. ID LIB3431-031-P1-N1-C6

Method BLASTX
NCBI GI g347451
BLAST score 386
E value 3.0e-37
Match length 71
% identity 99

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza

sativa]

Seq. No. 400242

Seq. ID LIB3431-031-P1-N1-C7

Method BLASTN
NCBI GI g2780342
BLAST score 419
E value 0.0e+00
Match length 427
% identity 100

NCBI Description Oryza sativa gene for PBZ1, complete cds

>gi 3251321 dbj E12488 E12488 Nucleotide sequence of Oryza

satīva PBZ1 gene

Seq. No. 400243

Seq. ID LIB3431-031-P1-N1-D1

Method BLASTN

```
NCBI GI g3126853
BLAST score 124
E value 2.0e-63
Match length 162
% identity 100
NCBI Description Oryza sa
```

NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89)

mRNA, nuclear gene encoding chloroplast protein, complete

cds

Seq. No. 400244

Seq. ID LIB3431-031-P1-N1-D10

Method BLASTX
NCBI GI g1296955
BLAST score 308
E value 3.0e-28
Match length 56
% identity 46

NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 400245

Seq. ID LIB3431-031-P1-N1-D6

Method BLASTN
NCBI GI g218154
BLAST score 117
E value 6.0e-59
Match length 169
% identity 100

NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,

clone:Aldp

Seq. No. 400246

Seq. ID LIB3431-031-P1-N1-D7

Method BLASTX
NCBI GI g289920
BLAST score 300
E value 3.0e-27
Match length 57
% identity 100

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 400247

Seq. ID LIB3431-031-P1-N1-D8

Method BLASTX
NCBI GI g131225
BLAST score 216
E value 2.0e-17
Match length 56
% identity 73

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi 167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 400248

Seq. ID LIB3431-031-P1-N1-D9

Method BLASTN

```
g3885887
NCBI GI
BLAST score
                  425
                  0.0e + 00
E value
                  429
Match length
% identity
                  100
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                  complete cds
                  400249
Seq. No.
Seq. ID
                  LIB3431-031-P1-N1-E12
Method
                  BLASTX
                  q1076422
NCBI GI
                  229
BLAST score
                  1.0e-18
E value
Match length
                  85
                  60
% identity
                  transcription factor OBF4 - Arabidopsis thaliana
NCBI Description
                  >gi 414613 emb CAA49524 (X69899) ocs-element binding
                  factor 4 [Arabidopsis thaliana]
                  400250
Seq. No.
Seq. ID
                  LIB3431-031-P1-N1-E2
                  BLASTX
Method
NCBI GI
                  g133019
                  256
BLAST score
                  4.0e-22
E value
                  79
Match length
% identity
                  56
                  60S RIBOSOMAL PROTEIN L7 >gi 71122_pir R5D07 ribosomal
NCBI Description
                  protein L7 - slime mold (Dictyostelium discoideum)
                  >qi 7357 emb CAA33035 (X14909) ribosomal protein L7 (AA 1
                  - 246) [Dictyostelium discoideum]
                  400251
Seq. No.
                  LIB3431-031-P1-N1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3126854
BLAST score
                  507
E value
                  1.0e-68
Match length
                  135
% identity
                  99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  400252
                  LIB3431-031-P1-N1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q218209
BLAST score
                  53
E value
                  9.0e-21
Match length
                   69
% identity
                  94
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
                   400253
Seq. No.
                  LIB3431-031-P1-N1-E8
Seq. ID
```



```
BLASTX
Method
                  g417260
NCBI GI
                  300
BLAST score
                  4.0e-27
E value
Match length
                  76
                  75
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir_S33632
NCBI Description
                  lir1 protein - rice >gi_20263 emb_CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
```

400254 Seq. No. LIB3431-031-P1-N1-E9 Seq. ID Method BLASTX NCBI GI g3914466 BLAST score 342 E value 4.0e-32

Match length 63 % identity 95

PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR NCBI Description

(PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN

subunit precursor [Zea mays]

Seq. No. 400255 LIB3431-031-P1-N1-F1 Seq. ID Method BLASTX NCBI GI g2407279 BLAST score 182 E value 2.0e-13

Match length 37 100 % identity

(AF017362) aldolase [Oryza sativa] NCBI Description

400256 Seq. No. LIB3431-031-P1-N1-F12 Seq. ID

BLASTX Method NCBI GI g132105 354 BLAST score 6.0e-44E value Match length 94 % identity 96

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone posss1139) - rice >gi 218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400257

LIB3431-031-P1-N1-F5 Seq. ID

Method BLASTX g115787 NCBI GI 459 BLAST score E value 8.0e-46 87 Match length

Seq. ID Method

```
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  400258
Seq. No.
Seq. ID
                  LIB3431-031-P1-N1-F6
                  BLASTX
Method
NCBI GI
                  q3036949
BLAST score
                  300
                  4.0e-27
E value
Match length
                  57
                  100
% identity
                  (AB012638) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
Seq. No.
                  400259
                  LIB3431-031-P1-N1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2911886
BLAST score
                  198
                  3.0e-15
E value
                  52
Match length
                  69
% identity
                  (AF047663) Contains similarity to Pfam domain: PF00448
NCBI Description
                   (SRP54), Score=14.7, E-value=2.7e-12, N=1 [Caenorhabditis
                  elegans]
                   400260
Seq. No.
                  LIB3431-031-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q82080
BLAST score
                   336
E value
                   2.0e-31
Match length
                  79
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >qi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   400261
                  LIB3431-031-P1-N1-G10
Seq. ID
Method
                   BLASTX
                   g606817
NCBI GI
BLAST score
                   266
                   3.0e-23
E value
Match length
                   50
                   100
% identity
                  (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                   >gi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic
                   anhydrase 3 [Oryza sativa]
                   400262
Seq. No.
```

51245

LIB3431-031-P1-N1-G3

BLASTX

```
q671740
NCBI GI
BLAST score
                  508
E value
                  2.0e-51
Match length
                  91
% identity
                  100
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  400263
Seq. No.
Seq. ID
                  LIB3431-031-P1-N1-G4
Method
                  BLASTN
NCBI GI
                  g455510
BLAST score
                  58
E value
                  8.0e-24
Match length
                  102
% identity
                  89
NCBI Description Rice mRNA for ferritin, partial sequence
Seq. No.
                  400264
                  LIB3431-031-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  300
E value
                  4.0e-27
Match length
                  57
% identity
                  100
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  400265
Seq. No.
                  LIB3431-031-P1-N1-G6
Seq. ID
Method
                  BLASTX
                  g132105
NCBI GI
BLAST score
                  301
                  2.0e-27
E value
Match length
                  57
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400266
Seq. No.
                  LIB3431-031-P1-N1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548603
BLAST score
                  449
E value
                  1.0e-44
Match length
                  89
                  97
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
```

>gi_478404_pir__JQ2247 photosystem I chain D precursor barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 400267 LIB3431-031-P1-N1-H1 Seq. ID Method BLASTX NCBI GI g4886443 BLAST score 219 1.0e-17 E value Match length 62 % identity 76 (AL050268) hypothetical protein [Homo sapiens] NCBI Description 400268 Seq. No. LIB3431-031-P1-N1-H11 Seq. ID Method BLASTX NCBI GI g1486472 BLAST score 168 9.0e-12 E value 33 Match length % identity (X99853) oxoglutarate malate translocator [Solanum NCBI Description tuberosum] Seq. No. 400269 Seq. ID LIB3431-031-P1-N1-H12 Method BLASTX NCBI GI g2570515 BLAST score 148 2.0e-09 E value Match length 38 % identity 71 (AF022740) glycolate oxidase [Oryza sativa] NCBI Description 400270 Seq. No. LIB3431-031-P1-N1-H6 Seq. ID Method BLASTX g733454 NCBI GI BLAST score 446 3.0e-44 E value Match length 91 95 % identity (U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description [Zea mays] 400271 Seq. No. LIB3431-031-P1-N1-H7 Seq. ID BLASTN Method g5295987 NCBI GI BLAST score 124 E value 4.0e-63

Seq. No. 400272

359

clone:S10304

84

Match length

NCBI Description

% identity

Oryza sativa mRNA for MADS box-like protein, complete cds,

% identity

95

```
LIB3431-031-P1-N1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587556
BLAST score
                  161
E value
                  7.0e-11
Match length
                  40
% identity
                  (AC006577) Similar to gi 1653162 (p)ppGpp
NCBI Description
                  3-pyrophosphohydrolase from Synechocystis sp genome
                  gb D90911. EST gb W43807 comes from this gene.
                  [Arabidopsis thaliana]
                  400273
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q3789948
BLAST score
                  673
E value
                  7.0e-71
Match length
                  133
                  95
% identity
                  (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
Seq. No.
                  400274
                  LIB3431-033-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  397
E value
                  1.0e-38
Match length
                  102
                  79
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  400275
Seq. No.
                  LIB3431-033-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  g548603
NCBI GI
BLAST score
                  223
                  3.0e-18
E value
                  93
Match length
                  58
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi 478404 pir__JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                  400276
Seq. No.
                  LIB3431-033-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076724
                   580
BLAST score
                   5.0e-60
E value
Match length
                  109
```

```
LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >qi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  400277
                  LIB3431-033-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  529
E value
                  4.0e-60
Match length
                  138
                  80
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                  400278
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q1419090
BLAST score
                  431
                  1.0e-42
E value
Match length
                  116
% identity
                  72
                  (X94968) 37kDa chloroplast inner envelope membrane
NCBI Description
                  polypeptide precursor [Nicotiana tabacum]
                  400279
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  q710308
BLAST score
                  377
E value
                  3.0e-36
Match length
                  72
% identity
NCBI Description (U11693) victorin binding protein [Avena sativa]
                  400280
Seq. No.
                  LIB3431-033-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  g5733866
NCBI GI
BLAST score
                  442
                  8.0e-44
E value
Match length
                  140
% identity
                  62
                  (AC007932) Contains similarity to gb M73488
NCBI Description
                   1-aminocyclopropane-1-carboxylate deaminase from
                   Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  400281
                  LIB3431-033-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  246
                  1.0e-136
E value
                  246
Match length
                  100
% identity
```

NCBI Description Oryza sativa mRNA for the small subunit of

```
ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
Seq. No.
                  400282
                  LIB3431-033-P1-K1-B4
Seq. ID
Method
                  BLASTX
                  g2244749
NCBI GI
BLAST score
                  574
E value
                  2.0e-59
Match length
                  132
% identity
                  81
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
                  400283
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q1421730
BLAST score
                  531
                  6.0e-63
E value
                  143
Match length
% identity
                  87
NCBI Description (U43082) RF2 [Zea mays]
                  400284
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-B6
                  BLASTX
Method
NCBI GI
                  q3212854
BLAST score
                  453
                  4.0e-45
E value
Match length
                  137
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  400285
                  LIB3431-033-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3281853
BLAST score
                  231
                  4.0e-19
E value
Match length
                  90
% identity
                  51
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                  400286
Seq. No.
                  LIB3431-033-P1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5915836
BLAST score
                  157
                  1.0e-10
E value
                  55
Match length
                  62
% identity
NCBI Description
                  CYTOCHROME P450 71D7 >gi 1762144 (U48435) putative
```

Seq. No. 400287

Seq. ID LIB3431-033-P1-K1-C2

Method BLASTX

cytochrome P450 [Solanum chacoense]

```
q6006363
NCBI GI
BLAST score
                  228
                  1.0e-18
E value
                  42
Match length
                  100
% identity
                  (AP000559) ESTs AU078183(C62904),C73912(E21020) correspond
NCBI Description
                  to a region of the predicted gene.; Similar to water stress
                  inducible protein (U74296) [Oryza sativa]
                  400288
Seq. No.
                  LIB3431-033-P1-K1-C3
Seq. ID
                  BLASTX
Method
                  g2501356
NCBI GI
                  475
BLAST score
                  1.0e-47
E value
                  115
Match length
                  79
% identity
                  TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
NCBI Description
                  >gi 1658322 emb CAA90427 (Z50099) transketolase precursor
                  [Solanum tuberosum]
                  400289
Seq. No.
                  LIB3431-033-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  q1076724
NCBI GI
                  655
BLAST score
                  8.0e-69
E value
                  141
Match length
                   85
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                   >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
                   400290
Seq. No.
                  LIB3431-033-P1-K1-C6
Seq. ID
                  BLASTN
Method
                   q3821780
NCBI GI
BLAST score
                   35
                   5.0e-10
E value
                   35
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   400291
                   LIB3431-033-P1-K1-C7
Seq. ID
                   BLASTX
Method
                   q131388
NCBI GI
BLAST score
                   329
E value
                   1.0e-30
                   115
Match length
% identity
                   65
```

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844 emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum



aestivum]

Seq. No. 400292 Seq. ID LIB3431-033-P1-K1-C8 Method BLASTX NCBI GI q131388 BLAST score 308 E value 4.0e-28 115

63 % identity OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831_pir__S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

400293 Seq. No.

Match length

Seq. ID LIB3431-033-P1-K1-C9

Method BLASTX NCBI GI q2507455 BLAST score 617 2.0e-64 E value Match length 141 82 % identity

FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE NCBI Description

SYNTHETASE) (FHS) (FTHFS) >gi 322401 pir A43350

formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi 170145 (M83940) 10-formyltetrahydrofolate synthetase

[Spinacia oleracea]

400294 Seq. No.

LIB3431-033-P1-K1-D1 Seq. ID

BLASTN Method g3789953 NCBI GI BLAST score 317 1.0e-178 E value 317 Match length 100 % identity

Oryza sativa chlorophyll a/b-binding protein precursor NCBI Description

(Cab26) mRNA, nuclear gene encoding chloroplast protein,

complete cds

400295 Seq. No.

LIB3431-033-P1-K1-D10 Seq. ID

Method BLASTX g3201656 NCBI GI 178 BLAST score 6.0e-13 E value 85 Match length % identity 47

(AF005933) galactokinase [Lactobacillus casei] NCBI Description

400296 Seq. No.

LIB3431-033-P1-K1-D11 Seq. ID

Method BLASTX

BLAST score

662

```
q3885888
NCBI GI
BLAST score
                  180
                  4.0e-13
E value
                  83
Match length
% identity
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
                  400297
Seq. No.
                  LIB3431-033-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2407281
                  674
BLAST score
                  5.0e-71
E value
                  127
Match length
                  98
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  400298
Seq. No.
                  LIB3431-033-P1-K1-D2
Seq. ID
                  BLASTN
Method
NCBI GI
                  q20262
BLAST score
                  225
                  1.0e-123
E value
                  225
Match length
                  100
% identity
NCBI Description O.sativa light-induced mRNA
                   400299
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-D4
                  BLASTX
Method
                   q5729802
NCBI GI
BLAST score
                  254
                   8.0e-22
E value
                   53
Match length
                   83
% identity
NCBI Description similar to S. pombe dim1+ >gi 2565275 (AF023611) Dim1p
                   homolog [Homo sapiens]
                   400300
Seq. No.
Seq. ID
                   LIB3431-033-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q1169798
BLAST score
                   688
E value
                   1.0e-72
Match length
                   145
% identity
                   92
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE
                   ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218)
                   phosphoglucose isomerase (Pgi-b) [Oryza sativa]
Seq. No.
                   400301
                   LIB3431-033-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   g3345477
NCBI GI
```

```
1.0e-69
E value
Match length
                  125
                  100
% identity
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  400302
                  LIB3431-033-P1-K1-D7
Seq. ID
                  BLASTX
Method
                  q5923670
NCBI GI
BLAST score
                  296
E value
                  8.0e-27
                  99
Match length
                  57
% identity
NCBI Description (AC009326) unknown protein [Arabidopsis thaliana]
                  400303
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3885513
                  276
BLAST score
                  2.0e-24
E value
Match length
                  74
% identity
                  62
                  (AF084201) similar to chloroplast 50S ribosomal protein L31
NCBI Description
                  [Medicago sativa]
Seq. No.
                  400304
                  LIB3431-033-P1-K1-E1
Seq. ID
                  BLASTX
Method
                  q3980417
NCBI GI
                  385
BLAST score
                  4.0e-37
E value
Match length
                  118
                  32
% identity
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.
                   400305
                  LIB3431-033-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885891
BLAST score
                   121
E value
                   2.0e-61
Match length
                   170
% identity
                   99
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                  mRNA, complete cds
                   400306
Seq. No.
                   LIB3431-033-P1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   579
E value
                   7.0e-60
Match length
                   106
                   100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

400307 Seq. No. LIB3431-033-P1-K1-E12 Seq. ID BLASTX Method NCBI GI g82080 436 BLAST score E value 4.0e-43124 Match length 68 % identity chlorophyll a/b-binding protein type III precursor - tomato NCBI Description >gi 226872 prf 1609235A chlorophyll a/b binding protein [Lycopersicon esculentum] 400308 Seq. No. LIB3431-033-P1-K1-E3 Seq. ID BLASTX Method NCBI GI g3345477 BLAST score 630 6.0e-66 E value 135 Match length 90 % identity (AB016283) carbonic anhydrase [Oryza sativa] NCBI Description 400309 Seq. No. Seq. ID LIB3431-033-P1-K1-E4 Method BLASTX NCBI GI q417260 BLAST score 410 5.0e-40E value Match length 128 65 % identity LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632 NCBI Description lir1 protein - rice >gi 20263_emb_CAA48706 (X68807) light-regulated gene [Oryza sativa] 400310 Seq. No. Seq. ID LIB3431-033-P1-K1-E5 Method BLASTX NCBI GI g115787 376 BLAST score 4.0e-36 E value Match length 73

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 400311

% identity

```
LIB3431-033-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  491
E value
                  1.0e-49
Match length
                  121
                  83
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  400312
Seq. No.
                  LIB3431-033-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  634
                  2.0e-66
E value
                  124
Match length
% identity
                  97
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  400313
Seq. No.
                  LIB3431-033-P1-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q132105
                  426
BLAST score
                  6.0e-42
E value
Match length
                  77
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400314
Seq. No.
                  LIB3431-033-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  q2072555
NCBI GI
                   237
BLAST score
                   9.0e-20
E value
Match length
                   44
                   100
% identity
```

(AF001396) metallothionein-like protein [Oryza sativa] NCBI Description >gi 6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

400315 Seq. No.

LIB3431-033-P1-K1-F1 Seq. ID

BLASTX Method NCBI GI g3249064

```
BLAST score
                  7.0e-48
E value
                  145
Match length
% identity
                  61
NCBI Description
                  (AC004473) Strong similarity to trehalose-6-phosphate
                  synthase homolog gb 2245136 from A. thaliana chromosome 4
                  contig gb Z97344. [Arabidopsis thaliana]
                  400316
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  638
E value
                  8.0e-67
Match length
                  124
                  94
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  400317
Seq. No.
                  LIB3431-033-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2921158
BLAST score
                  383
                  4.0e-37
E value
Match length
                  102
                  75
%'identity
NCBI Description (AF022909) ClpC [Arabidopsis thaliana]
                  400318
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g6056372
BLAST score
                  224
E value
                  2.0e-18
Match length
                  75
% identity
                  59
                  (AC009894) Very similar to receptor-like serine/threonine
NCBI Description
                  kinase [Arabidopsis thaliana]
Seq. No.
                  400319
                  LIB3431-033-P1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3273244
BLAST score
                  56
                  2.0e-22
E value
                  132
Match length
% identity
                  86
NCBI Description Oryza sativa DNA for NLS receptor, complete cds
                  400320
Seq. No.
                  LIB3431-033-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  277
E value
                  2.0e-24
Match length
                  70
```

Seq. No.

% identity NCBI Description (Z72488) CP12 [Nicotiana tabacum] 400321 Seq. No. LIB3431-033-P1-K1-F8 Seq. ID BLASTX Method NCBI GI g320618 380 BLAST score 4.0e-44 E value 108 Match length 86 % identity chlorophyll a/b-binding protein I precursor - rice NCBI Description >gi 218172 dbj BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi 227611 prf 1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 400322 Seq. No. LIB3431-033-P1-K1-F9 Seq. ID Method BLASTX g132105 NCBI GI 595 BLAST score 9.0e-62 E value 129 Match length 87 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 400323 Seq. No. LIB3431-033-P1-K1-G1 Seq. ID Method BLASTX g2662310 NCBI GI 173 BLAST score 3.0e-12 E value Match length 34 % identity 100 NCBI Description (AB009307) bpwl [Hordeum vulgare] 400324 Seq. No. LIB3431-033-P1-K1-G10 Seq. ID BLASTX Method NCBI GI g5824418 BLAST score 284 2.0e-25 E value 111 Match length % identity 49 (Z36948) similar to polypyrimidine tract binding protein NCBI Description [Caenorhabditis elegans] 400325

```
LIB3431-033-P1-K1-G11
Seq. ID
                  BLASTX
Method
                  g3075488
NCBI GI
                  592
BLAST score
E value
                  2.0e-61
Match length
                  115
% identity
                  96
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  400326
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-G12
                  BLASTX
Method
                  q4678927
NCBI GI
BLAST score
                  188
                  5.0e-14
E value
Match length
                  140
% identity
                  37
                  (AL049711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  400327
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-G2
                  BLASTX
Method
NCBI GI
                  q4079798
                   359
BLAST score
                   4.0e-34
E value
                  112
Match length
                   67
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   400328
Seq. No.
Seq. ID
                   LIB3431-033-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q2306981
BLAST score
                   482
                   2.0e-48
E value
Match length
                   86
% identity
                   98
                  (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
                   400329
Seq. No.
                   LIB3431-033-P1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4836892
BLAST score
                   427
E value
                   3.0e-46
Match length
                   136
% identity
                   72
                  (AC007369) Putative RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   400330
                   LIB3431-033-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1710551
BLAST score
                   277
                   2.0e-24
E value
Match length
                   51
```

% identity

57

```
% identity
                  60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728.1
NCBI Description
                  (X95458) ribosomal protein L39 [Zea mays]
Seq. No.
                  400331
Seq. ID
                  LIB3431-033-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  448
E value
                  1.0e-44
Match length
                  107
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  400332
Seq. ID
                  LIB3431-033-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3184098
BLAST score
                  393
E value
                  4.0e-38
Match length
                  143
% identity
                  51
NCBI Description
                  (AL023777) coenzyme a synthetase [Schizosaccharomyces
                  pombe]
Seq. No.
                  400333
Seq. ID
                  LIB3431-033-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q584741
BLAST score
                  377
E value
                  3.0e-36
Match length
                  107
% identity
                  69
NCBI Description
                  ANKYRIN REPEAT PROTEIN (AKRP) >gi 322461 pir JQ1729
                  ankyrin-repeat protein - Arabidopsis thaliana >qi 166744
                  (M82883) ankyrin repeat-containing protein [Arabidopsis
                  thaliana]
                  400334
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  286
E value
                  2.0e-25
Match length
                  76
% identity
                  74
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
                  400335
Seq. No.
                  LIB3431-033-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170745
BLAST score
                  384
                  4.0e-37
E value
Match length
                  116
```



NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326 (M88321) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167328 (M88322) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 400336

Seq. ID LIB3431-033-P1-K1-H2

Method BLASTX
NCBI GI g2570511
BLAST score 580
E value 4.0e-60
Match length 111
% identity 98

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 400337

Seq. ID LIB3431-033-P1-K1-H4

Method BLASTN
NCBI GI g2072554
BLAST score 173
E value 1.0e-92
Match length 249
% identity 92

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 400338

Seq. ID LIB3431-033-P1-K1-H7

Method BLASTX
NCBI GI g132105
BLAST score 582
E value 3.0e-60
Match length 125
% identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375 prf_1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400339

Seq. ID LIB3431-033-P1-K1-H9

Method BLASTX
NCBI GI g170131
BLAST score 383
E value 6.0e-37
Match length 98
% identity 71

NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No. 400340

Seq. ID LIB3431-033-P1-N1-A1

Method BLASTX

```
q3789948
NCBI GI
BLAST score
                  167
E value
                  1.0e-11
Match length
                  34
% identity
                  97
                  (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
                  400341
Seq. No.
                  LIB3431-033-P1-N1-A11 -
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115784
BLAST score
                  145
E value
                  4.0e-09
Match length
                  26
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB)
                   (LHCP) >gi 167525 (M16058) chlorophyll a/b-binding protein
                  [Cucumis sativus]
Seq. No.
                  400342
Seq. ID
                  LIB3431-033-P1-N1-A12
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  294
                  1.0e-26
E value
                  57
Match length
% identity
                  96
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi 478404 pir JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  400343
                  LIB3431-033-P1-N1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2306980
BLAST score
                  229
E value
                  1.0e-126
Match length
                  254
% identity
                   98
NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,
                  complete cds
                   400344
Seq. No.
                  LIB3431-033-P1-N1-A4
Seq. ID
Method
                  BLASTX
                  g2286153
NCBI GI
BLAST score
                  249
                  2.0e-21
E value
Match length
                  50
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                   400345
Seq. No.
                  LIB3431-033-P1-N1-A5
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2570514
```

```
BLAST score
                  2.0e-73
E value
                  227
Match length
                  91
% identity
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
Seq. No.
                  400346
                  LIB3431-033-P1-N1-A6
Seq. ID
                  BLASTN
Method
                  g728629
NCBI GI
                  269
BLAST score
                  1.0e-149
E value
                  288
Match length
                  99
% identity
NCBI Description O.sativa mRNA for PCR clone D
                  400347
Seq. No.
                  LIB3431-033-P1-N1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g710308
                  209
BLAST score
                  1.0e-16
E value
                  43
Match length
                  88
% identity
NCBI Description (U11693) victorin binding protein [Avena sativa]
                   400348
Seq. No.
                  LIB3431-033-P1-N1-A8
Seq. ID
                  BLASTX
Method
                  g5733866
NCBI GI
BLAST score
                  142
E value
                   5.0e-09
                   34
Match length
% identity
                   (AC007932) Contains similarity to gb_M73488
NCBI Description
                   1-aminocyclopropane-1-carboxylate deaminase from
                   Pseudomonas sp. ESTs gb Z18033 and gb Z34214 come from
                   this gene. [Arabidopsis thaliana]
                   400349
Seq. No.
                   LIB3431-033-P1-N1-A9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q218207
BLAST score
                   250
                   1.0e-138
E value
                   250
Match length
                   100
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS1139
                   400350
Seq. No.
Seq. ID
                   LIB3431-033-P1-N1-B1
Method
                   BLASTN
```

q20177

1.0e-167

299

NCBI GI

E value

BLAST score

```
321
Match length
                  99
% identity
                  Rice cab1R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  400351
Seq. ID
                  LIB3431-033-P1-N1-B5
Method
                  BLASTX
NCBI GI
                  q1421730
BLAST score
                  201
E value
                  1.0e-15
Match length
                  40
                  95
% identity
NCBI Description
                  (U43082) RF2 [Zea mays]
                  400352
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-C11
Method
                  BLASTX
                  q3281853
NCBI GI
                  200
BLAST score
                  1.0e-15
E value
Match length
                  70
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                  400353
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-C2
Method
                  BLASTN
NCBI GI
                  q6006355
BLAST score
                  221
E value
                  1.0e-121
Match length
                  331
% identity
                  100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  400354
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-C4
Method
                  BLASTX
                  g551047
NCBI GI
BLAST score
                  209
E value
                  1.0e-16
Match length
                  42
% identity
                  93
                  (X79277) type II LHCI [Lolium temulentum]
NCBI Description
                  400355
Seq. No.
                  LIB3431-033-P1-N1-C5
Seq. ID
Method
                  BLASTN
                  g218171
NCBI GI
BLAST score
                  72
                  2.0e-32
E value
Match length
                  112
% identity
                  91
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
```

```
400356
Seq. No.
                  LIB3431-033-P1-N1-C6
Seq. ID
                  BLASTN
Method
                  g5091597
NCBI GI
BLAST score
                  33
E value
                  4.0e-09
                  45
Match length
                   93
% identity
                  Oryza sativa chromosome 1 BAC 10A19I, complete sequence
NCBI Description
                   400357
Seq. No.
                  LIB3431-033-P1-N1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g482311
BLAST score
                   171
                   3.0e-12
E value
                   33
Match length
                   100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi 739292 prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   400358
Seq. No.
Seq. ID
                   LIB3431-033-P1-N1-C8
                   BLASTX
Method
                   g482311
NCBI GI
                   315
BLAST score
                   5.0e-29
E value
                   63
Match length
                   100
% identity
                   photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   400359
Seq. No.
Seq. ID
                   LIB3431-033-P1-N1-D1
                   BLASTN
Method
NCBI GI
                   g3789953
                   317
BLAST score
                   1.0e-178
E value
                   317
Match length
% identity
                   100
                   Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   400360
Seq. No.
                   LIB3431-033-P1-N1-D11
Seq. ID
Method
                   BLASTN
                   g3885887
NCBI GI
                   297
BLAST score
                   1.0e-166
E value
Match length
                   301
% identity
                   100
                   Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
```

```
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-D12
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                  134
E value
                  3.0e-69
Match length
                  285
                  99
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS2106
                  400362
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-D2
                  BLASTN
Method
                  g20262
NCBI GI
BLAST score
                  162
E value
                  5.0e-86
                  210
Match length
                  94
% identity
NCBI Description O.sativa light-induced mRNA
                   400363
Seq. No.
                  LIB3431-033-P1-N1-D4
Seq. ID
                  BLASTX
Method
                  g5729802
NCBI GI
                  154
BLAST score
                   3.0e-10
E value
Match length
                   32
                   84
% identity
                  similar to S. pombe dim1+ >gi_2565275 (AF023611) Dim1p
NCBI Description
                  homolog [Homo sapiens]
                   400364
Seq. No.
                   LIB3431-033-P1-N1-D5
Seq. ID
                   BLASTX
Method
                   q1169798
NCBI GI
BLAST score
                   233
                   2.0e-19
E value
                   46
Match length
                   100
% identity
                   GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE
                   ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218)
                   phosphoglucose isomerase (Pgi-b) [Oryza sativa]
                   400365
Seq. No.
Seq. ID
                   LIB3431-033-P1-N1-D6
Method
                   BLASTN
NCBI GI
                   g3345476
BLAST score
                   295
                   1.0e-165
E value
Match length
                   299
% identity
                   100
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
```

400366

Seq. No.

```
LIB3431-033-P1-N1-D7
Seq. ID
                  BLASTX
Method
                  g5923670
NCBI GI
                  177
BLAST score
                  7.0e-13
E value
                  70
Match length
% identity
NCBI Description (AC009326) unknown protein [Arabidopsis thaliana]
                  400367
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-E10
                  BLASTX
Method
                  g3885892
NCBI GI
                  258
BLAST score
                  2.0e-22
E value
                  51
Match length
                  100
% identity
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
                  400368
Seq. No.
                  LIB3431-033-P1-N1-E11
Seq. ID
                  BLASTX
Method
                  g132105
NCBI GI
BLAST score
                  186
                  6.0e-14
E value
                  35
Match length
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094 pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400369
Seq. No.
                  LIB3431-033-P1-N1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115813
BLAST score
                  176
                  1.0e-12
E value
Match length
                   41
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   400370
Seq. No.
                   LIB3431-033-P1-N1-E3
Seq. ID
                   BLASTX
Method
                   q606817
NCBI GI
BLAST score
                   182
E value
                   2.0e-13
                   34
Match length
% identity
                   97
```

```
(U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                  >gi 5917783_gb AAD56038.1_AF182806_1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
                  400371
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-E4
Method
                  BLASTN
                  g20262
NCBI GI
                  282
BLAST score
                  1.0e-157
E value
                  290
Match length
                  99
% identity
NCBI Description O.sativa light-induced mRNA
                  400372
Seq. No.
                  LIB3431-033-P1-N1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g421916
                  156
BLAST score
                  2.0e-10
E value
                  29
Match length
                   97
% identity
                  chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                  >gi 12582 emb CAA48410 (X68333) light harvesting
                   chlorophyll a /b binding protein [Hedera helix]
                   400373
Seq. No.
                   LIB3431-033-P1-N1-E6
Seq. ID
                   BLASTN
Method
                   g20181
NCBI GI
                   190
BLAST score
                   1.0e-102
E value
                   194
Match length
                   99
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   400374
Seq. No.
Seq. ID
                   LIB3431-033-P1-N1-E7
                   BLASTN
Method
                   q3126853
NCBI GI
BLAST score
                   128
                   1.0e-65
E value
Match length
                   189
                   97
% identity
                   Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                   mRNA, nuclear gene encoding chloroplast protein, complete
                   cds
                   400375
Seq. No.
                   LIB3431-033-P1-N1-E8
 Seq. ID
                   BLASTN
Method
NCBI GI
                   g218207
 BLAST score
                   205
 E value
                   1.0e-111
```

240

97

Match length

% identity

Oryza sativa mRNA for the small subunit of NCBI Description ribulose-1,5-bisphosphate carboxylase, complete cds, clone p0SSS1139 400376 Seq. No. Seq. ID LIB3431-033-P1-N1-E9 Method BLASTN g2072554 NCBI GI 157 BLAST score 4.0e-83 E value 185 Match length 96 % identity Oryza sativa metallothionein-like protein mRNA, complete NCBI Description 400377 Seq. No. LIB3431-033-P1-N1-F10 Seq. ID BLASTN Method g218209 NCBI GI 34 BLAST score 2.0e-09 E value 50 Match length 92 % identity Oryza sativa mRNA for the small subunit of NCBI Description ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106 400378 Seq. No. LIB3431-033-P1-N1-F8 Seq. ID BLASTN Method g20177 NCBI GI BLAST score 346 0.0e + 00E value Match length 365 99 % identity NCBI Description Rice cab1R gene for light harvesting chlorophyll a/b-binding protein 400379 Seq. No. LIB3431-033-P1-N1-F9 Seq. ID BLASTX Method NCBI GI q132105 BLAST score 293 E value 2.0e-26 57 Match length % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

Seq. No. 400380

51269

carboxylase S [Oryza sativa]

sativa] >gi_226375_prf__1508256A ribulose bisphosphate

Method

BLASTX

```
LIB3431-033-P1-N1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2662309
BLAST score
                  53
E value
                  8.0e-21
Match length
                  61
                  97
% identity
NCBI Description Hordeum vulgare mRNA for bpw1, complete cds
                  400381
Seq. No.
                  LIB3431-033-P1-N1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2326947
BLAST score
                  231
                   4.0e-19
E value
Match length
                  44
% identity
                  100
                   (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
                   400382
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-G2
                  BLASTN
Method
                   q4079797
NCBI GI
                   129
BLAST score
                   3.0e-66
E value
Match length
                   251
                   100
% identity
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                   complete cds
                   400383
Seq. No.
                   LIB3431-033-P1-N1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076724
BLAST score
                   268
E value
                   2.0e-23
Match length
                   52
% identity
                   96
                   LHCI-680, photosystem I antenna protein - barley
NCBI Description
                   >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
                   400384
Seq. No.
                   LIB3431-033-P1-N1-G4
Seq. ID
                   BLASTX
Method
                   g2673917
NCBI GI
                   154
BLAST score
                   4.0e-10
E value
                   43
Match length
% identity
                   (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   400385
Seq. No.
                   LIB3431-033-P1-N1-G6
Seq. ID
```

Method

BLASTX

```
g1710551
NCBI GI
BLAST score
                  248
                  4.0e-21
E value
Match length
                  46
% identity
                  98
                  60S RIBOSOMAL PROTEIN L39 >qi 1177369 emb CAA64728.1
NCBI Description
                  (X95458) ribosomal protein L39 [Zea mays]
                  400386
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-G7
Method
                  BLASTN
NCBI GI
                  g2073379
BLAST score
                  88
                  8.0e-42
E value
Match length
                  88
% identity
                  100
NCBI Description Rice CP26 mRNA, partial sequence
Seq. No.
                  400387
Seq. ID
                  LIB3431-033-P1-N1-G9
Method
                  BLASTX
NCBI GI
                  q586339
BLAST score
                  207
E value
                  3.0e-16
Match length
                  71
% identity
                  51
                  PEROXISOMAL-COENZYME A SYNTHETASE >gi 626794 pir $46098
NCBI Description
                  probable AMP-binding protein - yeast (Saccharomyces
                  cerevisiae) >qi 536615 emb CAA85185 (Z36091) ORF YBR222c
                   [Saccharomyces cerevisiae]
Seq. No.
                  400388
                  LIB3431-033-P1-N1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  152
                  6.0e-10
E value
Match length
                  30
                  90
% identity
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                  400389
                  LIB3431-033-P1-N1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170745
BLAST score
                  331
                  2.0e-33
E value
Match length
                  103
% identity
                  67
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi 167326
NCBI Description
                   (M88321) Group 4 late embryogenesis-abundant protein
                   [Gossypium hirsutum] >gi_167328 (M88322) Group 4 late
                  embryogenesis-abundant protein [Gossypium hirsutum]
                  400390
Seq. No.
                  LIB3431-033-P1-N1-H2
Seq. ID
```

```
NCBI GI
                  q4689380
BLAST score
                  258
                  3.0e-22
E value
                  52
Match length
% identity
NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein
                  [Vigna radiata]
                  400391
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-H4
Method
                  BLASTN
```

NCBI GI q2072554 BLAST score 290 E value 1.0e-162 Match length 294 100 % identity

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

400392

Seq. No. Seq. ID LIB3431-033-P1-N1-H7 Method BLASTX NCBI GI g132105 BLAST score 301 E value 2.0e-27 57 Match length 100 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >qi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400393

Seq. ID LIB3431-033-P1-N1-H9

Method BLASTX NCBI GI g170131 BLAST score 152 E value 6.0e-10 Match length 47 % identity

NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No. 400394

Seq. ID LIB3431-034-P1-K1-A11

Method BLASTX NCBI GI q4469021 BLAST score 268 E value 2.0e-23 Match length 78 % identity 69

NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. ID

Method

```
400395
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  310
                  2.0e-28
E value
Match length
                  71
% identity
                  83
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  400396
Seq. No.
                  LIB3431-034-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  g548605
NCBI GI
BLAST score
                  522
                  3.0e-53
E value
                  114
Match length
% identity
                  91
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                  400397
Seq. No.
                  LIB3431-034-P1-K1-A3
Seq. ID
Method
                  BLASTX
                  g3080375
NCBI GI
BLAST score
                   386
E value
                  3.0e-37
Match length
                  118
                  64
% identity
                  (AL022580) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  400398
                  LIB3431-034-P1-K1-A4
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
BLAST score
                   36
E value
                  1.0e-10
Match length
                  47
% identity
                   65
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   400399
                  LIB3431-034-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3420055
BLAST score
                   294
E value
                  2.0e-26
Match length
                   62
                  89
% identity
                  (AC004680) cyclophilin [Arabidopsis thaliana]
NCBI Description
                   400400
Seq. No.
```

51273

LIB3431-034-P1-K1-A7

BLASTN

```
q5091597
NCBI GI
BLAST score
                  141
E value
                  3.0e-73
Match length
                  225
% identity
                  26
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
                  400401
Seq. No.
                  LIB3431-034-P1-K1-A8
Seq. ID
                  BLASTX
```

Method BLASTX
NCBI GI g3123270
BLAST score 643
E value 2.0e-67
Match length 130
% identity 95

NCBI Description 40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)

>gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4

[Oryza sativa]

 Seq. No.
 400402

 Seq. ID
 LIB3431-034-P1-K1-A9

 Method
 BLASTX

 NCBI GI
 g1532168

 BLAST score
 179

 E value
 4.0e-13

Match length 53 % identity 60

NCBI Description (U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 400403

Seq. ID LIB3431-034-P1-K1-B1

Method BLASTN
NCBI GI g6015437
BLAST score 39
E value 2.0e-12
Match length 39
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 400404

Seq. ID LIB3431-034-P1-K1-B10

Method BLASTX
NCBI GI g320618
BLAST score 521
E value 4.0e-53
Match length 115
% identity 86

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

```
Seq. No.
                  400405
Seq. ID
                  LIB3431-034-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g2598589
BLAST score
                  250
E value
                  2.0e-21
                  94
Match length
                  51
% identity
                  (Y15367) MtN19 [Medicago truncatula]
NCBI Description
                  400406
Seq. No.
                  LIB3431-034-P1-K1-B2
Seq. ID
Method
                  BLASTX
                  g4079798
NCBI GI
BLAST score
                  342
E value
                  3.0e-32
Match length
                  104
% identity
                  66
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  400407
Seq. No.
                  LIB3431-034-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129231
BLAST score
                  740
                  9.0e-79
E value
Match length
                  142
                  98
% identity
NCBI Description
                  ORYZAIN ALPHA CHAIN PRECURSOR >gi 67644 pir KHRZOA oryzain
                   (EC 3.4.22.-) alpha precursor - rice
                  >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor
                   [Oryza sativa]
Seq. No.
                  400408
Seq. ID
                  LIB3431-034-P1-K1-B5
Method
                  BLASTN
                  g1815627
NCBI GI
BLAST score
                  166
E value
                  3.0e-88
Match length
                  166
                  100
% identity
                  Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  400409
                  LIB3431-034-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g480450
NCBI GI
BLAST score
                  352
E value
                  3.0e-33
Match length
                  76
% identity
                  89
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
```

reductoisomerase [Arabidopsis thaliana]

thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid

```
Seq. No.
                  400410
Seq. ID
                  LIB3431-034-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q4587571
BLAST score
                  148
                  2.0e-15
E value
Match length
                  82
% identity
                  56
                  (AC006550) Belongs to the PF 01027 Uncharacterized protein
NCBI Description
                  family UPF0005 with 7 transmembrane domains. [Arabidopsis
                  thaliana]
                  400411
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-B9
Method
                  BLASTX
                  g2492514
NCBI GI
                  672
BLAST score
                  7.0e-71
E value
                  141
Match length
                  94
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >gi 1483215 emb CAA68141_ (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
Seq. No.
                  400412
                  LIB3431-034-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  q5091509
NCBI GI
                  509
BLAST score
                  7.0e-52
E value
                  115
Match length
                  88
% identity
                  (AB023482) EST AU065533(C2174) corresponds to a region of
NCBI Description
                  the predicted gene.; Similar to Homo sapiens splicing
                   factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]
                  400413
Seq. No.
                  LIB3431-034-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  a464705
                   594
BLAST score
E value
                  1.0e-61
Match length
                  122
                   97
% identity
                  40S RIBOSOMAL PROTEIN S13 >gi 419802 pir S30146 ribosomal
NCBI Description
                  protein S13.e - maize >gi 288059 emb CAA44311 (X62455)
                   cytoplasmatic ribosomal protein S13 [Zea mays]
Seq. No.
                   400414
Seq. ID
                   LIB3431-034-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   q218218
BLAST score
                   67
                   4.0e-29
E value
Match length
                   95
% identity
                   93
NCBI Description Oryza sativa p-SINE1-r3 gene, repeat sequence
```

```
400415
Seq. No.
                  LIB3431-034-P1-K1-D11
Seq. ID
Method
                  BLASTX
                  q132096
NCBI GI
                  461
BLAST score
                  2.0e-50
E value
                  125
Match length
% identity
                  84
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_
                   (D00644) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa]
Seq. No.
                  400416
Seq. ID
                  LIB3431-034-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
E value
                  8.0e-20
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  400417
                  LIB3431-034-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q439879
BLAST score
                  285
                  2.0e-25
E value
                  121
Match length
% identity
                  51
                  (L15194) [Golden delicious apple fruit expressed mRNA,
NCBI Description
                   complete cds.], gene product [Malus domestica]
                   400418
Seq. No.
                  LIB3431-034-P1-K1-D3
Seq. ID
                  BLASTX
Method
                  q4539335
NCBI GI
BLAST score
                  546
                  5.0e-56
E value
Match length
                  142
                  70
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   400419
Seq. No.
                  LIB3431-034-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g671740
                   647
BLAST score
                   7.0e-68
E value
Match length
                   119
% identity
                   100
```

(X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description construct] 400420 Seq. No. LIB3431-034-P1-K1-D6 Seq. ID Method BLASTX NCBI GI g461899 BLAST score 506 2.0e-51 E value 134 Match length 69 % identity PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR NCBI Description (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi 405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi 1322278 (U42724) cyclophilin [Arabidopsis thaliana] 400421 Seq. No. LIB3431-034-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g115787 BLAST score 535 9.0e-55 E value Match length 122 % identity 88 CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi 20182 emb CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 400422 Seq. No. LIB3431-034-P1-K1-D9 Seq. ID Method BLASTX g132105 NCBI GI BLAST score 481 E value 2.0e-48 109 Match length % identity 85 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 400423

 Seq. No.
 400423

 Seq. ID
 LIB3431-034-P1-K1-E10

 Method
 BLASTX

 NCBI GI
 g320618

 BLAST score
 551

 E value
 1.0e-56

 Match length
 120

Match length

141

```
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  400424
Seq. No.
                  LIB3431-034-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g3036951
NCBI GI
BLAST score
                  333
                  4.0e-31
E value
                  64
Match length
% identity
                  100
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                  400425
Seq. No.
                  LIB3431-034-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  q505136
NCBI GI
BLAST score
                  564
                   4.0e-58
E value
                  108
Match length
% identity
                  98
                  (D30794) ferredoxin [Oryza sativa]
NCBI Description
Seq. No.
                   400426
                  LIB3431-034-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4887618
BLAST score
                   749
                   8.0e-80
E value
                   141
Match length
                   99
% identity
NCBI Description (AB007628) homeobox gene [Oryza sativa]
                   400427
Seq. No.
                  LIB3431-034-P1-K1-E5
Seq. ID
                   BLASTX
Method
                   g2492782
NCBI GI
                   594
BLAST score
                   1.0e-61
E value
                   138
Match length
                   76
% identity
                  ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)
NCBI Description
                   (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992)
                   alpha-galactosidase [Coffea arabica]
                   400428
Seq. No.
Seq. ID
                   LIB3431-034-P1-K1-E6
                   BLASTX
Method
NCBI GI
                   g3250675
BLAST score
                   367
E value
                   5.0e-35
```

```
% identity
NCBI Description
                  (AL024486) putative protein [Arabidopsis thaliana]
                  400429
Seq. No.
                  LIB3431-034-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2104959
BLAST score
                  188
                  4.0e-14
E value
Match length
                  42
                  81
% identity
NCBI Description
                  (U96925) immunophilin [Vicia faba]
Seq. No.
                  400430
                  LIB3431-034-P1-K1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q218171
BLAST score
                  159
                  4.0e-84
E value
Match length
                  279
% identity
                  89
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
                  400431
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-F1
Method
                  BLASTX
                  q320618
NCBI GI
BLAST score
                  435
                  4.0e-43
E value
                  89
Match length
                  94
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  400432
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3913018
                  723
BLAST score
E value
                  8.0e-77
Match length
                  139
% identity
                  99
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  400433
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g283971
BLAST score
                  365
E value
                  8.0e-35
```

Seq. No.

Seq. ID

400438

LIB3431-034-P1-K1-F7

```
Match length
% identity
                  aldehyde dehydrogenase (NAD(P)+) (EC 1.2.1.5) 3 - human
NCBI Description
                  >gi_178375 (M77477) aldehyde dehydrogenase [Homo sapiens]
                  >gi 300402 bbs 132241 (S61044) aldehyde dehydrogenase
                  isozyme 3, ALDH3 {EC 1.2.1.3} [human, stomach, Peptide, 453
                  aa] [Homo sapiens]
Seq. No.
                  400434
Seq. ID
                  LIB3431-034-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q6013233
BLAST score
                  301
                  3.0e-27
E value
Match length
                  140
% identity
                  41
NCBI Description
                  (AF183932) ionotropic glutamate receptor homolog
                  [Arabidopsis thaliana]
Seq. No.
                  400435
Seq. ID
                  LIB3431-034-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  675
E value
                  4.0e-71
Match length
                  127
                  100
% identity
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  400436
Seq. ID
                  LIB3431-034-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g115794
BLAST score
                  218
E value
                  1.0e-17
Match length
                  78
% identity
                  60
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
                  III CAB-13) >gi_72748_pir_CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi_19277_emb_CAA42818_ (X60275) LHCII type III
                  [Lycopersicon esculentum]
Seq. No.
                  400437
Seq. ID
                  LIB3431-034-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g6006363
BLAST score
                  271
E value
                  7.0e-24
Match length
                  51
% identity
                  100
NCBI Description
                  (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
                  to a region of the predicted gene.; Similar to water stress
                  inducible protein (U74296) [Oryza sativa]
```

```
BLASTY
```

Method BLASTX
NCBI GI g82080
BLAST score 408
E value 7.0e-40
Match length 116
% identity 68
NCBI Description chloroph

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 400439

Seq. ID LIB3431-034-P1-K1-F8

Method BLASTX
NCBI GI g548605
BLAST score 550
E value 1.0e-56
Match length 124
% identity 88

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir_ A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 400440

Seq. ID LIB3431-034-P1-K1-F9

Method BLASTX
NCBI GI g733454
BLAST score 247
E value 5.0e-21
Match length 67
% identity 76

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 400441

Seq. ID LIB3431-034-P1-K1-G10

Method BLASTX
NCBI GI g2827533
BLAST score 158
E value 1.0e-10
Match length 70
% identity 50

NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 400442

Seq. ID LIB3431-034-P1-K1-G11

Method BLASTX
NCBI GI g2407281
BLAST score 641
E value 3.0e-67
Match length 121
% identity 98

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 400443

```
Seq. ID
                   LIB3431-034-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   a6015437
BLAST score
                   34
                   2.0e-10
E value
Match length
                   38
% identity
                   97
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   400444
Seq. ID
                  LIB3431-034-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  338
E value
                  1.0e-31
Match length
                  110
% identity
                  63
NCBI Description
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
Seq. No.
                  400445
Seq. ID
                  LIB3431-034-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3319357
BLAST score
                  374
E value
                  7.0e-36
Match length
                  118
% identity
                  67
NCBI Description
                  (AF077407) contains similarity to phosphoenolpyruvate
                  synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
Seq. No.
                  400446
Seq. ID
                  LIB3431-034-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  675
E value
                  4.0e-71
Match length
                  127
% identity
                  100
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  400447
Seq. ID
                  LIB3431-034-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  2.0e-10
Match length
                  35
% identity
                  100
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  400448
Seq. ID
                  LIB3431-034-P1-K1-H1
Method
                  BLASTX
NCBI GI
```

51283

g2288988

6.0e-12

170

BLAST score

E value

Match length 66 % identity 47

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 400449

Seq. ID LIB3431-034-P1-K1-H11

Method BLASTX
NCBI GI g548605
BLAST score 594
E value 1.0e-61
Match length 130
% identity 91

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 400450

Seq. ID LIB3431-034-P1-K1-H3

Method BLASTX
NCBI GI 9417482
BLAST score 397
E value 1.0e-38
Match length 140
% identity 58

NCBI Description PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS

PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir__JQ2254

farnesyl-diphosphate_farnesyltransferase_(FC_2_5_1_21) be

farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta chain - garden pea >gi_169049 (L08664) farnesyl-protein

transferase beta-subunīt [Pisum sativum]

Seq. No. 400451

Seq. ID LIB3431-034-P1-K1-H5

Method BLASTX
NCBI GI g6006429
BLAST score 298
E value 6.0e-27
Match length 118
% identity 49

NCBI Description (AJ242958) SPL1-Related3 protein [Arabidopsis thaliana]

Seq. No. 400452

Seq. ID LIB3431-034-P1-K1-H7

Method BLASTX
NCBI GI g132105
BLAST score 547
E value 4.0e-56
Match length 119
% identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone posssilas) - rice >gi_218208 dbj_BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

Seq. No.

Seq. ID

400458

LIB3431-034-P1-N1-A8

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400453 Seq. ID LIB3431-034-P1-K1-H9 Method BLASTN NCBI GI g2073379 BLAST score 88 E value 5.0e-42 Match length 92 % identity 99 NCBI Description Rice CP26 mRNA, partial sequence 400454 Seq. No. Seq. ID LIB3431-034-P1-N1-A11 Method BLASTX NCBI GI g4469021 BLAST score 292 E value 4.0e-26 Match length 76 % identity 74 NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana] Seq. No. 400455 Seq. ID LIB3431-034-P1-N1-A12 Method BLASTX NCBI GI g1835731 BLAST score 273 E value 4.0e-24 Match length 65 % identity 82 NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa] Seq. No. 400456 Seq. ID LIB3431-034-P1-N1-A2 Method BLASTN NCBI GI q304219 BLAST score 49 E value 1.0e-18 Match length 71 % identity 92 NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit mRNA, complete cds Seq. No. 400457 LIB3431-034-P1-N1-A6 Seq. ID Method BLASTX NCBI GI g3420055 BLAST score 260 E value 2.0e-22 Match length 55 % identity 89 NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]

Seq. ID

Method

NCBI GI

```
Method
                   BLASTX
NCBI GI
                   q3914899
BLAST score
                   199
E value
                   2.0e-15
Match length
                   41
% identity
                   93
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 2331301 (AF013487) ribosomal
                   protein S4 type I [Zea mays]
Seq. No.
                   400459
Seq. ID
                   LIB3431-034-P1-N1-B10
Method
                   BLASTX
NCBI GI
                   q3036951
BLAST score
                   356
E value
                   8.0e-34
Match length
                   68
% identity
                   100
NCBI Description
                  (AB012639) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                   400460
Seq. ID
                   LIB3431-034-P1-N1-B2
Method
                   BLASTN
NCBI GI
                   g4079797
BLAST score
                   92
E value
                  2.0e-44
Match length
                  163
% identity
                   98
NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
                  complete cds
Seq. No.
                  400461
Seq. ID
                  LIB3431-034-P1-N1-B3
Method
                  BLASTN
NCBI GI
                  q218180
BLAST score
                  294
E value
                  1.0e-164
Match length
                  390
% identity
                  93
NCBI Description Rice mRNA for oryzain alpha (EC 3.4.22)
Seq. No.
                  400462
Seq. ID
                  LIB3431-034-P1-N1-B5
Method
                  BLASTN
NCBI GI
                  g1815627
BLAST score
                  116
E value
                  3.0e-58
Match length
                  151
% identity
                  97
NCBI Description
                  Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA,
                  complete cds
Seq. No.
                  400463
```

g480450 BLAST score 542

BLASTX

LIB3431-034-P1-N1-B6

```
E value 2.0e-55
Match length 150
% identity 74
NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No. 400464
```

Seq. ID LIB3431-034-P1-N1-B9
Method BLASTX
NCBI GI g5734790
BLAST score 337
E value 1.0e-31
Match length 74
% identity 89

NCBI Description (AC007980) ATP-dependent metalloprotease [Arabidopsis

thaliana]

 Seq. No.
 400465

 Seq. ID
 LIB3431-034-P1-N1-C1

 Method
 BLASTN

 NCBI GI
 g3789951

 BLAST score
 96

E value 1.0e-46
Match length 211
% identity 86

NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 400466

Seq. ID LIB3431-034-P1-N1-C10

Method BLASTX
NCBI GI g671740
BLAST score 431
E value 1.0e-42
Match length 79
% identity 99

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 400467

Seq. ID LIB3431-034-P1-N1-C11

Method BLASTX
NCBI GI g5091509
BLAST score 262
E value 8.0e-23
Match length 47
% identity 100

NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of

the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]

Seq. No. 400468

Seq. ID LIB3431-034-P1-N1-C3

Method BLASTX NCBI GI g3123295

NCBI GI

E value

BLAST score

Match length

```
BLAST score
                   231
E value
                   4.0e-19
Match length
                   57
                   70
% identity
NCBI Description
                  CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi 2583169
                   (AF026473) calmodulin-related protein [Arabidopsis
                   thaliana]
Seq. No.
                   400469
                  LIB3431-034-P1-N1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1296955
BLAST score
                   300
E value
                  3.0e-27
Match length
                  54
% identity
                   46
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.
                  400470
Seq. ID
                  LIB3431-034-P1-N1-C7
Method
                  BLASTN
NCBI GI
                  g1661159
BLAST score
                  157
E value
                  5.0e-83
Match length
                  237
% identity
                  92
NCBI Description Oryza sativa chlorophyll a/b binding protein (kcdl895)
                  mRNA, complete cds
                  400471
Seq. No.
Seq. ID
                  LIB3431-034-P1-N1-C8
Method
                  BLASTN
NCBI GI
                  g2072726
BLAST score
                  461
E value
                  0.0e + 00
Match length
                  503
% identity
                  98
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
Seq. No.
                  400472
Seq. ID
                  LIB3431-034-P1-N1-C9
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  211
E value
                  9.0e-17
Match length
                  44
% identity
                  91
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  400473
Seq. ID
                  LIB3431-034-P1-N1-D10
Method
                  BLASTN
```

% identity 95

q218218

6.0e-40

85



NCBI Description Oryza sativa p-SINE1-r3 gene, repeat sequence

Seq. No. 400474 Seq. ID LIB3431-034-P1-N1-D11 Method BLASTX NCBI GI g132105 BLAST score 451 E value 6.0e-45 Match length 93 89 % identity NCBI Description

Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone posss1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400475

Seq. ID LIB3431-034-P1-N1-D12

Method BLASTN
NCBI GI g2072554
BLAST score 277
E value 1.0e-154
Match length 293
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 400476

Seq. ID LIB3431-034-P1-N1-D3

Method BLASTX
NCBI GI g3786007
BLAST score 160
E value 7.0e-11
Match length 43
% identity 53

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 400477

Seq. ID LIB3431-034-P1-N1-D4

Method BLASTN
NCBI GI g218209
BLAST score 74
E value 1.0e-33
Match length 143
% identity 97

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

p0SSS2106

Seq. No. 400478

Seq. ID LIB3431-034-P1-N1-D6

Method BLASTX NCBI GI g992633

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The state of the s
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BLAST score
                  217
E value
                  1.0e-17
Match length
                  59
% identity
                  66
NCBI Description
                  (U30874) cyclophilin B [Schistosoma mansoni]
                  >gi 1588493 prf 2208425A B-like cyclophilin [Schistosoma
                  mansoni]
Seq. No.
                  400479
Seq. ID
                  LIB3431-034-P1-N1-D7
Method
                  BLASTN
                  q20181
```

Method BLASTN
NCBI GI g20181
BLAST score 128
E value 1.0e-65
Match length 215
% identity 91

NCBI Description Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein

 Seq. No.
 400480

 Seq. ID
 LIB3431-034-P1-N1-D8

 Method
 BLASTN

 NCBI GI
 g3819197

 BLAST score
 47

 E value
 3.0e-17

E value 3.00 Match length 103 % identity 86

NCBI Description Hordeum vulgare partial mRNA; clone cMWG0676.uni

 Seq. No.
 400481

 Seq. ID
 LIB3431-034-P1-N1-D9

 Method
 BLASTX

 NCBI GI
 g132105

 BLAST score
 179

BLAST score 179 E value 4.0e-13 Match length 34 % identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208 dbj_BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400482

Seq. ID LIB3431-034-P1-N1-E10

Method BLASTN
NCBI GI g20177
BLAST score 35
E value 4.0e-10
Match length 67
% identity 88

NCBI Description Rice cablR gene for light harvesting chlorophyll

a/b-binding protein

```
Seq. No.
                  400483
Seq. ID
                  LIB3431-034-P1-N1-E11
Method
                  BLASTX
NCBI GI
                  g1181599
BLAST score
                  144
E value
                  5.0e-09
Match length
                  39
% identity
                  72
NCBI Description (D83007) subunit of photosystem I [Cucumis sativus]
                  400484
Seq. No.
Seq. ID
                  LIB3431-034-P1-N1-E12
Method
                  BLASTX
NCBI GI
                  g5902389
BLAST score
                  170
E value
                  5.0e-12
                  49
Match length
% identity
                  55
NCBI Description (AC008148) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  400485
                  LIB3431-034-P1-N1-E2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1209384
BLAST score
                  337
E value
                  0.0e + 00
Match length
                  341
% identity
                  100
NCBI Description Oryza sativa mRNA for root ferredoxin, partial cds
Seq. No.
                  400486
                  LIB3431-034-P1-N1-E4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4887617
BLAST score
                  434
E value
                  0.0e + 00
Match length
                  449
% identity
                  99
NCBI Description Oryza sativa HOS59 mRNA, partial cds
Seq. No.
                  400487
Seq. ID
                  LIB3431-034-P1-N1-E5
Method
                  BLASTX
NCBI GI
                  g2204226
BLAST score
                  255
E value
                  6.0e-22
Match length
                  55
% identity
                  82
NCBI Description (Y13848) alpha-galactosidase [Hordeum vulgare]
Seq. No.
                  400488
Seq. ID
                  LIB3431-034-P1-N1-F1
Method
                  BLASTX
                  g3036949
NCBI GI
BLAST score
                  234
E value
                  1.0e-19
```

Match length 49 % identity 92 NCBI Description (AB012638) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris] Seq. No. 400489 Seq. ID LIB3431-034-P1-N1-F11 Method BLASTX NCBI GI q2407279 BLAST score 176 E value 1.0e-12 Match length 37 % identity 97 NCBI Description (AF017362) aldolase [Oryza sativa] Seq. No. 400490 Seq. ID LIB3431-034-P1-N1-F12 Method BLASTX NCBI GI q4455169 BLAST score 233 E value 3.0e-19 Match length 77 % identity 53 NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana] Seq. No. 400491 Seq. ID LIB3431-034-P1-N1-F2 Method BLASTX NCBI GI q548605 BLAST score 317 E value 3.0e-29 Match length 71 % identity 87 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare] Seq. No. 400492 Seq. ID LIB3431-034-P1-N1-F3 Method BLASTX NCBI GI g3036951 BLAST score 347 E value 9.0e-33 Match length 68 % identity 99 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 400493

Seq. ID LIB3431-034-P1-N1-F5

Method BLASTN NCBI GI g2570510 BLAST score 255 E value 1.0e-141

Match length % identity 98 Oryza sativa chlorophyll a-b binding protein mRNA, complete NCBI Description Seq. No. 400494 Seq. ID LIB3431-034-P1-N1-F6 Method BLASTN NCBI GI q6006355 BLAST score 374 E value 0.0e + 00Match length 380 % identity 99 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11 Seq. No. 400495 Seq. ID LIB3431-034-P1-N1-F7 Method BLASTX NCBI GI g115813 BLAST score 215 E value 3.0e-17 Match length 48 % identity 85 CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III NCBI Description CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum] Seq. No. 400496 LIB3431-034-P1-N1-F8

Seq. ID Method BLASTN NCBI GI g304219 BLAST score 40 E value 3.0e-13

Match length 68 % identity

NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit

mRNA, complete cds

Seq. No. 400497

Seq. ID LIB3431-034-P1-N1-F9

Method BLASTX NCBI GI g733456 BLAST score 371 E value 2.0e-35 Match length 76 % identity 95

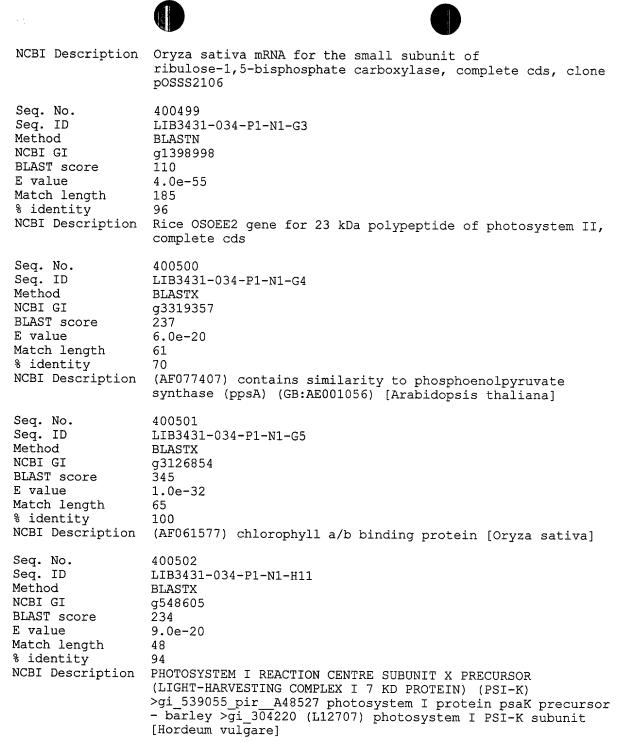
(U23189) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description

[Zea mays]

Seq. No. 400498

Seq. ID LIB3431-034-P1-N1-G11

Method BLASTN NCBI GI g218209 BLAST score 149 E value 4.0e-78 Match length 328 % identity 97



Seq. No. 400503

Seq. ID LIB3431-034-P1-N1-H3 Method BLASTX

NCBI GI g417482 BLAST score 371 E value 1.0e-35 Match length 91 % identity 75 NCBI Description PRO

PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS

PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir_JQ2254 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta chain - garden pea >gi_169049 (L08664) farnesyl-protein

transferase beta-subunit [Pisum sativum]

Seq. No. 400504

Seq. ID LIB3431-034-P1-N1-H4

Method BLASTN NCBI GI g3819197

BLAST score 47 E value 4.0e-17 Match length 103 % identity 86

NCBI Description Hordeum vulgare partial mRNA; clone cMWG0676.uni

Seq. No. 400505

Seq. ID LIB3431-034-P1-N1-H7

Method BLASTN
NCBI GI g218207
BLAST score 295
E value 1.0e-165
Match length 307
% identity 99

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS1139

Seq. No. 400506

Seq. ID LIB3431-035-P1-K1-A1

Method BLASTX
NCBI GI g548605
BLAST score 471
E value 3.0e-47
Match length 98
% identity 93

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 400507

Seq. ID LIB3431-035-P1-K1-A12

Method BLASTX
NCBI GI g1171579
BLAST score 239
E value 5.0e-20
Match length 91
% identity 48

NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 400508

Seq. ID LIB3431-035-P1-K1-A2

Method BLASTX

```
NCBI GI
                   q2582822
BLAST score
                   172
E value
                   3.0e-12
Match length
                   39
% identity
                   82
NCBI Description
                   (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
                   Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                   400509
Seq. ID
                  LIB3431-035-P1-K1-A3
Method
                  BLASTX
NCBI GI
                   a728744
BLAST score
                   271
E value
                   2.0e-46
Match length
                  132
% identity
NCBI Description
                  AUXIN-INDUCED PROTEIN PCNT115 >gi 100305 pir S16390
                  auxin-induced protein - common tobacco
                  >gi_19799_emb_CAA39708 (X56267) auxin-induced protein
                   [Nicotiana tabacum]
Seq. No.
                  400510
Seq. ID
                  LIB3431-035-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q5912299
BLAST score
                  464
                  8.0e-55
E value
Match length
                  123
% identity
NCBI Description
                  (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                  400511
Seq. ID
                  LIB3431-035-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q1076724
BLAST score
                  665
E value
                  6.0e-70
Match length
                  141
% identity
                  85
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  400512
Seq. ID
                  LIB3431-035-P1-K1-B3
                  BLASTX
                  g320618
                  578
```

Method NCBI GI BLAST score E value 1.0e-59 Match length 127 % identity 87

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

```
Seq. No.
                   400513
Seq. ID
                   LIB3431-035-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q3386621
BLAST score
                   513
E value
                   4.0e-52
Match length
                   119
% identity
                   83
NCBI Description
                  (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                   400514
Seq. ID
                   LIB3431-035-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   q3273202
BLAST score
                   394
E value
                   4.0e-38
Match length
                   115
% identity
                   74
NCBI Description
                  (AB010918) responce reactor4 [Arabidopsis thaliana]
Seq. No.
                   400515
Seq. ID
                   LIB3431-035-P1-K1-B7
Method
                   BLASTN
NCBI GI
                   q20181
BLAST score
                   92
E value
                   6.0e-44
Match length
                   243
% identity
                   86
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
Seq. No.
                   400516
Seq. ID
                  LIB3431-035-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g417488
BLAST score
                   608
E value
                   3.0e-63
Match length
                  152
% identity
                  75
NCBI Description
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
                  H) >gi_100452 pir A40995 starch phosphorylase (EC 2.4.1.1)
                  H - potato >gi_169473 (M69038) alpha-glucan phosphorylase
                  type H isozyme [Solanum tuberosum]
Seq. No.
                  400517
Seq. ID
                  LIB3431-035-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  600
E value
                  3.0e-62
Match length
                  135
% identity
                  88
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
```

[Oryza sativa]

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

```
Seq. No.
                  400518
Seq. ID
                  LIB3431-035-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  758
E value
                  7.0e-81
Match length
                  149
% identity
                  95
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  400519
Seq. ID
                  LIB3431-035-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q100454
BLAST score
                  664
E value
                  7.0e-70
Match length
                  146
% identity
                  86
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - potato
                  >gi 809113 emb CAA35601 (X17578) 33kDa precursor protein
                  of oxygen-evolving complex [Solanum tuberosum]
Seq. No.
                  400520
Seq. ID
                  LIB3431-035-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g544437
BLAST score
                  339
E value
                  1.0e-31
Match length
                  73
% identity
                  86
NCBI Description
                  GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
                  >gi_296358_emb CAA47018 (X66377) CIT-SAP [Citrus sinensis]
Seq. No.
                  400521
Seq. ID
                  LIB3431-035-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  g473980
BLAST score
                  76
E value
                  9.0e-35
Match length
                  113
% identity
                  90
NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
Seq. No.
                  400522
Seq. ID
                  LIB3431-035-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  415
E value
                  1.0e-40
Match length
                  141
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
```

[Lycopersicon esculentum]

```
Seq. No.
                  400523
Seq. ID
                  LIB3431-035-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q3345477
BLAST score
                  662
E value
                  1.0e-69
Match length
                  127
% identity
                  98
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  400524
Seq. ID
                  LIB3431-035-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q5042462
BLAST score
                  450
E value
                  9.0e-45
Match length
                  114
% identity
                  80
NCBI Description
                  (AC007789) putative negatively light-regulated protein
                  [Oryza sativa]
Seq. No.
                  400525
Seq. ID
                  LIB3431-035-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  676
E value
                  3.0e-71
Match length
                  144
% identity
                  89
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400526
Seq. ID
                  LIB3431-035-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  793
E value
                  6.0e-85
Match length
                  153
                  95
```

% identity 9 NCBI Description S

SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_(X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 400527

Seq. ID LIB3431-035-P1-K1-D10

Method BLASTX

E value

4.0e-52

```
NCBI GI
                   q82080
BLAST score
                   483
E value
                  1.0e-48
Match length
                  134
% identity
                   69
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                  400528
Seq. ID
                  LIB3431-035-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q170131
BLAST score
                  263
E value
                  8.0e-23
Match length
                  67
% identity
                  67
NCBI Description
                  (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
Seq. No.
                  400529
Seq. ID
                  LIB3431-035-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2773154
BLAST score
                  242
                  2.0e-20
E value
Match length
                  118
% identity
                  47
NCBI Description
                  (AF039573) abscisic acid- and stress-inducible protein
                  [Oryza sativa]
Seq. No.
                  400530
Seq. ID
                  LIB3431-035-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  744
E value
                  3.0e-79
Match length
                  141
% identity
                  99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  400531
Seq. No.
                  LIB3431-035-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6014904
BLAST score
                  372
E value
                  1.0e-35
Match length
                  70
% identity
                  97
NCBI Description
                  DAG PROTEIN, CHLOROPLAST PRECURSOR
                  >gi_1200205_emb_CAA65064_ (X95753) DAG [Antirrhinum majus]
Seq. No.
                  400532
                  LIB3431-035-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  512
```



Match length 108 % identity 94

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No.

400533

Seq. ID

LIB3431-035-P1-K1-D5

Method BLASTX
NCBI GI g543711
BLAST score 367
E value 5.0e-35
Match length 71
% identity 99

NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir_S30927 14-3-3

protein homolog - rice >gi 303859 dbj BAA03711 (D16140)

brain specific protein [Oryza sativa]

Seq. No.

400534

Seq. ID

LIB3431-035-P1-K1-D6

Method BLASTX
NCBI GI g1172874
BLAST score 204
E value 7.0e-16
Match length 135
% identity 38

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi_479589_pir__S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No.

400535

Seq. ID

LIB3431-035-P1-K1-D8

Method BLASTX
NCBI GI g132105
BLAST score 673
E value 7.0e-71
Match length 124
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400536

Seq. ID LIB3431-035-P1-K1-E1

Method BLASTX
NCBI GI g320618
BLAST score 544
E value 1.0e-55
Match length 128
% identity 84

NCBI Description

```
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  400537
Seq. No.
                  LIB3431-035-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  304
                  1.0e-27
E value
Match length
                  76
% identity
                  76
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                  400538
                  LIB3431-035-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2306980
BLAST score
                  98
                  7.0e-48
E value
Match length
                  122
% identity
                  95
                  Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                  complete cds
                  400539
Seq. No.
                  LIB3431-035-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2464852
BLAST score
                  205
                  5.0e-16
E value
                  100
Match length
% identity
                  46
NCBI Description
                  (Z99707) putative protein [Arabidopsis thaliana]
                  400540
Seq. No.
                  LIB3431-035-P1-K1-E3
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
BLAST score
                  38
E value
                  9.0e-12
Match length
                  38
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  400541
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-E4
Method
                  BLASTX
                  g115794
NCBI GI
BLAST score
                  374
E value
                  7.0e-36
                  77
Match length
% identity
                  91
```

51302

CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding



protein type III precursor (cab-13) - tomato
>gi_19277_emb_CAA42818_ (X60275) LHCII type III
[Lycopersicon esculentum]

Seq. No. 400542

Seq. ID LIB3431-035-P1-K1-E6

Method BLASTX
NCBI GI g320618
BLAST score 724
E value 8.0e-77
Match length 156
% identity 89

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi 218172 dbj BAA00536 (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 400543

Seq. ID LIB3431-035-P1-K1-E7

Method BLASTX
NCBI GI g3355476
BLAST score 246
E value 8.0e-21
Match length 72
% identity 60

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 400544

Seq. ID LIB3431-035-P1-K1-F1

Method BLASTX
NCBI GI g115787
BLAST score 423
E value 5.0e-42
Match length 116
% identity 83

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2D programmer wise Sei 20102 amb CAR22100

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 400545

Seq. ID LIB3431-035-P1-K1-F10

Method BLASTX
NCBI GI g4585882
BLAST score 522
E value 4.0e-53
Match length 143
% identity 72

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 400546

Seq. ID LIB3431-035-P1-K1-F4

Method BLASTX NCBI GI g5441881

Match length

127

```
BLAST score
                  175
                  2.0e-12
E value
                  115
Match length
% identity
                  39
                  (AP000367) Similar to putative receptor kinase. (AC002332)
NCBI Description
                  [Oryza sativa]
                  400547
Seq. No.
                  LIB3431-035-P1-K1-F6
Seq. ID
                  BLASTX
Method
                  g4049341
NCBI GI
                  285
BLAST score
                  2.0e-25
E value
Match length
                  87
% identity
                  66
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                  400548
Seq. No.
                  LIB3431-035-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  36
                  1.0e-10
E value
Match length
                  47
% identity
                  65
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  400549
                  LIB3431-035-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4079798
BLAST score
                  499
E value
                  1.0e-50
                  126
Match length
% identity
                  78
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
Seq. No.
                  400550
                  LIB3431-035-P1-K1-G1
Seq. ID
Method
                  BLASTX
                  g482311
NCBI GI
BLAST score
                  771
E value
                  2.0e-82
Match length
                  149
% identity
                  99
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  400551
                  LIB3431-035-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  565
E value
                  3.0e-58
```

```
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  400552
                  LIB3431-035-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score
                  507
E value
                  1.0e-51
Match length
                  95
                  99
% identity
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  400553
Seq. No.
                  LIB3431-035-P1-K1-G12
Seq. ID
Method
                  BLASTN
                  g2407282
NCBI GI
BLAST score
                  111
E value
                  2.0e-55
Match length
                  111
% identity
                  100
NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
Seq. No.
                  400554
                  LIB3431-035-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  300
                  4.0e-27
E value
Match length
                  69
% identity
                  88
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  400555
Seq. ID
                  LIB3431-035-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1352461
BLAST score
                  358
E value
                  4.0e-34
Match length
                  87
% identity
                  79
NCBI Description IN2-2 PROTEIN
Seq. No.
                  400556
Seq. ID
                  LIB3431-035-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1616659
BLAST score
                  512
```

51305

1.0e-56

146

E value Match length

```
% identity
NCBI Description
                  (U49387) adenylosuccinate synthetase [Triticum aestivum]
                  400557
Seq. No.
                  LIB3431-035-P1-K1-G5
Seq. ID
                  BLASTX
Method
                  g5031281
NCBI GI
BLAST score
                  314
                  9.0e-29
E value
                  98
Match length
                  62
% identity
                 (AF139499) unknown [Prunus armeniaca]
NCBI Description
                  400558
Seq. No.
                  LIB3431-035-P1-K1-G6
Seq. ID
                  BLASTN
Method
                  q1245938
NCBI GI
BLAST score
                  35
                  6.0e-10
E value
Match length
                  35
                  100
% identity
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
NCBI Description
                  heart atrium, mRNA, 2998 nt]
Seq. No.
                  400559
                  LIB3431-035-P1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3885888
BLAST score
                  347
                  1.0e-32
E value
Match length
                  70
                  97
% identity
NCBI Description (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                  400560
                  LIB3431-035-P1-K1-G9
Seq. ID
Method
                  BLASTX
                  g422029
NCBI GI
BLAST score
                  542
E value
                  2.0e-55
Match length
                  150
                  73
% identity
                  transcription factor OBF3.2, ocs element-binding - maize
NCBI Description
                  >gi 297018 emb CAA48904 (X69152) ocs-element binding
                  factor 3.2 [Zea mays]
                  400561
Seq. No.
                  LIB3431-035-P1-K1-H1
Seq. ID
Method
                  BLASTX
                  g2407281
NCBI GI
BLAST score
                  705
E value
                  1.0e-74
Match length
                  132
% identity
                  99
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
```

Seq. No. 400562 Seq. ID LIB3431-035-P1-K1-H10 Method BLASTX q132105 NCBI GI BLAST score 595 E value 9.0e-62 Match length 128 % identity 88 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 400563 Seq. No. LIB3431-035-P1-K1-H11 Seq. ID Method BLASTX NCBI GI g3914603 BLAST score 699 5.0e-74 E value Match length 134 % identity 99 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa] 400564 Seq. No. Seq. ID LIB3431-035-P1-K1-H12 Method BLASTX g6063542 NCBI GI BLAST score 351 E value 2.0e-33 Match length 109 % identity 72 NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa] Seq. No. 400565 Seq. ID LIB3431-035-P1-K1-H2 Method BLASTX g1172813 NCBI GI BLAST score 563 E value 5.0e-58

Match length 108 % identity 99

60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12) NCBI Description

>gi_1076752_pir__S49596 ribosomal protein L10.e, cytosolic - $rice > gi_575357$ emb_CAA57340 (X81692) putative tumor

supressor [Oryza sativa]

Seq. No. 400566

```
LIB3431-035-P1-K1-H4
Seq. ID
Method
                  BLASTX
                  g417260
NCBI GI
BLAST score
                  421
                  2.0e-41
E value
Match length
                  128
                  66
% identity
NCBI Description
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
                  400567
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-H5
Method
                  BLASTX
                  g4585882
NCBI GI
BLAST score
                  628
                  1.0e-65
E value
Match length
                  157
                  72
% identity
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  400568
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g4454459
BLAST score
                  433
                  1.0e-42
E value
Match length
                  112
% identity
                  76
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                  400569
Seq. No.
                  LIB3431-035-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402713
BLAST score
                  219
                  1.0e-17
E value
Match length
                  62
% identity
                  63
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  400570
                  LIB3431-035-P1-N1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  320
                  1.0e-29
E value
Match length
                  67
                  93
% identity
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
```

Seq. No. 400571

```
Seq. ID
                  LIB3431-035-P1-N1-A2
Method
                  BLASTX
                  g2582822
NCBI GI
BLAST score
                  169
                  6.0e-12
E value
                  39
Match length
                  79
% identity
                  (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                  Protein of 32kDa) [Solanum tuberosum]
                  400572
Seq. No.
                  LIB3431-035-P1-N1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  368
                  3.0e-35
E value
                  73
Match length
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  400573
                  LIB3431-035-P1-N1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417488
BLAST score
                  184
E value
                  9.0e-19
                  60
Match length
                  82
% identity
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                  H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1)
                  H - potato >gi 169473 (M69038) alpha-glucan phosphorylase
                  type H isozyme [Solanum tuberosum]
Seq. No.
                  400574
                  LIB3431-035-P1-N1-B9
Seq. ID
Method
                  BLASTX
                  g1085987
NCBI GI
BLAST score
                  179
                  4.0e-13
E value
Match length
                  34
                  94
% identity
NCBI Description
                  light harvesting chlorophyll a protein precursor - Norway
                  spruce >gi_607148_emb_CAA57407_ (X81808) light harvesting
                  chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]
Seq. No.
                  400575
Seq. ID
                  LIB3431-035-P1-N1-C11
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  406
                  1.0e-39
E value
Match length
                  79
% identity
                  96
```



```
(X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  400576
Seq. No.
                  LIB3431-035-P1-N1-C2
Seq. ID
                  BLASTX
Method
                  g482311
NCBI GI
                  171
BLAST score
                  4.0e-12
E value
                  33
Match length
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  400577
Seq. No.
                  LIB3431-035-P1-N1-C3
Seq. ID
                  BLASTX
Method
                  q1362150
NCBI GI
BLAST score
                  290
                  1.0e-33
E value
                  84
Match length
                  88
% identity
                  hypothetical protein (clone AFN3) - wild oat (fragment)
NCBI Description
                  >gi_726478 (U20000) putative ORF1 [Avena fatua]
                  400578
Seq. No.
                  LIB3431-035-P1-N1-C4
Seq. ID
Method
                  BLASTN
                  g2331130
NCBI GI
BLAST score
                  227
                  1.0e-125
E value
                  251
Match length
                  98
% identity
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
                  400579
Seq. No.
                  LIB3431-035-P1-N1-C7
Seq. ID
                  BLASTN
Method
                  g218209
NCBI GI
BLAST score
                  57
                  3.0e-23
E value
                  172
Match length
                  90
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
                   400580
Seq. No.
                  LIB3431-035-P1-N1-C8
Seq. ID
```

Method BLASTN
NCBI GI g5042437
BLAST score 325
E value 0.0e+00
Match length 389
% identity 100

```
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                  400581
                  LIB3431-035-P1-N1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g347451
BLAST score
                  237
                  7.0e-20
E value
Match length
                  47
                  98
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  400582
                  LIB3431-035-P1-N1-D1
Seq. ID
                  BLASTX
Method
                  q1173347
NCBI GI
                  190
BLAST score
                  2.0e-14
E value
                  41
Match length
                  95
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 100803 pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  400583
                  LIB3431-035-P1-N1-D10
Seq. ID
Method
                  BLASTX
                  g82080
NCBI GI
BLAST score
                  256
                  3.0e-25
E value
                  76
Match length
% identity
                  82
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   400584
Seq. No.
                  LIB3431-035-P1-N1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q170131
BLAST score
                   152
E value
                   6.0e-10
Match length
                   47
                   66
% identity
                   (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
NCBI Description
Seq. No.
                   400585
                   LIB3431-035-P1-N1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2773153
BLAST score
                   364
E value
                   0.0e + 00
Match length
                   388
```



% identity

Oryza sativa abscisic acid- and stress-inducible protein NCBI Description

(Asr1) mRNA, complete cds

400586 Seq. No.

LIB3431-035-P1-N1-D2 Seq. ID

BLASTN Method g3126853 NCBI GI 160 BLAST score 1.0e-84 E value 210 Match length 99 % identity

Oryza sativa chlorophyll a/b binding protein (RCABP89) NCBI Description

mRNA, nuclear gene encoding chloroplast protein, complete

cds

400587 Seq. No.

LIB3431-035-P1-N1-D4 Seq. ID

BLASTX Method g3789952 NCBI GI 168 BLAST score 1.0e-11 E value Match length 30 100 % identity

(AF094775) chlorophyll a/b-binding protein presursor [Oryza NCBI Description

sativa]

400588 Seq. No.

LIB3431-035-P1-N1-D5 Seq. ID

BLASTX Method g543711 NCBI GI 367 BLAST score 6.0e-35 E value 71 Match length 99 % identity

NCBI Description

14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)

brain specific protein [Oryza sativa]

400589 Seq. No.

LIB3431-035-P1-N1-D8 Seq. ID

Method BLASTN q218209 NCBI GI 34 BLAST score E value 2.0e-09 Match length 50 92 % identity

Oryza sativa mRNA for the small subunit of NCBI Description

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS2106

400590 Seq. No.

LIB3431-035-P1-N1-D9 Seq. ID

Method BLASTX NCBI GI g259138 BLAST score 242 2.0e-20 E value

Match length 45 % identity 100

NCBI Description oryzacystatin=cysteine protease inhibitor [Oryza=rice,

Peptide Recombinant, 90 aa]

Seq. No. 400591

Seq. ID LIB3431-035-P1-N1-E1

Method BLASTX
NCBI GI g115787
BLAST score 410
E value 4.0e-40
Match length 77
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 400592

Seq. ID LIB3431-035-P1-N1-E10

Method BLASTX
NCBI GI g1617197
BLAST score 286
E value 2.0e-25
Match length 71
% identity 73

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 400593

Seq. ID LIB3431-035-P1-N1-E11

Method BLASTX
NCBI GI g1076724
BLAST score 263
E value 6.0e-23
Match length 51
% identity 96

NCBI Description LHCI-680, photosystem I antenna protein - barley

>gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I

antenna protein [Hordeum vulgare]

Seq. No. 400594

Seq. ID LIB3431-035-P1-N1-E2

Method BLASTX
NCBI GI g2464852
BLAST score 171
E value 5.0e-12
Match length 80
% identity 49

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 400595

Seq. ID LIB3431-035-P1-N1-E4

Method BLASTX NCBI GI g115794 BLAST score 467 E value 1.0e-46



Match length % identity 91 NCBI Description

CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDT033 chlorophyll a/b-binding
protein type III precursor (cab-13) - tomato

>gi_19277_emb_CAA42818_ (X60275) LHCII type III

[Lycopersicon esculentum]

Seq. No.

400596

LIB3431-035-P1-N1-E6 Seq. ID

Method BLASTX NCBI GI g115768 BLAST score 223 E value 4.0e-18 Match length 43 98 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB) (LHCP) >gi_72743_pir_CDKV chlorophyll a/b-binding

protein precursor - cucumber (fragment) >gi 167523 (M16057)

chlorophyll a/b-binding protein [Cucumis sativus]

Seq. No.

400597

LIB3431-035-P1-N1-E9 Seq. ID

Method BLASTX NCBI GI g2582822 BLAST score 362 2.0e-34 E value 79 Match length 85 % identity

(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress NCBI Description

Protein of 32kDa) [Solanum tuberosum]

Seq. No.

LIB3431-035-P1-N1-F1 Seq. ID

400598

Method BLASTX g671737 NCBI GI BLAST score 199 E value 2.0e-15 Match length 37 100 % identity

NCBI Description (X74731) Chloropyll a/b binding protein [Amaranthus

hypochondriacus]

Seq. No. 400599

Seq. ID LIB3431-035-P1-N1-F10

Method BLASTX NCBI GI q115813 BLAST score 230 E value 6.0e-19 Match length 55 % identity 82

CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III NCBI Description

CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 400600

Seq. ID LIB3431-035-P1-N1-F7

NCBI GI

g733454



```
BLASTX
Method
NCBI GI
                  g2262116
                  152
BLAST score
                   6.0e-10
E value
                  92
Match length
                  39
% identity
                  (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
                  400601
Seq. No.
                  LIB3431-035-P1-N1-F9
Seq. ID
                  BLASTX
Method
                   g4079798
NCBI GI
                   322
BLAST score
                   5.0e-34
E value
Match length
                   81
                   96
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   400602
Seq. No.
                   LIB3431-035-P1-N1-G1
Seq. ID
                   BLASTX
Method
                   g482311
NCBI GI
                   303
BLAST score
                   2.0e-27
E value
Match length
                   64
                   95
% identity
                   photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   400603
Seq. No.
                   LIB3431-035-P1-N1-G10
Seq. ID
                   BLASTX
Method
                   g289920
NCBI GI
                   154
BLAST score
                   4.0e-10
E value
                   29
Match length
                   97
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   400604
Seq. No.
                   LIB3431-035-P1-N1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3789954
                   410
BLAST score
                   5.0e-40
E value
                   78
Match length
                   97
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   400605
Seq. No.
                   LIB3431-035-P1-N1-G2
Seq. ID
Method
                   BLASTX
```

E value

2.0e-36

```
289
BLAST score
                  6.0e-26
E value
Match length
                  62
                  92
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  400606
Seq. No.
                  LIB3431-035-P1-N1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462750
BLAST score
                  184
                  1.0e-13
E value
Match length
                  53
% identity
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  400607
Seq. No.
Seq. ID
                  LIB3431-035-P1-N1-G4
Method
                  BLASTX
NCBI GI
                   q1616659
BLAST score
                   343
E value
                   4.0e-32
                   75
Match length
% identity
                  (U49387) adenylosuccinate synthetase [Triticum aestivum]
NCBI Description
                   400608
Seq. No.
                   LIB3431-035-P1-N1-G8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3885887
BLAST score
                   304
                   1.0e-170
E value
Match length
                   315
% identity
                   99
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
                   400609
Seq. No.
                   LIB3431-035-P1-N1-H1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g218209
                   152
BLAST score
                   7.0e-80
E value
                   343
Match length
                   97
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
                   400610
Seq. No.
                   LIB3431-035-P1-N1-H10
Seq. ID
                   BLASTX
Method
                   g347451
NCBI GI
                   380
BLAST score
```

```
Match length
                  100
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
                  400611
Seq. No.
                  LIB3431-035-P1-N1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3377792
BLAST score
                  263
                  1.0e-146
E value
                   334
Match length
                  95
% identity
                  Oryza sativa ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
                   400612
Seq. No.
```

LIB3431-035-P1-N1-H12 Seq. ID

Method BLASTN NCBI GI g6063530 BLAST score 364 0.0e + 00E value 389 Match length 98 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01

400613 Seq. No. LIB3431-035-P1-N1-H2 Seq. ID Method BLASTX g1172813 NCBI GI BLAST score 450 1.0e-44 E value Match length 88

98 % identity 60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12) NCBI Description

>gi_1076752_pir__S49596 ribosomal protein L10.e, cytosolic - rice >gi 575357 emb CAA57340 (X81692) putative tumor

supressor [Oryza sativa]

400614 Seq. No.

LIB3431-035-P1-N1-H4 Seq. ID

Method BLASTX g417260 NCBI GI 300 BLAST score E value 3.0e-27 Match length 81 70 % identity

LIGHT REGULATED PROTEIN PRECURSOR >gi 422003_pir__\$33632 NCBI Description

lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)

light-regulated gene [Oryza sativa]

400615 Seq. No.

Seq. ID LIB3431-035-P1-N1-H5

Method BLASTX NCBI GI g115813 BLAST score 171 E value 4.0e-12

Match length 42 79 % identity CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III NCBI Description CAB-8) >gi 19182 emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum] 400616 Seq. No. LIB3431-036-P1-K1-A1 Seq. ID Method BLASTX NCBI GI g2997684 BLAST score 245 1.0e-20 E value Match length 85 56 % identity NCBI Description (AF053302) putative transcriptional co-activator [Arabidopsis thaliana] 400617 Seq. No. LIB3431-036-P1-K1-A11 Seq. ID Method BLASTX NCBI GI g2072555 BLAST score 237 9.0e-20 E value Match length 44 100 % identity NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like protein [Oryza sativa] Seq. No. 400618 LIB3431-036-P1-K1-A12 Seq. ID Method BLASTX NCBI GI q871931 399 BLAST score E value 7.0e-39 Match length 95 % identity 86 NCBI Description (D30763) ferredoxin [Oryza sativa] 400619 Seq. No. Seq. ID LIB3431-036-P1-K1-A4 Method BLASTX NCBI GI q1709846 BLAST score 180 E value 4.0e-13 122

Match length % identity 47

PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336) NCBI Description

22 kDa component of photosystem II [Lycopersicon

esculentum]

400620 Seq. No.

LIB3431-036-P1-K1-A5 Seq. ID

Method BLASTN NCBI GI q6016845 BLAST score 301 E value 1.0e-168 Match length 426 % identity 93 NCBI Description Orv

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 400621

Seq. ID LIB3431-036-P1-K1-A6

Method BLASTN
NCBI GI g218207
BLAST score 227

E value 1.0e-124 Match length 259 % identity 97

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS1139

Seq. No. 400622

Seq. ID LIB3431-036-P1-K1-A8

Method BLASTX
NCBI GI g132105
BLAST score 470
E value 3.0e-47
Match length 107
% identity 85

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400623

Seq. ID LIB3431-036-P1-K1-A9

Method BLASTX
NCBI GI 9730456
BLAST score 663
E value 9.0e-70
Match length 128
% identity 98

NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 400624

Seq. ID LIB3431-036-P1-K1-B12

Method BLASTX
NCBI GI g2407281
BLAST score 556
E value 3.0e-57
Match length 108
% identity 97

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 400625

Seq. ID LIB3431-036-P1-K1-B2

% identity

96

```
BLASTN
Method
                   g19094
NCBI GI
                   52
BLAST score
                   4.0e-20
E value
                   64
Match length
                   95
% identity
                  H.vulgare mRNA PsaN for photosystem I subunit N
NCBI Description
                   400626
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-B3
                   BLASTX
Method
                   g2072555
NCBI GI
                   237
BLAST score
                   9.0e-20
E value
                   44
Match length
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   400627
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-B4
Method
                   BLASTX
                   q2306981
NCBI GI
                   385
BLAST score
                   4.0e-37
E value
                   68
Match length
                   99
% identity
                   (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
                   400628
Seq. No.
                   LIB3431-036-P1-K1-B5
Seq. ID
                   BLASTX
Method
                   q132105
NCBI GI
                   567
BLAST score
                   2.0e-58
E value
Match length
                   122
                   87
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{EC} 4.\overline{1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400629
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-B6
                   BLASTX
Method
NCBI GI
                   q4760553
BLAST score
                   703
                   2.0e-74
E value
Match length
                   142
```

NCBI Description (AB019533) Nad-dependent formate dehydrogenase [Oryza

NCBI Description



sativa]

```
Seq. No.
                   400630
                   LIB3431-036-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2570511
BLAST score
                   637
E value
                   1.0e-66
Match length
                   123
                   98
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   LIB3431-036-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   486
E value
                   5.0e-49
Match length
                   111
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
                    400632
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-C1
Method
                    BLASTX
NCBI GI
                    g1835731
BLAST score
                    378
                    3.0e-36
E value
Match length
                    122
% identity
                    67
                    (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                    400633
Seq. No.
Seq. ID
                    LIB3431-036-P1-K1-C11
                    BLASTX
Method
                    q3126854
NCBI GI
BLAST score
                    715
                    7.0e-76
E value
                    136
Match length
                    99
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                    400634
Seq. No.
Seq. ID
                    LIB3431-036-P1-K1-C12
Method
                    BLASTX
                    q82080
NCBI GI
BLAST score
                    425
                    7.0e-42
E value
Match length
                    121
                    68
% identity
```

51321

[Lycopersicon esculentum]

chlorophyll a/b-binding protein type III precursor - tomato

>gi_226872_prf__1609235A chlorophyll a/b binding protein

BLAST score

356

```
400635
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q3914468
BLAST score
                  536
                  7.0e-55
E value
                  142
Match length
% identity
                  75
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                  >gi 478411 pir JQ2257 nuclear antigen 21D7 - carrot
                  >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus
                  carota]
                  400636
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g119784
                  221
BLAST score
                  6.0e-18
E value
                  92
Match length
                  55
% identity
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
NCBI Description
                  (BETA-KETOACYL-ACP SYNTHASE I) (KAS I)
                  >gi 100555 pir _A39356 3-oxoacyl-[acyl-carrier-protein]
                  synthase (EC 2.3.1.41) I beta chain precursor, chloroplast
                  - barley >gi 167065 (M60410) beta-ketoacyl-ACP synthase I
                  [Hordeum vulgare]
                  400637
Seq. No.
                  LIB3431-036-P1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q131225
BLAST score
                  663
                  1.0e-69
E value
                  147
Match length
                  85
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir_ A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  400638
                  LIB3431-036-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097547
BLAST score
                  261
E value
                  1.0e-22
Match length
                  124
                   48
% identity
                  (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   400639
                  LIB3431-036-P1-K1-C9
Seq. ID
                   BLASTX
Method
                   q3024440
NCBI GI
```

```
E value
                  7.0e-34
Match length
                  75
% identity
                  PROTEASOME DELTA CHAIN PRECURSOR (MULTICATALYTIC
NCBI Description
                  ENDOPEPTIDASE COMPLEX DELTA CHAIN)
                  >gi 1743356 emb CAA70699 (Y09505) proteasome delta subunit
                  [Nicotiana tabacum]
                  400640
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4105561
BLAST score
                  186
                  8.0e-14
E value
Match length
                  80
                  54
% identity
NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
Seq. No.
                  400641
                  LIB3431-036-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  592
                  5.0e-64
E value
Match length
                  133
                  94
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  400642
Seq. ID
                  LIB3431-036-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g131388
BLAST score
                  283
E value
                  3.0e-25
Match length
                  107
                  63
% identity
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
Seq. No.
                  400643
                  LIB3431-036-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4759278
BLAST score
                  301
E value
                  3.0e-27
Match length
                  144
```

51323

NCBI Description prp28, U5 snRNP 100 kd protein >gi 2655202 (AF026402) U5

43

% identity

snRNP 100 kD protein [Homo sapiens]

```
400644
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-D4
Method
                  BLASTX
NCBI GI
                   q2529682
                   238
BLAST score
                   6.0e-20
E value
                   143
Match length
                   42
% identity
NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]
                   400645
Seq. No.
                   LIB3431-036-P1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4519936
BLAST score
                   481
                   2.0e-48
E value
Match length
                   136
                   71
% identity
NCBI Description (AB019186) RPR1 [Oryza sativa]
                   400646
Seq. No.
                   LIB3431-036-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   g4678279
NCBI GI
                   311
BLAST score
                   2.0e-28
E value
                   97
Match length
                   67
% identity
                   (AL049660) carboxyl terminal protease-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   400647
Seq. No.
                   LIB3431-036-P1-K1-D7
Seq. ID
                   BLASTX
Method
                   g3789954
NCBI GI
BLAST score
                   582
                   3.0e-60
E value
                   109
Match length
% identity
                   100
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   400648
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-D8
                   BLASTX
Method
                   g3126854
NCBI GI
BLAST score
                   662
                   1.0e-69
E value
                   124
Match length
                   100
 % identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
 Seq. No.
                   400649
                   LIB3431-036-P1-K1-E1
 Seq. ID
```

51324

BLASTX

Method

```
g115787
NCBI GI
                  531
BLAST score
                  3.0e-54
E value
                  121
Match length
                  88
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  400650
Seq. No.
                  LIB3431-036-P1-K1-E10
Seq. ID
Method
                  BLASTX
                  g4263714
NCBI GI
                  536
BLAST score
                  7.0e-55
E value
                  142
Match length
% identity
                  77
                  (AC006223) putative integral membrane protein [Arabidopsis
NCBI Description
                  thaliana]
                  400651
Seq. No.
                  LIB3431-036-P1-K1-E11
Seq. ID
Method
                  BLASTX
                  q6006310
NCBI GI
                  751
BLAST score
                   5.0e-80
E value
                  144
Match length
% identity
                   99
                  (AB018443) nonphototrophic hypocotyl 1b [Oryza sativa]
NCBI Description
                   400652
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-E12
Method
                  BLASTX
NCBI GI
                   q1421751
BLAST score
                   175
                   2.0e-12
E value
                   36
Match length
                   92
% identity
                   (U60592) putative ORF; conserved in 5' leaders of plant
NCBI Description
                   SAMdC [Pisum sativum]
                   400653
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-E3
Method
                   BLASTX
                   q3047090
NCBI GI
                   419
BLAST score
                   4.0e-41
E value
                   138
Match length
                   55
% identity
NCBI Description (AF058826) T26D22.18 gene product [Arabidopsis thaliana]
                   400654
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-E4
                   BLASTX
Method
```

51325

g2944180

NCBI GI

NCBI GI

```
454
BLAST score
E value
                  3.0e-45
Match length
                  114
% identity
                  76
                  (AF007779) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  400655
Seq. ID
                  LIB3431-036-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  g1835730
BLAST score
                  274
E value
                  1.0e-152
Match length
                  290
% identity
                  99
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                  complete cds
                  400656
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3461848
BLAST score
                  210
E value
                  1.0e-16
Match length
                  75
% identity
                  64
NCBI Description
                  (AC005315) putative ATPase [Arabidopsis thaliana]
Seq. No.
                  400657
Seq. ID
                  LIB3431-036-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                  490
E value
                  2.0e-49
Match length
                  127
% identity
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
NCBI Description
                   - spinach >gi 1066153 dbj BAA07177 (D37963) cysteine
                  synthase [Spinacia oleracea]
Seq. No.
                   400658
Seq. ID
                  LIB3431-036-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g461595
BLAST score
                  262
E value
                  8.0e-23
Match length
                  94
                   55
% identity
                  ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
NCBI Description
                  >qi 479533 pir S34473 H+-transporting ATP synthase (EC
                   3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520
                   (X71397) CF(o) II ATP synthase subunit 9 [Spinacia oleracea]
Seq. No.
                   400659
Seq. ID
                  LIB3431-036-P1-K1-F11
Method
                  BLASTX
```

51326

g2072555

BLAST score 9.0e-20 E value Match length 44 100 % identity (AF001396) metallothionein-like protein [Oryza sativa] NCBI Description >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa] 400660 Seq. No. LIB3431-036-P1-K1-F12 Seq. ID BLASTN Method g1245938 NCBI GI 36 BLAST score 1.0e-10 E value 36 Match length 100 % identity rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, NCBI Description heart atrium, mRNA, 2998 nt] 400661 Seq. No. LIB3431-036-P1-K1-F2 Seq. ID BLASTX Method g6017100 NCBI GI 588 BLAST score 6.0e-61 E value 142 Match length % identity (AC009895) unknown protein [Arabidopsis thaliana] NCBI Description 400662 Seq. No. LIB3431-036-P1-K1-F3 Seq. ID BLASTX Method g131388 NCBI GI BLAST score 383 6.0e-37 E value 127 Match length 66 % identity OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir__S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum] 400663 Seq. No. LIB3431-036-P1-K1-F4 Seq. ID BLASTX Method NCBI GI g3789952 BLAST score 275 E value 3.0e-24

Match length 55 96 % identity

(AF094775) chlorophyll a/b-binding protein presursor [Oryza NCBI Description

sativa]

400664 Seq. No.

Seq. No.

400669

```
LIB3431-036-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4558549
BLAST score
                  627
E value
                  2.0e-65
Match length
                  144
                  83
% identity
NCBI Description
                  (AC007138) putative SecA-type chloroplast protein transport
                  factor [Arabidopsis thaliana]
                  400665
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-F7
                  BLASTX
Method
NCBI GI
                  g2191152
BLAST score
                  149
E value
                  2.0e-09
Match length
                  105
                  39
% identity
                  (AF007269) A IG002N01.31 gene product [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  400666
Seq. ID
                  LIB3431-036-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  682
E value
                  6.0e-72
                  127
Match length
% identity
                  99
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  400667
Seq. ID
                  LIB3431-036-P1-K1-G1
Method
                  BLASTX
                  g2130052
NCBI GI
BLAST score
                  451
                  7.0e-45
E value
Match length
                  99
                  89
% identity
                  xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                  >gi_1296809_emb_CAA64545_ (X95257) xylose isomerase
                   [Hordeum vulgare]
Seq. No.
                  400668
                  LIB3431-036-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

NCBI GI

```
Seq. ID
                  LIB3431-036-P1-K1-G2
                  BLASTX
Method
NCBI GI
                  g3913808
                  590
BLAST score
                  4.0e-61
E value
Match length
                  132
% identity
                  89
                  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
NCBI Description
                  SYNTHETASE) >gi 2429618 dbj BAA22284 (AB007120)
                  ferrochelatase [Oryza sativa]
                  400670
Seq. No.
                  LIB3431-036-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4079798
BLAST score
                  496
                  4.0e-50
E value
Match length
                  127
                  77
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  400671
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-G5
                  BLASTX
Method
NCBI GI
                  g3126854
BLAST score
                  511
                  6.0e-52
E value
                  99
Match length
                  97
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  400672
Seq. No.
                  LIB3431-036-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4895205
                  248
BLAST score
                  4.0e-21
E value
Match length
                  61
% identity
                  (AC007661) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   400673
Seq. ID
                  LIB3431-036-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q2695931
BLAST score
                  350
E value
                  5.0e-33
Match length
                  141
% identity
                   53
NCBI Description (AJ222779) hypothetical protein [Hordeum vulgare]
Seq. No.
                  400674
                  LIB3431-036-P1-K1-G8
Seq. ID
Method
                  BLASTN
```

51329

q6015437

```
BLAST score
                  1.0e-10
E value
                  36
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  400675
Seq. No.
                  LIB3431-036-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789952
                  578
BLAST score
                  8.0e-60
E value
Match length
                  116
% identity
                  98
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  400676
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  591
                  3.0e-61
E value
                  127
Match length
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400677
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-H7
                  BLASTN
Method
NCBI GI
                   g5917782
BLAST score
                   36
                   5.0e-11
E value
                  120
Match length
                   82
% identity
NCBI Description Oryza sativa carbonic anhydrase 3 mRNA, complete cds
                   400678
Seq. No.
                  LIB3431-036-P1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g548605
BLAST score
                   561
E value
                   8.0e-58
                   127
Match length
                   89
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi 539055 pir A48527 photosystem I protein psak precursor
```

- barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

```
400679
Seq. No.
                  LIB3431-036-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g1709846
NCBI GI
BLAST score
                  164
                  3.0e-11
E value
                  121
Match length
% identity
                  44
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)
NCBI Description
                  22 kDa component of photosystem II [Lycopersicon
                  esculentum]
                  400680
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-A1
                  BLASTN
Method
NCBI GI
                  g576770
                  280
BLAST score
                   1.0e-156
E value
                  304
Match length
% identity
                   98
                  Oryza sativa clone ST1 sucrose-regulated mRNA, 3'-end
NCBI Description
                   sequence
                   400681
Seq. No.
                  LIB3431-036-P1-N1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2072555
                   237
BLAST score
                   1.0e-19
E value
Match length
                   44
% identity
                   100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   400682
Seq. No.
Seq. ID
                   LIB3431-036-P1-N1-A4
                   BLASTX
Method
NCBI GI
                   g6103011
BLAST score
                   515
                   2.0e-52
E value
Match length
                   115
% identity
                   48
                  (X84225) precursor of photosystem II subunit (22KDa)
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   400683
                   LIB3431-036-P1-N1-A5
Seq. ID
Method
                   BLASTN
                   g6016845
NCBI GI
BLAST score
                   206
E value
                   1.0e-112
Match length
                   347
```

51331

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

89

% identity

BLAST score

237

```
400684
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  402
E value
                  4.0e-39
Match length
                  73
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400685
Seq. ID
                  LIB3431-036-P1-N1-A9
Method
                  BLASTX
NCBI GI
                  g730456
BLAST score
                  335
E value
                  3.0e-31
Match length
                  65
                  100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                  400686
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-B12
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  532
                  2.0e-54
E value
                  103
Match length
% identity
NCBI Description
                 (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  400687
Seq. ID
                  LIB3431-036-P1-N1-B2
Method
                  BLASTX
NCBI GI
                  g3914466
BLAST score
                  369
E value
                  3.0e-35
Match length
                  67
% identity
                  99
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                  (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  400688
Seq. ID
                  LIB3431-036-P1-N1-B3
Method
                  BLASTX
NCBI GI
                  g2072555
```

```
E value 1.0e-19
Match length 44
% identity 100
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 400689
Seq. ID LIB3431-036-P1-N1-B4
```

Method BLASTX
NCBI GI g2306981
BLAST score 236
E value 1.0e-19

Match length 52 % identity 87

NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 400690

Seq. ID LIB3431-036-P1-N1-B5

Method BLASTX
NCBI GI g132105
BLAST score 443
E value 7.0e-44
Match length 80
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400691

Seq. ID LIB3431-036-P1-N1-B6

Method BLASTX
NCBI GI g4760553
BLAST score 429
E value 3.0e-42
Match length 82
% identity 95

NCBI Description (AB019533) Nad-dependent formate dehydrogenase [Oryza

sativa]

Seq. No. 400692

Seq. ID LIB3431-036-P1-N1-B7

Method BLASTX
NCBI GI g115794
BLAST score 550
E value 2.0e-56
Match length 111
% identity 94

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE

III CAB-13) >gi 72748 pir CDTO33 chlorophyll a/b-binding

protein type III precursor (cab-13) - tomato



>gi_19277_emb_CAA42818_ (X60275) LHCII type III
[Lycopersicon esculentum]

Seq. No. 400693

Seq. ID LIB3431-036-P1-N1-B9

Method BLASTX
NCBI GI g115787
BLAST score 501
E value 1.0e-50
Match length 97
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 400694

Seq. ID LIB3431-036-P1-N1-C1

Method BLASTN
NCBI GI g1835730
BLAST score 197
E value 1.0e-106
Match length 277
% identity 93

NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,

complete cds

Seq. No. 400695

Seq. ID LIB3431-036-P1-N1-C11

Method BLASTX
NCBI GI g3126854
BLAST score 190
E value 3.0e-14
Match length 71
% identity 55

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 400696

Seq. ID LIB3431-036-P1-N1-C12

Method BLASTX
NCBI GI g115813
BLAST score 209
E value 2.0e-16
Match length 69
% identity 67

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 400697

Seq. ID LIB3431-036-P1-N1-C5

Method BLASTX
NCBI GI g119784
BLAST score 312
E value 2.0e-28
Match length 62

```
% identity
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
NCBI Description
                  (BETA-KETOACYL-ACP SYNTHASE I) (KAS I)
                  >gi 100555 pir A39356 3-oxoacyl-[acyl-carrier-protein]
                  synthase (EC 2.3.1.41) I beta chain precursor, chloroplast
                  - barley >gi 167065 (M60410) beta-ketoacyl-ACP synthase I
                  [Hordeum vulgare]
Seq. No.
                  400698
                  LIB3431-036-P1-N1-C9
Seq. ID
Method
                  BLASTX
                  g2511594
NCBI GI
BLAST score
                  326
                  4.0e-30
E value
Match length
                  95
% identity
                  66
                  (Y13694) multicatalytic endopeptidase complex, proteasome
NCBI Description
                  precursor, beta subunit [Arabidopsis thaliana]
                  >gi_2827525_emb_CAA16533.1_ (AL021633) multicatalytic
                  endopeptidase complex, proteasome precursor, beta subunit
                  [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                  proteasome subunit PBA1 [Arabidopsis thaliana]
                  400699
Seq. No.
                  LIB3431-036-P1-N1-D1
Seq. ID
Method
                  BLASTX
                  q4105561
NCBI GI
BLAST score
                  391
                  9.0e-38
E value
Match length
                  85
                  88
% identity
                  (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
NCBI Description
                  400700
Seq. No.
                  LIB3431-036-P1-N1-D10
Seq. ID
Method
                  BLASTX
                  g3036942
NCBI GI
BLAST score
                  363
E value
                  2.0e-34
Match length
                  71
% identity
                  97
                  (AB012636) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
                  400701
Seq. No.
                  LIB3431-036-P1-N1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q482311
BLAST score
                  428
                  4.0e-42
E value
```

Match length 86 99 % identity

photosystem II oxygen-evolving complex protein 1 - rice NCBI Description

(strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 400702

E value

2.0e-24

```
Seq. ID
                  LIB3431-036-P1-N1-D4
                  BLASTX
Method
NCBI GI
                  g2529682
                  202
BLAST score
                  1.0e-15
E value
                  104
Match length
                  38
% identity
                  (AC002535) unknown protein [Arabidopsis thaliana]
NCBI Description
                  400703
Seq. No.
                  LIB3431-036-P1-N1-D7
Seq. ID
Method
                  BLASTX
                  g3789954
NCBI GI
BLAST score
                  181
E value
                  4.0e-13
Match length
                  32
% identity
                  100
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  400704
                  LIB3431-036-P1-N1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  405
E value
                  1.0e-39
Match length
                  78
% identity
                  97
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  400705
Seq. No.
                  LIB3431-036-P1-N1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036946
BLAST score
                  321
                  1.0e-29
E value
Match length
                  63
                  97
% identity
                  (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
Seq. No.
                  400706
                  LIB3431-036-P1-N1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6006310
BLAST score
                  454
E value
                  4.0e-45
Match length
                  86
                  100
% identity
                  (AB018443) nonphototrophic hypocotyl 1b [Oryza sativa]
NCBI Description
                  400707
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-E2
Method
                  BLASTX
NCBI GI
                  q4966372
BLAST score
                  277
```

E value

Match length

1.0e-19

44

```
Match length
                  83
% identity
                  67
NCBI Description
                  (AC006341) ESTs gb N38586 and gb N38613 come from this
                  gene. [Arabidopsis thaliana]
                  400708
Seq. No.
                  LIB3431-036-P1-N1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3047125
BLAST score
                  205
                  6.0e-16
E value
Match length
                  75
                  48
% identity
NCBI Description
                  (AF058919) No definition line found [Arabidopsis thaliana]
                  400709
Seq. No.
                  LIB3431-036-P1-N1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3461848
BLAST score
                  210
                  1.0e-16
E value
Match length
                  75
% identity
                  64
NCBI Description
                  (AC005315) putative ATPase [Arabidopsis thaliana]
                  400710
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-F1
Method
                  BLASTX
NCBI GI
                  q1071913
BLAST score
                  365
E value
                  1.0e-34
Match length
                  103
                  70
% identity
NCBI Description
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
                  - spinach >gi_1066153_dbj_BAA07177 (D37963) cysteine
                  synthase [Spinacia oleracea]
Seq. No.
                  400711
Seq. ID
                  LIB3431-036-P1-N1-F10
Method
                  BLASTX
NCBI GI
                  q461595
BLAST score
                  220
E value
                  9.0e-18
Match length
                  98
% identity
                  49
                  ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
NCBI Description
                  >gi_479533_pir__S34473 H+-transporting ATP synthase (EC
                  3.6.1.34) Chain 9 - spinach >gi_394755_emb_CAA50520
                  (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]
Seq. No.
                  400712
Seq. ID
                  LIB3431-036-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
```



% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 400713

Seq. ID LIB3431-036-P1-N1-F3

Method BLASTX
NCBI GI g482311
BLAST score 302
E value 2.0e-27
Match length 60
% identity 100

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice

(strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 400714

Seq. ID LIB3431-036-P1-N1-F4

Method BLASTX
NCBI GI g3789952
BLAST score 273
E value 6.0e-24
Match length 52
% identity 100

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No. 400715

Seq. ID LIB3431-036-P1-N1-F5

Method BLASTN
NCBI GI g2662340
BLAST score 71
E value 1.0e-31
Match length 215
% identity 83

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 400716

Seq. ID LIB3431-036-P1-N1-F6

Method BLASTX
NCBI GI g2500724
BLAST score 182
E value 3.0e-13
Match length 39
% identity 87

NCBI Description PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR

>gi_2129894_pir__S72453 secA protein precursor - garden pea >gi_1122325_emb_CAA57798 (X82404) chloroplast SecA protein

[Pisum sativum]

Seq. No. 400717

Seq. ID LIB3431-036-P1-N1-F8

Method BLASTX
NCBI GI g671740
BLAST score 382
E value 1.0e-36

Match length 70 99 % identity NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct] 400718 Seq. No. LIB3431-036-P1-N1-F9 Seq. ID Method BLASTX NCBI GI g4314378 BLAST score 175 2.0e-12 E value Match length 57 60 % identity (AC006232) putative lipase [Arabidopsis thaliana] NCBI Description >gi 5306262 gb AAD41994.1 AC006233 5 (AC006233) putative lipase [Arabidopsis thaliana] 400719 Seq. No. LIB3431-036-P1-N1-G10 Seq. ID Method BLASTX g2072555 NCBI GI BLAST score 237 E value 1.0e-19 Match length 44 100 % identity NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like protein [Oryza sativa] 400720 Seq. No. LIB3431-036-P1-N1-G4 Seq. ID Method BLASTX g4079798 NCBI GI BLAST score 354 E value 2.0e-33 Match length 68 100 % identity NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa] Seq. No. 400721 LIB3431-036-P1-N1-G5 Seq. ID Method BLASTX NCBI GI q3126854 BLAST score 520 E value 6.0e-53 Match length 99 % identity 98

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 400722

LIB3431-036-P1-N1-G6 Seq. ID

Method BLASTX NCBI GI q3378650 BLAST score 335 E value 3.0e-31 Match length 95

```
% identity
NCBI Description
                  (X97606) abscisic acid activated [Medicago sativa]
                  400723
Seq. No.
                  LIB3431-036-P1-N1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2695931
                  504
BLAST score
                  5.0e-51
E value
Match length
                  106
% identity
                  89
NCBI Description
                  (AJ222779) hypothetical protein [Hordeum vulgare]
Seq. No.
                  400724
                  LIB3431-036-P1-N1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6063542
BLAST score
                  390
                  1.0e-37
E value
Match length
                  71
                  100
% identity
NCBI Description
                  (AP000615) EST C74302(E30840) corresponds to a region of
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
Seq. No.
                  400725
                  LIB3431-036-P1-N1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115774
                  189
BLAST score
                  4.0e-14
E value
Match length
                  65
% identity
                  57
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE I
                  CAB-13) (LHCP) >gi_72731_pir__CDPJ13 chlorophyll
                  a/b-binding protein 13 precursor - petunia
                  >gi_20471_emb_CAA26210_ (X02357) cab 13 precursor
                  polypeptide (aa -33 to 233) [Petunia sp.]
Seq. No.
                  400726
Seq. ID
                  LIB3431-036-P1-N1-H12
Method
                  BLASTX
NCBI GI
                  q552740
BLAST score
                  197
E value
                  2.0e-15
Match length
                  56
                  75
% identity
NCBI Description
                  (M17841) ribosomal protein S7 [Zea mays]
                  400727
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-H2
Method
                  BLASTX
NCBI GI
                  q6016428
BLAST score
                  301
E value
                  3.0e-27
Match length
                  63
% identity
                  83
```



NCBI Description PUTATIVE CASEIN KINASE II BETA-4 CHAIN (CK II) >gi_3341688

(AC003672) putative casein kinase II beta subunit

[Arabidopsis thaliana]

Seq. No. 400728

Seq. ID LIB3431-036-P1-N1-H3

Method BLASTX
NCBI GI g2582822
BLAST score 393
E value 5.0e-38
Match length 83
% identity 86

NCBI Description (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress

Protein of 32kDa) [Solanum tuberosum]

Seq. No. 400729

Seq. ID LIB3431-036-P1-N1-H4

Method BLASTX
NCBI GI g3126854
BLAST score 287
E value 1.0e-25
Match length 54
% identity 100

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 400730

Seq. ID LIB3431-036-P1-N1-H5

Method BLASTX
NCBI GI g3789954
BLAST score 431
E value 2.0e-42
Match length 81
% identity 98

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 400731

Seq. ID LIB3431-036-P1-N1-H6

Method BLASTN
NCBI GI g902200
BLAST score 44
E value 4.0e-16
Match length 48
% identity 49

NCBI Description Z.mays complete chloroplast genome

Seq. No. 400732

Seq. ID LIB3431-036-P1-N1-H7

Method BLASTX
NCBI GI g606817
BLAST score 491
E value 2.0e-49
Match length 92
% identity 100

NCBI Description (U08404) carbonic anhydrase [Oryza sativa]

>gi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic

anhydrase 3 [Oryza sativa]

```
Seq. No.
                    400733
 Seq. ID
                    LIB3431-036-P1-N1-H8
 Method
                    BLASTX
 NCBI GI
                    q548605
 BLAST score
                    473
 E value
                    2.0e-47
 Match length
                    113
 % identity
                    85
 NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                    (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                    >gi_539055_pir__A48527 photosystem I protein psaK precursor
                    - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                    [Hordeum vulgare]
 Seq. No.
                    400734
 Seq. ID
                    LIB3431-037-P1-K1-A1
 Method
                    BLASTX
 NCBI GI
                    g671740
 BLAST score
                    471
 E value
                    2.0e-47
 Match length
                    89
 % identity
                    97
 NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                    construct]
 Seq. No.
                    400735
 Seq. ID
                   LIB3431-037-P1-K1-A11
 Method
                   BLASTX
 NCBI GI
                    q5262946
 BLAST score
                    661
 E value
                    2.0e-69
 Match length
                    149
 % identity
                    79
 NCBI Description (Y19104) beta-alanine synthase [Lycopersicon esculentum]
 Seq. No.
                    400736
 Seq. ID
                   LIB3431-037-P1-K1-A12
 Method
                   BLASTX
 NCBI GI
                   q2984709
 BLAST score
                   154
 E value
                   1.0e-12
` Match length
                   105
 % identity
                    49
 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
 Seq. No.
                   400737
 Seq. ID
                   LIB3431-037-P1-K1-A4
 Method
                   BLASTX
 NCBI GI
                   q4996105
 BLAST score
                   386
 E value
                   3.0e-37
 Match length
                   93
 % identity
                   76
 NCBI Description (AB014076) histidine decarboxylase [Brassica napus]
 Seq. No.
                   400738
```

Seq. ID LIB3431-037-P1-K1-A5

Method BLASTX
NCBI GI g132105
BLAST score 290
E value 1.0e-40
Match length 138
% identity 71

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400739

Seq. ID LIB3431-037-P1-K1-A7
Method BLASTX
NCBI GI g1076724
BLAST score 387

E value 2.0e-37
Match length 74
% identity 95

NCBI Description LHCI-680, photosystem I antenna protein - barley

>gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I

antenna protein [Hordeum vulgare]

Seq. No. 400740

Seq. ID LIB3431-037-P1-K1-A8

Method BLASTX
NCBI GI g3914603
BLAST score 735
E value 4.0e-78
Match length 142
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,

CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase [Oryza sativa]

Seq. No. 400741

Seq. ID LIB3431-037-P1-K1-B1

Method BLASTX
NCBI GI g482311
BLAST score 320
E value 1.0e-29
Match length 64
% identity 100

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice

(strain Nihonbare) >qi 739292 prf 2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 400742

Seq. ID LIB3431-037-P1-K1-B10

Method BLASTX



NCBI GI a132105 BLAST score 614 6.0e-64 E value Match length 132 % identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094_pir RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375_prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400743

Seq. ID LIB3431-037-P1-K1-B12

Method BLASTX NCBI GI q3377815 BLAST score 258 3.0e-22 E value Match length 76 % identity 68

NCBI Description (AF076275) similar to protein kinases (Pfam: pkinase.hmm,

score: 255.71) [Arabidopsis thaliana]

Seq. No. 400744

Seq. ID LIB3431-037-P1-K1-B2

Method BLASTX NCBI GI g115787 BLAST score 558 E value 2.0e-57 Match length 140 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 400745

Seq. ID LIB3431-037-P1-K1-B3

Method BLASTN NCBI GI q3885891 BLAST score 129 E value 2.0e-66 182 Match length % identity 99

Oryza sativa photosystem-1 F subunit precursor (PSI-F) NCBI Description

mRNA, complete cds

Seq. No. 400746

Seq. ID LIB3431-037-P1-K1-B4

Method BLASTX NCBI GI q3789954 BLAST score 388 E value 2.0e-37



```
73
Match length
                  97
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  400747
Seq. ID
                  LIB3431-037-P1-K1-B5
Method
                  BLASTX
                  g733454
NCBI GI
BLAST score
                  418
E value
                  5.0e-41
Match length
                  84
% identity
                  95
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  400748
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q100293
BLAST score
                  320
                  2.0e-29
E value
Match length
                  80
% identity
                  40
                  ribonucleoprotein A, 29K - wood tobacco
NCBI Description
                  >gi_19754_emb_CAA43427_ (X61113) 29kD A ribonucleoprotein
                  [Nicotiana sylvestris]
Seq. No.
                  400749
                  LIB3431-037-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913641
BLAST score
                  442
E value
                  8.0e-44
Match length
                  108
% identity
                  82
                  FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >qi 3041777 dbj BAA25423 (AB007194)
                  fructose-1,6-bisphosphatase [Oryza sativa]
                  400750
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-C10
Method
                  BLASTX
                  q2191138
NCBI GI
BLAST score
                  148
                  2.0e-09
E value
Match length
                  56
```

% identity 46

(AF007269) A IG002N01.18 gene product [Arabidopsis NCBI Description

thaliana]

400751 Seq. No.

Seq. ID LIB3431-037-P1-K1-C12

BLASTX Method g1617197 NCBI GI BLAST score 148

```
E value
                  2.0e-09
Match length
                  29
                  90
% identity
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
                  400752
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q5042409
                  425
BLAST score
E value
                  9.0e-42
Match length
                  139
% identity
                  61
                  (AC006193) Putative membrane related protein [Arabidopsis
NCBI Description
                  thaliana]
                  400753
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q3776557
BLAST score
                  389
                  1.0e-37
E value
Match length
                  142
% identity
                  51
                  (AC005388) Contains similarity to gi_2924495 hypothetical
NCBI Description
                  protein Rv1920 from Mycobacterium tuberculosis genome
                  gb_AL022020. [Arabidopsis thaliana]
Seq. No.
                  400754
Seq. ID
                  LIB3431-037-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q3885892
BLAST score
                  284
E value
                  2.0e-35
Match length
                  104
% identity
                  72
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
Seq. No.
                  400755
Seq. ID
                  LIB3431-037-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g5882720
BLAST score
                  294
                  2.0e-26
E value
                  99
Match length
                  60
% identity
NCBI Description
                  (AC008263) Similar to gb D86180 phosphoribosylanthranilate
                  transferase from Pisum sativum and contains 2 PF 00168 C2
                   (phospholipid binding) domains. ESTs gb H76726, gb T45544
                  and gb N96377 come from this gene. [Arab
                  400756
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  506
E value
                  3.0e-51
```

Match length % identity 70 (AB016283) carbonic anhydrase [Oryza sativa] NCBI Description 400757 Seq. No. Seq. ID LIB3431-037-P1-K1-D1 Method BLASTX NCBI GI q3789952 BLAST score 490 E value 2.0e-49 Match length 114 % identity 86 NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza satival 400758 Seq. No. LIB3431-037-P1-K1-D10 Seq. ID Method BLASTX NCBI GI g132105 BLAST score 631 E value 6.0e-66 Match length 116 % identity 100 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 400759 Seq. ID LIB3431-037-P1-K1-D11 Method BLASTX NCBI GI g115796 BLAST score 785 E value 5.0e-84 Match length 148 % identity 98 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 218174 dbj BAA00537 (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa] Seq. No. 400760 Seq. ID LIB3431-037-P1-K1-D12 Method BLASTX

NCBI GI g115787
BLAST score 557
E value 3.0e-57
Match length 133
% identity 84

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

```
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa]

400761
LIB3431-037-P1-K1-D5
BLASTX
g5734758
321
```

 Seq. No.
 400762

 Seq. ID
 LIB3431-037-P1-K1-D6

 Method
 BLASTX

 NCBI GI
 q3335335

1.0e-29

155

NCBI GI g3335335
BLAST score 190
E value 3.0e-14
Match length 61
% identity 62

Seq. No. Seq. ID

Method

NCBI GI

E value Match length

BLAST score

NCBI Description (AC004512) ESTs gb_F14113 and gb_T42122 come from this

region. [Arabidopsis thaliana]

Seq. No. 400763

Seq. ID LIB3431-037-P1-K1-D7

Method BLASTX
NCBI GI g3435096
BLAST score 273
E value 6.0e-24
Match length 101
% identity 55

NCBI Description (AF033587) SRZ21 [Arabidopsis thaliana]

Seq. No. 400764

Seq. ID LIB3431-037-P1-K1-E1

Method BLASTX
NCBI GI g1653513
BLAST score 158
E value 2.0e-10
Match length 81
% identity 41

NCBI Description (D90914) hypothetical protein [Synechocystis sp.]

Seq. No. 400765

Seq. ID LIB3431-037-P1-K1-E10

Method BLASTN
NCBI GI g6015437
BLAST score 35
E value 6.0e-10
Match length 35
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 400766

Seq. ID LIB3431-037-P1-K1-E11



Method BLASTX
NCBI GI g132105
BLAST score 748
E value 1.0e-79
Match length 157
% identity 90

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400767

Seq. ID LIB3431-037-P1-K1-E12

Method BLASTX
NCBI GI g3894193
BLAST score 152
E value 9.0e-10
Match length 117
% identity 38

NCBI Description (AC005662) putative strictosidine synthase [Arabidopsis

thaliana]

Seq. No. 400768

Seq. ID LIB3431-037-P1-K1-E2

Method BLASTN
NCBI GI g3075487
BLAST score 59
E value 2.0e-24
Match length 187
% identity 83

NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)

mRNA, complete cds

Seq. No. 400769

Seq. ID LIB3431-037-P1-K1-E3

Method BLASTN
NCBI GI g2239152
BLAST score 290
E value 1.0e-162
Match length 306
% identity 99

NCBI Description O.sativa mRNA for putative T3/T7-like RNA polymerase,

partial

Seq. No. 400770

Seq. ID LIB3431-037-P1-K1-E5

Method BLASTX
NCBI GI g132105
BLAST score 667
E value 4.0e-70
Match length 142
% identity 89



NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor (clone posss1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400771

Seq. ID LIB3431-037-P1-K1-E6

Method BLASTX
NCBI GI g132105
BLAST score 286
E value 2.0e-25
Match length 118
% identity 59

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400772

Seq. ID LIB3431-037-P1-K1-E7

Method BLASTX
NCBI GI g1076724
BLAST score 410
E value 5.0e-40
Match length 78
% identity 95

NCBI Description LHCI-680, photosystem I antenna protein - barley

>gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I

antenna protein [Hordeum vulgare]

Seq. No. 400773

Seq. ID LIB3431-037-P1-K1-E8

Method BLASTX
NCBI GI g461999
BLAST score 708
E value 6.0e-75
Match length 154
% identity 90

NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No. 400774

Seq. ID LIB3431-037-P1-K1-E9

Method BLASTX
NCBI GI g118170
BLAST score 429
E value 3.0e-42
Match length 102



```
% identity
                   CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
NCBI Description
                   >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784
(J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
                   oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967)
                   oryzacystatin=cysteine protease inhibitor [Oryza=rice,
                   Peptide, 102 aa] [Oryza] >gi 1280613 (U54702) oryzacystatin
                   [Oryza sativa]
                   400775
Seq. No.
                   LIB3431-037-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076724
BLAST score
                   548
                   3.0e-56
E value
                   102
Match length
                   96
% identity
                   LHCI-680, photosystem I antenna protein - barley
NCBI Description
                   >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
                   400776
Seq. No.
                   LIB3431-037-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2288969
BLAST score
                   390
                   1.0e-37
E value
Match length
                   118
% identity
                   65
NCBI Description (Y12862) glutathione transferase [Zea mays]
                   400777
Seq. No.
                   LIB3431-037-P1-K1-F11
Seq. ID
Method
                   BLASTX
                   q4469020
NCBI GI
BLAST score
                   314
E value
                   9.0e-29
Match length
                   72
% identity
                   82
NCBI Description
                   (AL035602) putative protein (fragment) [Arabidopsis
                   thaliana]
                   400778
Seq. No.
Seq. ID
                   LIB3431-037-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   470
E value
                   4.0e-47
Match length
                   126
                   75
% identity
```

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 400779

```
LIB3431-037-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706260
BLAST score
                   768
                  5.0e-82
E value
Match length
                  156
% identity
                  89
NCBI Description
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__$59597
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
Seq. No.
                  400780
Seq. ID
                  LIB3431-037-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  q11957
BLAST score
                  467
E value
                  0.0e+00
Match length
                  475
                  100
% identity
NCBI Description Rice complete chloroplast genome
Seq. No.
                  400781
Seq. ID
                  LIB3431-037-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  a548605
BLAST score
                  472
E value
                  3.0e-47
Match length
                  125
                  78
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor

    barley >gi_304220 (L12707) photosystem I PSI-K subunit

                   [Hordeum vulgare]
Seq. No.
                  400782
Seq. ID
                  LIB3431-037-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q3738304
BLAST score
                  270
E value
                  1.0e-23
Match length
                  143
% identity
                  42
NCBI Description
                  (AC005309) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  400783
Seq. ID
                  LIB3431-037-P1-K1-F8
```

Method BLASTX NCBI GI g2072555 BLAST score 237 E value 1.0e-19 Match length 44 100 % identity

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441 gb AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Match length

99

```
Seq. No.
                  400784
Seq. ID
                  LIB3431-037-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  421
E value
                  3.0e-41
Match length
                  128
% identity
                  66
NCBI Description
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  400785
Seq. ID
                  LIB3431-037-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q2347098
BLAST score
                  448
E value
                  2.0e-44
Match length
                  94
% identity
                  86
NCBI Description
                  (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
                  >gi_4490742_emb_CAB38904.1 (AL035708) ubiquitin-specific
                  protease (AtUBP3) [Arabidopsis thaliana]
Seq. No.
                  400786
Seq. ID
                  LIB3431-037-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  1.0e-19
Match length
                  44
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  400787
Seq. ID
                  LIB3431-037-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  520
E value
                  6.0e-53
Match length
                  138
% identity
                  76
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  400788
Seq. ID
                  LIB3431-037-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2565436
BLAST score
                  159
E value
                  1.0e-10
```

51353



% identity 39

NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No. 400789

Seq. ID LIB3431-037-P1-K1-G5

Method BLASTX
NCBI GI g1708191
BLAST score 428
E value 4.0e-42
Match length 135

% identity 55
NCBI Description HEXOSE CARRIER PROTEIN HEX6 >qi 467319 (L08188) hexose

carrier protein [Ricinus communis]

Seq. No. 400790

Seq. ID LIB3431-037-P1-K1-G7

Method BLASTX
NCBI GI g548603
BLAST score 698
E value 2.0e-75
Match length 148
% identity 97

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

>gi_478404_pir__JQ2247 photosystem I chain D precursor barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 400791

Seq. ID LIB3431-037-P1-K1-G8

Method BLASTX
NCBI GI g3603401
BLAST score 414
E value 2.0e-40
Match length 131
% identity 61

NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No. 400792

Seq. ID LIB3431-037-P1-K1-G9

Method BLASTX
NCBI GI g320618
BLAST score 546
E value 6.0e-56
Match length 123
% identity 85

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 400793

Seq. ID LIB3431-037-P1-K1-H1

Method BLASTX
NCBI GI g3294467
BLAST score 682
E value 6.0e-72

```
Match length
% identity
                  89
NCBI Description
                  (U89341) phosphoglucomutase 1 [Zea mays]
                  400794
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  660
E value
                  5.0e-75
Match length
                  143
% identity
                  99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  400795
Seq. No.
                  LIB3431-037-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  569
                  1.0e-58
E value
Match length
                  131
% identity
                  82
NCBI Description
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
                  400796
Seq. No.
                  LIB3431-037-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131388
BLAST score
                  294
E value
                  1.0e-26
Match length
                  115
% identity
                  61
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
                  400797
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1561774
BLAST score
                  733
E value
                  7.0e-78
Match length
                  161
% identity
                  81
NCBI Description
                  (U67426) malate dehydrogenase [Vitis vinifera]
                  400798
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-H7
```

Method BLASTX NCBI GI g548605 BLAST score 485 E value 6.0e-54 Match length

% identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR NCBI Description

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi 539055 pir A48527 photosystem I protein psaK precursor - barley >gi 304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 400799

Seq. ID LIB3431-037-P1-K1-H8

87

Method BLASTX NCBI GI q3757515 BLAST score 536 E value 8.0e-55 130 Match length % identity 75

(AC005167) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi_4581130_gb_AAD24620.1_AC005825_27 (AC005825)

hypothetical protein [Arabidopsis thaliana]

400800 Seq. No.

Seq. ID LIB3431-037-P1-K1-H9

Method BLASTX NCBI GI q132105 BLAST score 604 9.0e-63 E value 130 Match length % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400801

Seq. ID LIB3431-037-P1-N1-A1

Method BLASTX NCBI GI g347451 BLAST score 202 E value 8.0e-16 Match length 38 % identity 100

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza

sativa]

400802 Seq. No.

Seq. ID LIB3431-037-P1-N1-A12

Method BLASTN NCBI GI g11957 BLAST score 168 3.0e-89 E value Match length 284 % identity 45

```
NCBI Description Rice complete chloroplast genome
Seq. No.
                  400803
Seq. ID
                  LIB3431-037-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  g4996105
BLAST score
                  316
                  5.0e-29
E value
                  77
Match length
% identity
                  73
NCBI Description (AB014076) histidine decarboxylase [Brassica napus]
Seq. No.
                  400804
Seq. ID
                  LIB3431-037-P1-N1-A5
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  336
E value
                  3.0e-31
Match length
                  84
% identity
                  80
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  400805
Seq. ID
                  LIB3431-037-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  q167097
BLAST score
                  151
E value
                  7.0e-22
Match length
                  70
% identity
                  79
NCBI Description
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
                  [Hordeum vulgare]
Seq. No.
                  400806
Seq. ID
                  LIB3431-037-P1-N1-B1
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  320
E value
                  2.0e-29
Match length
                  64
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  400807
Seq. ID
                  LIB3431-037-P1-N1-B10
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  397
E value
                  2.0e-38
Match length
                  72
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
```

ribulose-bisphosphate carboxy \overline{l} ase ($\overline{E}C$ 4.1.1.39) small chain

precursor (clone pOSSS1139) - rice >qi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. Seq. ID LIB3431-037-P1-N1-B2 Method BLASTX NCBI GI q693920 BLAST score 374 E value 9.0e-36 Match length 71 % identity 100

NCBI Description (U21113) chlorophyll a/b binding protein [Solanum

tuberosum]

400808

400809 Seq. No. Seq. ID LIB3431-037-P1-N1-B3 Method BLASTN

NCBI GI q3885891 BLAST score 262 E value 1.0e-145 Match length 330 95 % identity

NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)

mRNA, complete cds

Seq. No. 400810

Seq. ID LIB3431-037-P1-N1-B5

Method BLASTX NCBI GI q733454 BLAST score 397 E value 1.0e-38 Match length 84 % identity

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 400811

Seq. ID LIB3431-037-P1-N1-C10

Method BLASTX NCBI GI g2191138 BLAST score 253 E value 1.0e-21 Match length 73 % identity 70

NCBI Description (AF007269) A IG002N01.18 gene product [Arabidopsis

thaliana]

Seq. No. 400812

Seq. ID LIB3431-037-P1-N1-C3

Method BLASTX NCBI GI g5042409 BLAST score 147 E value 4.0e-09

Match length

NCBI Description

% identity

100

construct]

```
Match length
% identity
                  66
                  (AC006193) Putative membrane related protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  400813
                  LIB3431-037-P1-N1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885892
BLAST score
                  471
E value
                  4.0e-47
Match length
                  89
% identity
                  100
NCBI Description
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
                  400814
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-C8
Method
                  BLASTX
NCBI GI
                  q3345477
                  182
BLAST score
                  2.0e-13
E value
Match length
                  34
% identity
                  97
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                  400815
Seq. No.
                  LIB3431-037-P1-N1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885886
BLAST score
                  199
E value
                  3.0e-15
Match length
                  35
                  100
% identity
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.
                  400816
                  LIB3431-037-P1-N1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789952
BLAST score
                  203
E value
                  1.0e-15
Match length
                  37
% identity
                  100
NCBI Description
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
Seq. No.
                  400817
Seq. ID
                  LIB3431-037-P1-N1-D10
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  263
                  9.0e-23
E value
                  51
```

51359

(X84730) ribulose-bisphosphate carboxylase [synthetic

```
400818
Seq. No.
Seq. ID
                    LIB3431-037-P1-N1-D11
                    BLASTX
Method
                    g3126854
NCBI GI
BLAST score
                    345
                    2.0e-32
E value
Match length
                    65
                    100
% identity
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                    400819
Seq. No.
Seq. ID
                    LIB3431-037-P1-N1-D12
Method
                    BLASTX
NCBI GI
                    q3036942
BLAST score
                    216
                    2.0e-17
E value
Match length
                    45
% identity
                    89
                    (AB012636) light harvesting chlorophyll a/b-binding protein
NCBI Description
                    [Nicotiana sylvestris]
Seq. No.
                    400820
Seq. ID
                    LIB3431-037-P1-N1-D3
Method
                    BLASTN
NCBI GI
                    q342643
BLAST score
                    34
E value
                    2.0e-09
Match length
                    106
% identity
NCBI Description
                    Maize mitochondrion with chloroplast insert containing
                    rRNAs
Seq. No.
                    400821
                    LIB3431-037-P1-N1-D8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2501190
BLAST score
                    202
                    1.0e-15
E value
Match length
                    60
% identity
                    72
                    THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                    >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                    [Zea mays]
Seq. No.
                    400822
Seq. ID
                    LIB3431-037-P1-N1-E11
Method
                    BLASTX
NCBI GI
                    g132105
BLAST score
                    443
                    7.0e-44
E value
                    80
Match length
                    100
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
```

51360

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 400823 Seq. ID LIB3431-037-P1-N1-E2

Method BLASTN
NCBI GI g3075487
BLAST score 60
E value 5.0e-25
Match length 92
% identity 91

NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)

mRNA, complete cds

Seq. No. 400824

Seq. ID LIB3431-037-P1-N1-E5

Method BLASTX
NCBI GI g671740
BLAST score 637
E value 1.0e-66
Match length 117
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 400825

Seq. ID LIB3431-037-P1-N1-E6

Method BLASTX
NCBI GI g671740
BLAST score 462
E value 4.0e-46
Match length 84
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

constructl

Seq. No. 400826

Seq. ID LIB3431-037-P1-N1-E7

Method BLASTX
NCBI GI g1076724
BLAST score 405
E value 2.0e-39
Match length 78
% identity 94

NCBI Description LHCI-680, photosystem I antenna protein - barley

>gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I

antenna protein [Hordeum vulgare]

Seq. No. 400827

Seq. ID LIB3431-037-P1-N1-E8

Method BLASTX NCBI GI g461999 BLAST score 169 E value 6.0e-12

```
Match length
                   75
% identity
NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)
Seq. No.
                   400828
Seq. ID
                  LIB3431-037-P1-N1-F1
Method
                  BLASTX
NCBI GI
                   g2306981
BLAST score
                   342
E value
                   5.0e-32
Match length
                  87
% identity
                  72
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
                  400829
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-F10
Method
                  BLASTX
NCBI GI
                  g2288969
BLAST score
                  281
E value
                  7.0e-25
Match length
                  127
                  47
% identity
NCBI Description (Y12862) glutathione transferase [Zea mays]
Seq. No.
                  400830
Seq. ID
                  LIB3431-037-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  q4469020
BLAST score
                  258
E value
                  3.0e-22
Match length
                  59
% identity
                  83
NCBI Description
                  (AL035602) putative protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  400831
Seq. ID
                  LIB3431-037-P1-N1-F2
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  87
E value
                  4.0e-41
Match length
                  167
% identity
                  88
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
Seq. No.
                  400832
Seq. ID
                  LIB3431-037-P1-N1-F3
Method
                  BLASTX
NCBI GI
                  g1706260
BLAST score
                  442
                  9.0e-44
E value
Match length
                  82
% identity
                  95
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir $59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
```



mays]

 Seq. No.
 400833

 Seq. ID
 LIB3431-037-P1-N1-F4

 Method
 BLASTX

 NCBI GI
 g128690

 BLAST score
 533

 E value
 2.0e-54

 Match length
 120

88

% identity NCBI Description

CBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST

>gi_66161_pir__DERZN3 NADH dehydrogenase (ubiquinone) (EC

1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_

(X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]

>gi_226610_prf__1603356AG NADH dehydrogenase ND3 [Oryza

satīva]

Seq. No. 400834

Seq. ID LIB3431-037-P1-N1-F5 Method BLASTX NCBI GI g131176

BLAST score 333 E value 6.0e-31 Match length 65 % identity 97

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR

(PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)

>gi_72683_pir__F1BH4 photosystem I chain IV precursor barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A

10.8kD photosystem I protein [Hordeum vulgare var.

distichum]

Seq. No. 400835

Seq. ID LIB3431-037-P1-N1-F6

Method BLASTX
NCBI GI g548605
BLAST score 277
E value 2.0e-24
Match length 59
% identity 90

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 400836

Seq. ID LIB3431-037-P1-N1-F8

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

Match length

NCBI Description

% identity

76

89

complete cds



protein [Oryza sativa]

Seq. No. 400837 Seq. ID LIB3431-037-P1-N1-F9 Method BLASTX NCBI GI q417260 BLAST score 400 E value 7.0e-39 Match length 120 % identity 68 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa] 400838 Seq. No. Seq. ID LIB3431-037-P1-N1-G1 Method BLASTN NCBI GI q2950394 BLAST score 35 5.0e-10 E value Match length 51 % identity 92 NCBI Description Zea mays me gene, exons 1 to 400839 Seq. No. Seq. ID LIB3431-037-P1-N1-G10 Method BLASTX NCBI GI q2347098 BLAST score 245 E value 1.0e-20 Match length 52 85 % identity NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana] Seq. No. 400840 Seq. ID LIB3431-037-P1-N1-G12 Method BLASTN NCBI GI g2072554 BLAST score 220 E value 1.0e-120 Match length 243 % identity 98 NCBI Description Oryza sativa metallothionein-like protein mRNA, complete Seq. No. 400841 Seq. ID LIB3431-037-P1-N1-G2 Method BLASTN NCBI GI q596079 BLAST score 44 E value 2.0e-15

51364

Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA,

```
Seq. No.
                   400842
Seq. ID
                  LIB3431-037-P1-N1-G3
Method
                  BLASTX
NCBI GI
                   g2565436
BLAST score
                   158
E value
                   2.0e-10
                   91
Match length
% identity
                   40
                  (AF028842) DegP protease precursor [Arabidopsis thaliana]
NCBI Description
                   400843
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-G5
Method
                   BLASTX
                   q1708191
NCBI GI
                   396
BLAST score
                   2.0e-38
E value
Match length
                   104
% identity
                   68
                  HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose
NCBI Description
                   carrier protein [Ricinus communis]
                   400844
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G7
Method
                   BLASTX
                   q548603
NCBI GI
BLAST score
                   565
                   3.0e-58
E value
Match length
                   110
% identity
                   97
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                   barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                   400845
Seq. ID
                   LIB3431-037-P1-N1-G8
Method
                   BLASTX
NCBI GI
                   q1168732
BLAST score
                   289
E value
                   8.0e-26
Match length
                   128
                   49
% identity
NCBI Description
                   CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 421914 pir S28045
                   ELI3 protein - parsley (fragment) >gi_836638_emb_CAA48028_ (X67817) Eli3 [Petroselinum crispum]
Seq. No.
                   400846
Seq. ID
                   LIB3431-037-P1-N1-G9
Method
                   BLASTX
                   g115787
NCBI GI
BLAST score
                   513
                   4.0e-52
E value
Match length
                   98
```

51365

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

100

% identity

NCBI Description

% identity

NCBI Description

100

```
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  400847
Seq. No.
                  LIB3431-037-P1-N1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3294467
                  369
BLAST score
                  3.0e-35
E value
                  78
Match length
                  95
% identity
NCBI Description
                  (U89341) phosphoglucomutase 1 [Zea mays]
                  400848
Seq. No.
                  LIB3431-037-P1-N1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g517500
BLAST score
                  190
                  5.0e-23
E value
                  94
Match length
                   68
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  400849
Seq. No.
                  LIB3431-037-P1-N1-H11
Seq. ID
                  BLASTX
Method
                  g3126854
NCBI GI
BLAST score
                   415
E value
                  1.0e-40
Match length
                  79
                  99
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   400850
                  LIB3431-037-P1-N1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q733454
BLAST score
                   402
                   3.0e-39
E value
Match length
                   81
                   95
% identity
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                   400851
Seq. ID
                   LIB3431-037-P1-N1-H3
Method
                   BLASTX
NCBI GI
                   q482311
BLAST score
                   374
E value
                   8.0e-36
Match length
                   74
```

protein 2R precursor - rice >gi_20182_emb_CAA32109

51366

photosystem II oxygen-evolving complex protein 1 - rice

(strain Nihonbare) >gi 739292 prf__2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 400852 LIB3431-037-P1-N1-H4 Seq. ID Method BLASTX g1708924 NCBI GI BLAST score 252 2.0e-21 E value Match length 54 87 % identity NCBI Description MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi 515759 (L34836) malate dehydrogenase (NADP+) [Vitis vinifera] 400853 Seq. No. Seq. ID LIB3431-037-P1-N1-H5 Method BLASTX NCBI GI g671740 BLAST score 202 E value 1.0e-15 38 Match length 100 % identity (X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description construct] Seq. No. 400854 LIB3431-037-P1-N1-H6 Seq. ID Method BLASTX g4206195 NCBI GI BLAST score 213 E value 5.0e-17 Match length 54 % identity 67 NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein [Arabidopsis thaliana] Seq. No. 400855 Seq. ID LIB3431-037-P1-N1-H7 Method BLASTX NCBI GI a548605 BLAST score 493 E value 8.0e-50 Match length 109 % identity NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi 539055_pir_ A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare] Seq. No. 400856

Seq. ID LIB3431-037-P1-N1-H8

Method BLASTX
NCBI GI g3757515
BLAST score 305
E value 8.0e-28

NCBI Description

```
Match length
                   77
% identity
NCBI Description
                   (AC005167) hypothetical protein [Arabidopsis thaliana]
                   >gi 4581130 gb AAD24620.1 AC005825 27 (AC005825)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   400857
Seq. ID
                  LIB3431-037-P1-N1-H9
Method
                  BLASTX
NCBI GI
                   q671740
BLAST score
                  264
E value
                   5.0e-23
Match length
                   53
                  96
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  constructl
Seq. No.
                   400858
Seq. ID
                  LIB3431-038-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q166410
BLAST score
                   443
E value
                   6.0e-44
Match length
                  118
% identity
                  71
NCBI Description
                  (L07291) Alfin-1 [Medicago sativa]
Seq. No.
                   400859
Seq. ID
                  LIB3431-038-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                   634
E value
                  2.0e-66
Match length
                  117
% identity
                  100
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  400860
Seq. ID
                  LIB3431-038-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g3367596
BLAST score
                  394
E value
                  3.0e-38
Match length
                  121
% identity
                  59
NCBI Description
                  (AL031135) putative protein [Arabidopsis thaliana]
Seq. No.
                  400861
Seq. ID
                  LIB3431-038-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g729535
BLAST score
                  223
E value
                  4.0e-18
Match length
                  76
% identity
                  58
```

51368

FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR

(FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)

```
(FTR-B)
Seq. No.
                   400862
Seq. ID
                  LIB3431-038-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  79
E value
                  3.0e-36
Match length
                  150
% identity
                  34
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
Seq. No.
                  400863
Seq. ID
                  LIB3431-038-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q3548808
BLAST score
                  322
E value
                  8.0e-30
Match length
                  81
% identity
                  67
NCBI Description
                  (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                  400864
Seq. ID
                  LIB3431-038-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q5031281
BLAST score
                  274
E value
                  4.0e-24
Match length
                  71
% identity
                  75
NCBI Description
                  (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  400865
Seq. ID
                  LIB3431-038-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  431
E value
                  2.0e-42
Match length
                  85
% identity
                  98
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  400866
Seq. ID
                  LIB3431-038-P1-K1-A7
Method
                  BLASTX
```

Method BLASTX
NCBI GI g282882
BLAST score 175
E value 2.0e-12
Match length 105
% identity 37

NCBI Description receptor-like protein kinase precursor - Arabidopsis

thaliana >gi_166848 (M84659) receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 400867

Seq. ID LIB3431-038-P1-K1-A8

Match length

142

```
BLASTX
Method
NCBI GI
                   q3822223
BLAST score
                   444
                   4.0e-44
E value
Match length
                   123
% identity
                   61
NCBI Description
                   (AF077955) branched-chain alpha keto-acid dehydrogenase E1
                  alpha subunit [Arabidopsis thaliana]
                   400868
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-B1
Method
                  BLASTX
                   g2293480
NCBI GI
BLAST score
                   431
E value
                   1.0e-42
Match length
                   85
                   98
% identity
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
                   400869
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-B10
Method
                  BLASTX
NCBI GI
                   g4689384
BLAST score
                   231
E value
                   4.0e-19
Match length
                   43
                   100
% identity
NCBI Description
                   (AF139467) LHCII type I chlorophyll a/b binding protein
                   [Vigna radiata]
Seq. No.
                   400870
Seq. ID
                   LIB3431-038-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g5734748
BLAST score
                   206
E value
                   4.0e-16
Match length
                   129
% identity
                   36
NCBI Description
                  (AC007651) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   400871
Seq. ID
                   LIB3431-038-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   g4959460
BLAST score
                   35
E value
                   5.0e-10
Match length
                   35
% identity
                   100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
                   400872
Seq. ID
                   LIB3431-038-P1-K1-B4
Method
                  BLASTX
NCBI GI
                   g2501190
BLAST score
                   602
E value
                   1.0e-62
```

51370

BLAST score

Match length

E value

759

139

5.0e-81

```
% identity
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                  >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi 596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
                  400873
Seq. No.
                  LIB3431-038-P1-K1-B5
Seq. ID
Method
                  BLASTX
                  g448445
NCBI GI
BLAST score
                  229
E value
                  7.0e-19
Match length
                  62
% identity
                  69
NCBI Description CFO ATP synthase:SUBUNIT=9 [Spinacia oleracea]
                  400874
Seq. No.
                  LIB3431-038-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g710308
NCBI GI
BLAST score
                  732
E value
                  8.0e-78
Match length
                  143
% identity
                  97
NCBI Description
                  (U11693) victorin binding protein [Avena sativa]
                  400875
Seq. No.
                  LIB3431-038-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q400879
BLAST score
                  383
                  6.0e-37
E value
Match length
                  135
% identity
                  60
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >gi_479690_pir__S35159 photosystem I chain psaN -
                  barley >gi_19095_emb_CAA47056_ (X66428) photosystem I
                  subunit N [Hordeum vulgare]
Seq. No.
                  400876
Seq. ID
                  LIB3431-038-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q4115918
BLAST score
                  213
E value
                  6.0e-17
Match length
                  50
                  82
% identity
NCBI Description
                  (AF118222) similar to nascent polypeptide associated
                  complex alpha chain [Arabidopsis thaliana]
                  400877
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g132105
```

51371

```
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
Seq. No.
                    400878
Seq. ID
                    LIB3431-038-P1-K1-C10
Method
                   BLASTX
NCBI GI
                    a167097
BLAST score
                    188
E value
                    9.0e-27
Match length
                    76
% identity
                    82
NCBI Description
                    (M55449) ribulose 1,5-bisphosphate carboxylase activase
                    [Hordeum vulgare]
Seq. No.
                    400879
Seq. ID
                    LIB3431-038-P1-K1-C11
Method
                    BLASTX
NCBI GI
                    q4204263
BLAST score
                    349
E value
                    6.0e-33
Match length
                    113
% identity
NCBI Description
                   (AC005223) 40409 [Arabidopsis thaliana]
Seq. No.
                    400880
Seq. ID
                    LIB3431-038-P1-K1-C12
Method
                    BLASTX
NCBI GI
                    q2072555
BLAST score
                    237
E value
                    8.0e-20
Match length
                    44
                    100
% identity
NCBI Description
                    (AF001396) metallothionein-like protein [Orvza sativa]
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                    400881
Seq. ID
                   LIB3431-038-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                    333
E value
                    4.0e-31
Match length
                   92
                   74
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
```

51372

[Oryza sativa]

>gi_227611_prf 1707316A chlorophyll a/b binding protein 1

```
Seq. No.
                  400882
Seq. ID
                  LIB3431-038-P1-K1-C3
Method
                  BLASTX
                  g733454
NCBI GI
                  191
BLAST score
E value
                  2.0e-14
Match length
                  38
                  97
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  400883
                  LIB3431-038-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  q417260
NCBI GI
BLAST score
                  176
E value
                  7.0e-13
Match length
                  38
                  84
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632
NCBI Description
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  400884
                  LIB3431-038-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  508
                  1.0e-51
E value
                  135
Match length
                  73
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  400885
Seq. ID
                  LIB3431-038-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q4678364
BLAST score
                  220
E value
                  8.0e-18
Match length
                  71
% identity
                  63
NCBI Description
                  (AL049659) putative protein [Arabidopsis thaliana]
Seq. No.
                  400886
Seq. ID
                  LIB3431-038-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g130274
BLAST score
                  337
E value
                  1.0e-31
Match length
                  63
                  100
% identity
NCBI Description PLASTOCYANIN >gi 82500 pir S06105 plastocyanin - rice
                  400887
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-D1
Method
                  BLASTX
```

51373

```
NCBI GI
                  q4056488
BLAST score
                  477
                  6.0e-48
E value
Match length
                  105
% identity
                  76
NCBI Description
                 (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                  400888
Seq. ID
                  LIB3431-038-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  q3063523
BLAST score
                  50
E value
                  6.0e-19
Match length
                  138
% identity
NCBI Description
                 Oryza sativa ribulose 1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
Seq. No.
                  400889
                  LIB3431-038-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3075488
BLAST score
                  483
E value
                  1.0e-48
                  93
Match length
                  100
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  400890
Seq. ID
                  LIB3431-038-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  552
E value
                  9.0e-57
Match length
                  117
% identity
                  90
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400891
                  LIB3431-038-P1-K1-D2
                  BLASTX
NCBI GI
                  q3914587
BLAST score
                  254
E value
                  9.0e-22
```

Seq. ID

Method

Match length 112 % identity 50 NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 1076711 pir S49992

ribulose-1,5-bisphosphate carboxylase/oxygenase - Aegilops

```
[Aegilops squarrosa]
                  400892
Seq. No.
                  LIB3431-038-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  586
E value
                  1.0e-60
Match length
                  144
                  78
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  400893
Seq. ID
                  LIB3431-038-P1-K1-D7
Method
                  BLASTX
                  g4582445
NCBI GI
BLAST score
                  269
E value
                  2.0e-23
Match length
                  64
% identity
                  70
NCBI Description
                  (AC007071) unknown protein [Arabidopsis thaliana]
                  >gi 4589952 gb AAD26470.1 AC007169 2 (AC007169) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  400894
                  LIB3431-038-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760334
BLAST score
                  294
E value
                  2.0e-26
                  76
Match length
% identity
                  64
NCBI Description
                  (AC002130) F1N21.5 [Arabidopsis thaliana]
Seq. No.
                  400895
Seq. ID
                  LIB3431-038-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1001532
BLAST score
                  251
E value
                  2.0e-21
Match length
                  93
                  52
% identity
NCBI Description
                  (D64000) hypothetical protein [Synechocystis sp.]
Seq. No.
                  400896
Seq. ID
                  LIB3431-038-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  638
                  8.0e-67
E value
Match length
                  140
% identity
                  81
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
```

squarrosa >gi 599620 emb CAA58150 (X83095) rbcS gene



>gi_226872_prf__1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 400897

Seq. ID LIB3431-038-P1-K1-E11

Method BLASTX
NCBI GI g115787
BLAST score 580
E value 5.0e-60
Match length 130
% identity 88

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 400898

Seq. ID LIB3431-038-P1-K1-E4

Method BLASTX
NCBI GI g3075488
BLAST score 518
E value 9.0e-53
Match length 117
% identity 85

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 400899

Seq. ID LIB3431-038-P1-K1-E5

Method BLASTX
NCBI GI g1617197
BLAST score 304
E value 1.0e-27
Match length 76
% identity 76

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 400900

Seq. ID LIB3431-038-P1-K1-E6

Method BLASTX
NCBI GI g4544399
BLAST score 597
E value 5.0e-62
Match length 128
% identity 84

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 400901

Seq. ID LIB3431-038-P1-K1-E7

Method BLASTX
NCBI GI g1777312
BLAST score 196
E value 5.0e-15
Match length 122
% identity 37

NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

400902 Seq. No. Seq. ID LIB3431-038-P1-K1-E9 Method BLASTX NCBI GI q542200 BLAST score 431 E value 1.0e-42 Match length 138 % identity 55 hypothetical protein - garden asparagus NCBI Description >gi 452714 emb CAA54526 (X77320) unknown [Asparagus officinalis] 400903 Seq. No. LIB3431-038-P1-K1-F1 Seq. ID Method BLASTX NCBI GI q132105 BLAST score 591 E value 3.0e-61 Match length 127 87 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 400904 Seq. No. Seq. ID LIB3431-038-P1-K1-F10 Method BLASTX NCBI GI q224293 BLAST score 409 E value 6.0e-40Match length 82 % identity 100 NCBI Description histone H4 [Triticum aestivum] Seq. No. 400905 Seq. ID LIB3431-038-P1-K1-F11 Method BLASTX NCBI GI g132105 BLAST score 322 E value 4.0e-46 Match length 110 % identity 87 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

```
sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
```

Seq. No. 400906 Seq. ID LIB3431-038-P1-K1-F2 Method BLASTN g6015437 NCBI GI BLAST score 35 E value 5.0e-10 Match length 35 % identity 100 NCBI Description Homo sapiens PEX1 mRNA, complete cds Seq. No. 400907 Seq. ID LIB3431-038-P1-K1-F3 Method BLASTX NCBI GI q2497903 BLAST score 220 E value 8.0e-18 Match length 59 % identity 68 NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like protein [Oryza sativa] >gi_1815628 (U43530) metallothionein-like type $\overline{2}$ [Oryza sativa] Seq. No. 400908 Seq. ID LIB3431-038-P1-K1-F4 Method BLASTX NCBI GI q3928097 BLAST score 213 E value 6.0e-17 Match length 94 % identity 47 NCBI Description (AC005770) unknown protein, 5' partial [Arabidopsis thaliana] Seq. No. 400909 Seq. ID LIB3431-038-P1-K1-F5 Method BLASTX NCBI GI q2407281 BLAST score 653 E value 1.0e-68 Match length 127 % identity NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] Seq. No. 400910 Seq. ID LIB3431-038-P1-K1-F6 Method BLASTX NCBI GI g548603 BLAST score 407 E value 1.0e-39 Match length 118 71 % identity

51378

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor -barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 400911

Seq. ID LIB3431-038-P1-K1-F9

Method BLASTX
NCBI GI g5360953
BLAST score 519
E value 7.0e-53
Match length 137
% identity 79

NCBI Description (AJ225059) v-ATPase subunit D [Arabidopsis thaliana]

Seq. No. 400912

Seq. ID LIB3431-038-P1-K1-G1

Method BLASTX
NCBI GI g1362150
BLAST score 546
E value 5.0e-56
Match length 112
% identity 89

NCBI Description hypothetical protein (clone AFN3) - wild oat (fragment)

>gi_726478 (U20000) putative ORF1 [Avena fatua]

Seq. No. 400913

Seq. ID LIB3431-038-P1-K1-G11

Method BLASTX
NCBI GI g5734640
BLAST score 550
E value 2.0e-56
Match length 145
% identity 81

NCBI Description (AP000391) Similar to Arabidopsis thaliana chromosome II

BAC F17K2 genomic sequence; hypothetical protein (AC003680)

[Oryza sativa]

Seq. No. 400914

Seq. ID LIB3431-038-P1-K1-G12

Method BLASTX
NCBI GI g132105
BLAST score 595
E value 9.0e-62
Match length 128
% identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 400915

Seq. ID LIB3431-038-P1-K1-G2

Seq. ID

400920

LIB3431-038-P1-K1-H12

```
Method
                   BLASTN
NCBI GI
                   q6015437
BLAST score
                   38
E value
                   8.0e-12
Match length
                   38
% identity
                   100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   400916
Seq. ID
                   LIB3431-038-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q3345477
BLAST score
                   476
E value
                   8.0e-48
Match length
                   137
% identity
                   69
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                   400917
Seq. ID
                  LIB3431-038-P1-K1-G8
Method
                  BLASTX
NCBI GI
                   q733454
BLAST score
                   604
E value
                  8.0e-63
Match length
                  138
% identity
                  83
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                   400918
Seq. ID
                  LIB3431-038-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q3024440
BLAST score
                  368
E value
                  3.0e-35
Match length
                  77
% identity
                  88
                  PROTEASOME DELTA CHAIN PRECURSOR (MULTICATALYTIC
NCBI Description
                  ENDOPEPTIDASE COMPLEX DELTA CHAIN)
                  >gi_1743356_emb_CAA70699_ (Y09505) proteasome delta subunit
                   [Nicotiana tabacum]
Seq. No.
                  400919
Seq. ID
                  LIB3431-038-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  760
E value
                  4.0e-81
Match length
                  144
% identity
                  100
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
```

400925

```
Method
                  BLASTX
NCBI GI
                  q2245109
BLAST score
                  361
E value
                  2.0e-34
                  117
Match length
% identity
                  60
NCBI Description
                  (Z97343) carboxyl-terminal proteinase like protein
                   [Arabidopsis thaliana]
Seq. No.
                  400921
Seq. ID
                  LIB3431-038-P1-K1-H2
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  400922
Seq. ID
                  LIB3431-038-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3834310
BLAST score
                  530
E value
                  4.0e-54
Match length
                  103
% identity
                  98
NCBI Description
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
                  gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                  gb N37265, gb H36151, gb Z34711, gb AA040983, and gb T22122
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  400923
Seq. ID
                  LIB3431-038-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  745
E value
                  2.0e-79
Match length
                  145
% identity
                  99
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  400924
Seq. ID
                  LIB3431-038-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q4335761
BLAST score
                  238
E value
                  7.0e-20
Match length
                  142
% identity
                  38
NCBI Description
                  (AC006284) unknown protein [Arabidopsis thaliana]
```

E value

5.0e-11

```
LIB3431-038-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  591
E value
                  3.0e-61
Match length
                  127
                  87
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400926
Seq. No.
                  LIB3431-038-P1-K1-H7
Seq. ID
Method
                  BLASTN
                  g1245938
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
% identity
                  100
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
NCBI Description
                  heart atrium, mRNA, 2998 nt]
                  400927
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g5007084
BLAST score
                  729
E value
                  2.0e-77
Match length
                  137
                  100
% identity
NCBI Description
                  (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
                  sativa]
Seq. No.
                  400928
                  LIB3431-038-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6006363
BLAST score
                  267
E value
                  3.0e-23
Match length
                  50
% identity
                  100
                  (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
NCBI Description
                  to a region of the predicted gene.; Similar to water stress
                  inducible protein (U74296) [Oryza sativa]
Seq. No.
                  400929
Seq. ID
                  LIB3431-038-P1-N1-A10
Method
                  BLASTX
NCBI GI
                  q3153151
BLAST score
                  162
```

```
Match length
                  100
% identity
NCBI Description
                   (AJ006296) chlorophyll a/b-binding protein [Hordeum
                  vulgare]
                  400930
Seq. No.
                  LIB3431-038-P1-N1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729535
BLAST score
                  416
E value
                  9.0e-41
Match length
                  80
% identity
                  91
NCBI Description
                  FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR
                   (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)
                   (FTR-B)
                  400931
Seq. No.
                  LIB3431-038-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6103011
BLAST score
                  394
E value
                  3.0e-38
Match length
                  84
% identity
                  48
NCBI Description
                  (X84225) precursor of photosystem II subunit (22KDa)
                  [Nicotiana tabacum]
                  400932
Seq. No.
                  LIB3431-038-P1-N1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3548808
BLAST score
                  244
E value
                  1.0e-20
Match length
                  69
% identity
                  64
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                  400933
Seq. ID
                  LIB3431-038-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  q5031281
BLAST score
                  181
E value
                  3.0e-13
Match length
                  41
% identity
                  76
NCBI Description (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  400934
Seq. ID
                  LIB3431-038-P1-N1-A5
Method
                  BLASTN
NCBI GI
                  q2331130
BLAST score
                  129
E value
                  3.0e-66
Match length
                  181
% identity
                  93
```

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete



cds

```
400935
Seq. No.
                  LIB3431-038-P1-N1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3822223
BLAST score
                  323
                  6.0e-30
E value
Match length
                  96
                  56
% identity
NCBI Description
                  (AF077955) branched-chain alpha keto-acid dehydrogenase E1
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  400936
Seq. ID
                  LIB3431-038-P1-N1-B1
Method
                  BLASTN
                  g2331130
NCBI GI
BLAST score
                  187
E value
                  1.0e-101
Match length
                  235
% identity
                  95
NCBI Description
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
Seq. No.
                  400937
Seq. ID
                  LIB3431-038-P1-N1-B10
Method
                  BLASTX
NCBI GI
                  g4689384
BLAST score
                  231
                  4.0e-19
E value
Match length
                  43
% identity
                  100
NCBI Description
                  (AF139467) LHCII type I chlorophyll a/b binding protein
                  [Vigna radiata]
Seq. No.
                  400938
Seq. ID
                  LIB3431-038-P1-N1-B3
Method
                  BLASTX
NCBI GI
                  g3192019
BLAST score
                  146
E value
                  4.0e-09
Match length
                  50
% identity
                  52
NCBI Description
                  (AL023797) uridylate kinase [Streptomyces coelicolor]
Seq. No.
                  400939
Seq. ID
                  LIB3431-038-P1-N1-B4
Method
                  BLASTX
NCBI GI
                  g2501190
BLAST score
                  155
E value
                  4.0e-10
Match length
                  51
% identity
                  69
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                  >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
```

NCBI GI

g11957

```
Seq. No.
                  400940
Seq. ID
                  LIB3431-038-P1-N1-B5
Method
                  BLASTX
NCBI GI
                  q461595
BLAST score
                  188
E value
                  5.0e-14
Match length
                  98
% identity
                  44
                  ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
NCBI Description
                  >gi_479533_pir__S34473 H+-transporting ATP synthase (EC
                  3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520
                  (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]
Seq. No.
                  400941
                  LIB3431-038-P1-N1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q710308
BLAST score
                  338
E value
                  1.0e-31
Match length
                  63
% identity
                  95
NCBI Description (U11693) victorin binding protein [Avena sativa]
                  400942
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-B8
Method
                  BLASTX
                  g1658271
NCBI GI
BLAST score
                  147
                  2.0e-09
E value
Match length
                  40
% identity
                  78
NCBI Description
                  (U74622) nascent polypeptide associated complex alpha chain
                  [Nicotiana tabacum]
Seq. No.
                  400943
Seq. ID
                  LIB3431-038-P1-N1-B9
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  354
E value
                  2.0e-33
Match length
                  65
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400944
Seq. ID
                  LIB3431-038-P1-N1-C1
Method
                  BLASTN
```

Method

NCBI GI

BLASTX

g417260

```
BLAST score
E value
                   1.0e-179
Match length
                   391
% identity
                   98
NCBI Description Rice complete chloroplast genome
Seq. No.
                   400945
Seq. ID
                   LIB3431-038-P1-N1-C10
Method
                   BLASTX
NCBI GI
                   q167097
BLAST score
                   151
E value
                   1.0e-21
Match length
                   63
% identity
                   86
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
Seq. No.
                   400946
Seq. ID
                   LIB3431-038-P1-N1-C12
Method
                  BLASTN
NCBI GI
                   q2072554
BLAST score
                   393
E value
                   0.0e + 00
Match length
                   393
% identity
                   100
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                   cds
Seq. No.
                   400947
Seq. ID
                  LIB3431-038-P1-N1-C2
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                   409
E value
                   6.0e-40
Match length
                   77
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  400948
Seq. ID
                  LIB3431-038-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  191
                  2.0e-14
E value
Match length
                  38
                  97
% identity
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                  400949
Seq. ID
                  LIB3431-038-P1-N1-C4
```

```
BLAST score
                   7.0e-13
E value
Match length
                   38
% identity
                   84
                  LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__$33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   400950
Seq. ID
                   LIB3431-038-P1-N1-C5
Method
                   BLASTX
NCBI GI
                   q3345477
BLAST score
                   188
                   4.0e-14
E value
Match length
                   34
% identity
                   100
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
                   400951
Seq. No.
                  LIB3431-038-P1-N1-C6
Seq. ID
Method
                  BLASTX
                   g4678364
NCBI GI
BLAST score
                   221
E value
                   7.0e-18
Match length
                   91
                  55
% identity
NCBI Description
                  (AL049659) putative protein [Arabidopsis thaliana]
Seq. No.
                   400952
                  LIB3431-038-P1-N1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q130274
BLAST score
                   492
E value
                   1.0e-49
Match length
                   96
% identity
                   98
NCBI Description PLASTOCYANIN >gi_82500_pir S06105 plastocyanin - rice
Seq. No.
                   400953
Seq. ID
                  LIB3431-038-P1-N1-D10
Method
                  BLASTX
NCBI GI
                   q671740
BLAST score
                   165
E value
                   2.0e-11
Match length
                   65
% identity
                  54
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                   400954
                  LIB3431-038-P1-N1-D11
```

Seq. ID LIB3431-03
Method BLASTX
NCBI GI g3075488
BLAST score 198
E value 3.0e-15

Match length 44 % identity 86

Match length

% identity

56

86

```
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  400955
Seq. ID
                  LIB3431-038-P1-N1-D12
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  197
E value
                  4.0e-15
Match length
                  62
                  63
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
Seq. No.
                  400956
Seq. ID
                  LIB3431-038-P1-N1-D2
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  208
E value
                  2.0e-16
Match length
                  48
% identity
                  85
NCBI Description
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
Seq. No.
                  400957
Seq. ID
                  LIB3431-038-P1-N1-D5
Method
                  BLASTX
NCBI GI
                  a131225
BLAST score
                  311
E value
                  2.0e-28
Match length
                  81
% identity
                  75
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  400958
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-D7
Method
                  BLASTX
NCBI GI
                  q4582445
BLAST score
                  269
                  1.0e-23
E value
Match length
                  64
% identity
                  70
NCBI Description
                  (AC007071) unknown protein [Arabidopsis thaliana]
                  >gi_4589952 gb AAD26470.1 AC007169 2 (AC007169) unknown
                  protein [Arabidopsis thaliana]
                  400959
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-E10
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  248
E value
                  4.0e-21
```

400965

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III CAB-8) >gi_19182_emb_CAA33330 (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum] Seq. No. 400960 Seq. ID LIB3431-038-P1-N1-E11 Method BLASTX NCBI GI g3036946 BLAST score 287 E value 1.0e-25 Match length 54 % identity 100 NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris] Seq. No. 400961 Seq. ID LIB3431-038-P1-N1-E4 Method BLASTX NCBI GI q3075488 BLAST score 326 3.0e-30 E value Match length 63 % identity 100 NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa] Seq. No. 400962 Seq. ID LIB3431-038-P1-N1-E5 Method BLASTX NCBI GI g1617197 BLAST score 244 E value 1.0e-20 Match length 50 % identity 90 NCBI Description (Z72488) CP12 [Nicotiana tabacum] Seq. No. 400963 Seq. ID LIB3431-038-P1-N1-E7 Method BLASTX NCBI GI g3256035 BLAST score 195 7.0e-15 E value Match length 67 % identity 55 NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum bicolor] Seq. No. 400964 Seq. ID LIB3431-038-P1-N1-E9 Method BLASTX NCBI GI q2586153 BLAST score 179 5.0e-13 E value 48 Match length % identity 65 NCBI Description (AF001530) ripening-associated protein [Musa acuminata]

```
Seq. ID
                   LIB3431-038-P1-N1-F1
Method
                   BLASTN
                   q3063523
NCBI GI
BLAST score
                   192
E value
                   1.0e-103
Match length
                   271
% identity
                   93
                   Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   400966
Seq. ID
                   LIB3431-038-P1-N1-F10
Method
                   BLASTX
NCBI GI
                   q70772
BLAST score
                   236
E value
                   9.0e-20
Match length
                   60
% identity
                   82
                  histone H4 - wheat >gi 70773 pir HSPM4 histone H4 - garden
NCBI Description
                   400967
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-F11
Method
                   BLASTX
                   g132105
NCBI GI
BLAST score
                   331
                   8.0e-31
E value
Match length
                   62
% identity
                   100
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400968
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-F4
Method
                   BLASTX
                   g3928097
NCBI GI
BLAST score
                   207
                   3.0e-16
E value
Match length
                   66
% identity
                   62
NCBI Description
                   (AC005770) unknown protein, 5' partial [Arabidopsis
                   thaliana]
                   400969
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-F5
Method
                   BLASTX
NCBI GI
                   g347451
BLAST score
                   197
                   4.0e-15
E value
                   37
Match length
```

```
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
                   400970
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-F6
Method
                  BLASTX
NCBI GI
                  g548603
BLAST score
                  535
E value
                   1.0e-54
Match length
                   109
% identity
                   94
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi 478404 pir JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                   400971
Seq. ID
                  LIB3431-038-P1-N1-G1
Method
                  BLASTX
NCBI GI
                   q1362150
BLAST score
                   388
E value
                   2.0e-37
Match length
                   81
% identity
                  hypothetical protein (clone AFN3) - wild oat (fragment)
NCBI Description
                  >gi 726478 (U20000) putative ORF1 [Avena fatua]
Seq. No.
                   400972
Seq. ID
                   LIB3431-038-P1-N1-G11
Method
                   BLASTN
NCBI GI
                   q5734616
BLAST score
                   397
E value
                   0.0e + 00
Match length
                   409
% identity
                   99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                   400973
Seq. ID
                   LIB3431-038-P1-N1-G12
Method
                   BLASTX
                   g132105
NCBI GI
BLAST score
                   315
E value
                   6.0e-29
Match length
                   60
% identity
                   98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

carboxylase S [Oryza sativa]

sativa] >gi 226375 prf 1508256A ribulose bisphosphate

```
Seq. ID
                  LIB3431-038-P1-N1-G3
Method
                  BLASTN
NCBI GI
                  q3789951
BLAST score
                  174
                  6.0e-93
E value
Match length
                  407
% identity
                  95
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  400975
Seq. ID
                  LIB3431-038-P1-N1-G6
Method
                  BLASTX
NCBI GI
                  q3345477
BLAST score
                  249
E value
                  3.0e-21
Match length
                  47
                  100
% identity
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  400976
Seq. ID
                  LIB3431-038-P1-N1-G8
Method
                  BLASTX
NCBI GI
                  q733456
BLAST score
                  352
E value
                  3.0e-33
Match length
                  73
% identity
                  95
NCBI Description
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
Seq. No.
                  400977
Seq. ID
                  LIB3431-038-P1-N1-H1
Method
                  BLASTX
NCBI GI
                  g2511594
BLAST score
                  337
                  2.0e-31
E value
Match length
                  84
                  75
% identity
NCBI Description
                  (Y13694) multicatalytic endopeptidase complex, proteasome
                  precursor, beta subunit [Arabidopsis thaliana]
                  >gi 2827525 emb CAA16533.1 (AL021633) multicatalytic
                  endopeptidase complex, proteasome precursor, beta subunit
                  [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                  proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.
                  400978
Seq. ID
                  LIB3431-038-P1-N1-H11
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  290
                  5.0e-26
E value
Match length
                  52
                  100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
```

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 400979

Seq. ID LIB3431-038-P1-N1-H12

Method BLASTX
NCBI GI g5174741
BLAST score 165
E value 2.0e-11
Match length 64
% identity 52

NCBI Description ubiquitin carboxyl-terminal esterase L3 (ubiquitin

thiolesterase) >gi_136682_sp_P15374_UBL3_HUMAN_UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (UCH-L3) (UBIQUITIN

THIOLESTERASE L3) >gi_108014_pir__A40085 ubiquitin carboxyl-terminal proteinase (EC 3.4.-.-) L3 - human >gi_2914274_pdb_1UCH__ Deubiquitinating Enzyme Uch-L3 (Human) At 1.8 Angstrom Resolution >gi_340074 (M30496) ubiquitin carboxyl-terminal hydrolase [Homo sapiens]

Seq. No. 400980

Seq. ID LIB3431-038-P1-N1-H3

Method BLASTX
NCBI GI g5381319
BLAST score 271
E value 9.0e-24
Match length 55
% identity 95

NCBI Description (AF091621) ubiquitin-conjugating enzyme E2 [Catharanthus

roseus]

Seq. No. 400981

Seq. ID LIB3431-038-P1-N1-H4

Method BLASTX
NCBI GI g289920
BLAST score 291
E value 4.0e-26
Match length 55
% identity 100

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 400982

Seq. ID LIB3431-038-P1-N1-H6

Method BLASTN
NCBI GI g3063523
BLAST score 58
E value 9.0e-24
Match length 146
% identity 85

NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 400983

Seq. ID LIB3431-038-P1-N1-H8

Method BLASTX NCBI GI g5007084



```
BLAST score
E value
                   3.0e-14
Match length
                   39
                  100
% identity
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
Seq. No.
                   400984
Seq. ID
                  LIB3431-038-P1-N1-H9
Method
                  BLASTN
NCBI GI
                  q6006355
BLAST score
                  198
E value
                  1.0e-107
Match length
                  391
% identity
                   99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  400985
Seq. ID
                  LIB3431-039-P1-K2-A10
Method
                  BLASTX
NCBI GI
                  q3885894
BLAST score
                  177
E value
                  3.0e-24
Match length
                  69
                  90
% identity
NCBI Description
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                  400986
Seq. ID
                  LIB3431-039-P1-K2-A6
Method
                  BLASTN
NCBI GI
                  g1835730
BLAST score
                  75
E value
                  2.0e-34
Match length
                  93
% identity
                  97
NCBI Description
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                  complete cds
Seq. No.
                  400987
Seq. ID
                  LIB3431-039-P1-K2-A7
Method
                  BLASTX
NCBI GI
                  g3808101
BLAST score
                  532
E value
                  2.0e-54
Match length
                  125
% identity
                  82
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
                  400988
Seq. ID
                  LIB3431-039-P1-K2-B1
Method
                  BLASTN
NCBI GI
                  q606816
BLAST score
                  53
E value
                  3.0e-21
Match length
                  57
```

NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete

98

% identity

Match length

% identity

30

100

```
Seq. No.
                   400989
Seq. ID
                   LIB3431-039-P1-K2-B10
Method
                   BLASTN
NCBI GI
                   g11957
BLAST score
                   378
E value
                   0.0e+00
Match length
                   411
% identity
                   98
NCBI Description Rice complete chloroplast genome
Seq. No.
                   400990
Seq. ID
                   LIB3431-039-P1-K2-B11
Method
                  BLASTN
NCBI GI
                   q11957
BLAST score
                   127
E value
                   4.0e-65
Match length
                   251
% identity
                   88
NCBI Description Rice complete chloroplast genome
Seq. No.
                   400991
Seq. ID
                  LIB3431-039-P1-K2-B2
Method
                  BLASTX
NCBI GI
                   q115772
BLAST score
                   189
E value
                   1.0e-25
Match length
                   62
% identity
                   94
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                  CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll a/b-binding
                  protein 1R precursor - rice >gi_20178_emb_CAA32108
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
                   400992
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-B3
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                   483
E value
                   9.0e-49
Match length
                  111
% identity
                   82
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
                   400993
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-B6
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  149
                  7.0e-10
E value
```

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

```
400994
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-B7
Method
                  BLASTX
NCBI GI
                  q3345477
BLAST score
                  626
                  2.0e-65
E value
Match length
                  120
% identity
                  99
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                  400995
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-B8
Method
                  BLASTX
NCBI GI
                  g131166
BLAST score
                  503
E value
                  3.0e-51
Match length
                  97
% identity
                  96
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi 82100 pir
                                                                         S00449
                  photosystem I chain II precursor - tomato >gi_170492
                   (M21344) photosystem I subunit II protein precursor
                  [Lycopersicon esculentum] >gi_226544_prf__1601516A
                  photosystem I reaction center II [Lycopersicon esculentum]
Seq. No.
                  400996
                  LIB3431-039-P1-K2-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541950
                  237
BLAST score
                  8.0e-20
E value
Match length
                  69
% identity
                  67
NCBI Description
                  SPCP1 protein - soybean >gi_310576 (L12257) nodulin-26
                  [Glycine max]
Seq. No.
                  400997
Seq. ID
                  LIB3431-039-P1-K2-C10
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  238
E value
                  5.0e-20
Match length
                  44
                  100
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  400998
Seq. ID
                  LIB3431-039-P1-K2-C3
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  612
E value
                  8.0e-64
Match length
                  114
% identity
                  96
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
```

```
Seq. No.
                   400999
Seq. ID
                   LIB3431-039-P1-K2-C4
Method
                   BLASTX
NCBI GI
                   g1706260
BLAST score
                   363
E value
                   6.0e-35
Match length
                   81
                   85
% identity
                   CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir $59597
NCBI Description
                   cysteine proteinase 1 precursor - maize
                   >gi_643597_dbj_BAA08244 (D45402) cysteine proteinase [Zea
                   mays]
                   401000
Seq. No.
                   LIB3431-039-P1-K2-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   772
                   2.0e-82
E value
Match length
                   144
% identity
                   99
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   401001
                   LIB3431-039-P1-K2-C6
Seq. ID
Method
                   BLASTX
                   g320618
NCBI GI
BLAST score
                   464
E value
                   2.0e-46
                   107
Match length
% identity
                   82
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   401002
Seq. ID
                   LIB3431-039-P1-K2-C7
Method
                   BLASTN
NCBI GI
                   q6015437
BLAST score
                   37
                   2.0e-11
E value
Match length
                   48
% identity
                   66
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   401003
Seq. ID
                   LIB3431-039-P1-K2-C8
Method
                   BLASTX
NCBI GI
                   g733454
BLAST score
                   369
E value
                   2.0e-35
                   100
Match length
% identity
                   71
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
```

```
Seq. No.
                  401004
Seq. ID
                  LIB3431-039-P1-K2-C9
Method
                  BLASTX
NCBI GI
                  q2072555
                  237
BLAST score
E value
                  7.0e-20
Match length
                  44
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  401005
Seq. No.
                  LIB3431-039-P1-K2-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  386
E value
                  1.0e-37
Match length
                  83
                  90
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  401006
Seq. ID
                  LIB3431-039-P1-K2-D3
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  225
E value
                  2.0e-18
Match length
                  43
% identity
                  100
NCBI Description
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  satival
Seq. No.
                  401007
Seq. ID
                  LIB3431-039-P1-K2-D4
Method
                  BLASTX
NCBI GI
                  q4680193
BLAST score
                  226
E value
                  4.0e-19
Match length
                  60
% identity
NCBI Description
                  (AF111710) putative farnesyl pyrophosphate synthase [Oryza
                  sativa subsp. indica]
Seq. No.
                  401008
Seq. ID
                  LIB3431-039-P1-K2-D6
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  5.0e-20
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
```

>qi 6103441 qb AAF03603.1 (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 401009

LIB3431-039-P1-K2-D7 Seq. ID

Method BLASTX NCBI GI g320618 BLAST score 254 E value 8.0e-22 Match length 72 % identity

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 401010

LIB3431-039-P1-K2-E2 Seq. ID

Method BLASTX NCBI GI q1235664 BLAST score 549 E value 9.0e-57 Match length 121 % identity 56

(U37936) novel calmodulin-like protein [Oryza sativa] NCBI Description

>qi 3171148 (AF064456) calmodulin-like protein [Oryza

satīva subsp. indica]

Seq. No. 401011

Seq. ID LIB3431-039-P1-K2-E6

Method BLASTN NCBI GI g2570510 BLAST score 137 E value 3.0e-71 Match length 148 % identity 98

Oryza sativa chlorophyll a-b binding protein mRNA, complete NCBI Description

cds

401012 Seq. No.

Seq. ID LIB3431-039-P1-K2-E7

Method BLASTX NCBI GI q132105 BLAST score 600 2.0e-62 E value Match length 129 % identity 88

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase ($\overline{\text{EC}}$ 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

```
Seq. No.
                  401013
Seq. ID
                  LIB3431-039-P1-K2-E9
Method
                  BLASTX
                  g1332579
NCBI GI
                  239
BLAST score
                  5.0e-20
E value
                  47
Match length
% identity
                  10
                 (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                  401014
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-F1
Method
                  BLASTX
NCBI GI
                  q1729971
BLAST score
                  233
E value
                  9.0e-20
Match length
                  59
% identity
                  80
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
Seq. No.
                  401015
Seq. ID
                  LIB3431-039-P1-K2-F2
Method
                  BLASTX
NCBI GI
                  q3885886
BLAST score
                  665
E value
                  4.0e-70
Match length
                  123
                  99
% identity
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.
                  401016
Seq. ID
                  LIB3431-039-P1-K2-F4
Method
                  BLASTN
NCBI GI
                  q4519191
BLAST score
                  35
E value
                  3.0e-10
Match length
                  71
                  87
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K9P8, complete sequence
Seq. No.
                  401017
Seq. ID
                  LIB3431-039-P1-K2-F6
Method
                  BLASTX
NCBI GI
                  q2598589
BLAST score
                  227
                  3.0e-21
E value
Match length
                  82
% identity
                  65
NCBI Description (Y15367) MtN19 [Medicago truncatula]
                  401018
Seq. No.
                  LIB3431-039-P1-K2-F7
Seq. ID
```

```
Method
                  BLASTX
NCBI GI
                  a5729704
BLAST score
                  249
E value
                  3.0e-21
                  102
Match length
% identity
                  45
NCBI Description
                  (AC007927) unknown protein, 5' partial [Arabidopsis
                  thaliana]
                  401019
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-F8
Method
                  BLASTX
                  g1773330
NCBI GI
BLAST score
                  636
                  2.0e-66
E value
Match length
                  148
% identity
                  84
NCBI Description (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
Seq. No.
                  401020
                  LIB3431-039-P1-K2-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2073379
BLAST score
                  228
                  1.0e-125
E value
Match length
                  243
% identity
                  98
NCBI Description Rice CP26 mRNA, partial sequence
                  401021
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-G10
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  35
E value
                  5.0e-10
Match length
                  35
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  401022
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-G12
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  417
                  6.0e-41
E value
Match length
                  122
% identity
```

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

401023 Seq. No.

Seq. ID LIB3431-039-P1-K2-G2

Method BLASTX NCBI GI g1729971 BLAST score 238 4.0e-20 E value

```
Match length
                    66
% identity
                    74
NCBI Description
                   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                    (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                    rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                    401024
Seq. No.
                   LIB3431-039-P1-K2-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                    g2462762
BLAST score
                    337
E value
                    3.0e-39
Match length
                    121
% identity
                    69
                    (AC002292) Highly similar to auxin-induced protein
NCBI Description
                    (aldo/keto reductase family) [Arabidopsis thaliana]
                    401025
Seq. No.
                   LIB3431-039-P1-K2-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                    g3063524
BLAST score
                    184
E value
                    3.0e-14
Match length
                    51
                    75
% identity
                    (AF052305) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                    subunit [Oryza sativa]
Seq. No.
                    401026
Seq. ID
                   LIB3431-039-P1-K2-G5
Method
                   BLASTX
NCBI GI
                    g82080
BLAST score
                    364
                    9.0e-35
E value
Match length
                    113
% identity
                    64
                    chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                    >gi 226872 prf 1609235A chlorophyll a/b binding protein
                    [Lycopersicon esculentum]
                    401027
Seq. No.
Seq. ID
                    LIB3431-039-P1-K2-G6
Method
                    BLASTX
NCBI GI
                    q320618
BLAST score
                    199
E value
                    9.0e-16
Match length
                    57
% identity
                    72
                   chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                    >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
```

401028

LIB3431-039-P1-K2-G8

Seq. No. Seq. ID

NCBI GI

g132105

```
Method
                  BLASTX
NCBI GI
                  q2464852
BLAST score
                  206
E value
                  4.0e-16
Match length
                  104
                  45
% identity
NCBI Description
                  (Z99707) putative protein [Arabidopsis thaliana]
                  401029
Seq. No.
                  LIB3431-039-P1-K2-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  544
                  6.0e-56
E value
Match length
                  103
                  99
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  401030
Seq. No.
                  LIB3431-039-P1-K2-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3395440
BLAST score
                  229
                  6.0e-19
E value
Match length
                  76
% identity
                  50
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  401031
Seq. No.
                  LIB3431-039-P1-K2-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3328122
BLAST score
                  245
E value
                  2.0e-21
Match length
                   95
% identity
                   65
NCBI Description
                   (AF073473) phosphoglycerate kinase precursor [Solanum
                  tuberosum]
                   401032
Seq. No.
                  LIB3431-039-P1-K2-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4835754
                  220
BLAST score
                   4.0e-18
E value
Match length
                  83
% identity
                  59
                   (AC007202) Is a member of the PF 00162 Phosphoglycerate
NCBI Description
                  kinase family. ESTs gb_N38721, gb_T22178, gb_R90345,
                  gb R90715, gb T21140, gb T46295, gb H37082, gb T46076,
                  gb N37132, gb AA597649, gb AI100648 and gb Z48462 c
                   401033
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-H6
                  BLASTX
Method
```



BLAST score 349 E value 4.0e-33 Match length 87 % identity 80

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 401034

Seq. ID LIB3431-039-P1-K2-H8

Method BLASTX
NCBI GI g129915
BLAST score 562
E value 6.0e-58
Match length 122
% identity 89

NCBI Description PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR

>gi_66912_pir__TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
precursor, chloroplast - wheat >gi_21833_emb_CAA33303_
(X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum

aestivum] >gi_3293043_emb_CAA51931_ (X73528)
phosphoglycerate kinase [Triticum aestivum]

Seq. No. 401035

Seq. ID LIB3431-039-P1-N1-A10

Method BLASTN
NCBI GI g3885893
BLAST score 216
E value 1.0e-118
Match length 259
% identity 96

NCBI Description Oryza sativa photosystem-1 H subunit GOS5 (PSI-H) mRNA,

complete cds

Seq. No. 401036

Seq. ID LIB3431-039-P1-N1-A4

Method BLASTX
NCBI GI g3913641
BLAST score 358
E value 4.0e-34
Match length 69
% identity 100

NCBI Description FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)

>gi 3041777 dbj BAA25423_ (AB007194)

fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 401037

Seq. ID LIB3431-039-P1-N1-A5

Method BLASTX NCBI GI g417744



BLAST score 287 E value 1.0e-25 Match length 56 % identity 96

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi 169663 (M81885)

S-adenosylhomocysteine hydrolase [Petroselinum crispum]

Seq. No. 401038

Seq. ID LIB3431-039-P1-N1-A6

Method BLASTX
NCBI GI g1835731
BLAST score 403
E value 3.0e-39
Match length 89
% identity 88

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401039

Seq. ID LIB3431-039-P1-N1-A7

Method BLASTX
NCBI GI g3808101
BLAST score 350
E value 5.0e-33
Match length 80
% identity 90

NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 401040

Seq. ID LIB3431-039-P1-N1-A9

Method BLASTX
NCBI GI g1707008
BLAST score 384
E value 4.0e-37
Match length 92
% identity 78

NCBI Description (U78721) 30S ribosomal protein S5 isolog [Arabidopsis

thaliana]

Seq. No. 401041

Seq. ID LIB3431-039-P1-N1-B10

Method BLASTN
NCBI GI g11957
BLAST score 256
E value 1.0e-142
Match length 464
% identity 97

NCBI Description Rice complete chloroplast genome

Seq. No. 401042

Seq. ID LIB3431-039-P1-N1-B2

Method BLASTX
NCBI GI g3036951
BLAST score 333
E value 4.0e-31
Match length 64
% identity 100

(AB012639) light harvesting chlorophyll a/b-binding protein NCBI Description [Nicotiana sylvestris] 401043 Seq. No. LIB3431-039-P1-N1-B3 Seq. ID BLASTX Method g733454 NCBI GI 383 BLAST score 6.0e-37 E value 78 Match length 95 % identity (U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description [Zea mays] Seq. No. 401044 LIB3431-039-P1-N1-B5 Seq. ID BLASTX Method g113170 NCBI GI BLAST score 239 5.0e-20 E value Match length 66 71 % identity ACYL CARRIER PROTEIN II PRECURSOR (ACP II) NCBI Description >gi_99531_pir__S12310 acyl carrier protein II - spinach >gi 21232 emb CAA36288 (X52065) acyl carrier protein II [Spinacia oleracea] 401045 Seq. No. LIB3431-039-P1-N1-B6 Seq. ID BLASTX Method g3126854 NCBI GI 345 BLAST score 2.0e-32 E value Match length 65 100 % identity (AF061577) chlorophyll a/b binding protein [Oryza sativa] NCBI Description 401046 Seq. No. LIB3431-039-P1-N1-B7 Seq. ID Method BLASTX q3345477 NCBI GI

Method BLASTX
NCBI GI g3345477
BLAST score 226
E value 2.0e-18
Match length 42
% identity 100

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 401047

Seq. ID LIB3431-039-P1-N1-B8

Method BLASTN
NCBI GI g167084
BLAST score 35
E value 3.0e-10
Match length 47
% identity 94

NCBI Description Barley PSI-D subunit of photosystem I (PsaD) mRNA, complete

cds

401053

```
401048
Seq. No.
                  LIB3431-039-P1-N1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541951
BLAST score
                  421
E value
                  2.0e-41
Match length
                  95
                  80
% identity
                  SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
NCBI Description
                  [Glycine max]
Seq. No.
                  401049
                  LIB3431-039-P1-N1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q289920
BLAST score
                  177
                  7.0e-13
E value
Match length
                  34
                  94
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  401050
Seq. No.
                  LIB3431-039-P1-N1-C11
Seq. ID
Method
                  BLASTX
                  g2911043
NCBI GI
                  143
BLAST score
                  9.0e-09
E value
Match length
                  59
                  47
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
                  401051
Seq. No.
                  LIB3431-039-P1-N1-C3
Seq. ID
Method
                  BLASTX
                  g3868758
NCBI GI
                  552
BLAST score
                  1.0e-56
E value
Match length
                  112
% identity
                   91
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  401052
Seq. No.
Seq. ID
                  LIB3431-039-P1-N1-C4
Method
                  BLASTX
NCBI GI
                  q1706260
BLAST score
                   349
E value
                   7.0e-33
Match length
                   67
                  94
% identity
NCBI Description
                  CYSTEINE PROTEINASE 1 PRECURSOR >qi 2118131 pir S59597
                   cysteine proteinase 1 precursor - maize
                  >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                  mays]
```



```
LIB3431-039-P1-N1-C5
Seq. ID
                  BLASTX
Method
                  g3126854
NCBI GI
                  299
BLAST score
                  5.0e-27
E value
                  58
Match length
                  98
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  401054
                  LIB3431-039-P1-N1-C6
Seq. ID
                  BLASTX
Method
                  q3036946
NCBI GI
                  313
BLAST score
E value
                  8.0e-29
Match length
                  61
% identity
                  98
                  (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
Seq. No.
                  401055
                  LIB3431-039-P1-N1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2073379
BLAST score
                  71
E value
                  1.0e-31
Match length
                  139
                  86
% identity
NCBI Description Rice CP26 mRNA, partial sequence
                  401056
Seq. No.
                  LIB3431-039-P1-N1-C9
Seq. ID
                  BLASTN
Method
                  g2072554
NCBI GI
                  277
BLAST score
E value
                  1.0e-154
                  341
Match length
                  95
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
Seq. No.
                  401057
                  LIB3431-039-P1-N1-D3
Seq. ID
                  BLASTN
Method
                  g218209
NCBI GI
BLAST score
                  48
                  8.0e-18
E value
Match length
                  68
                  93
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
```

Seq. ID LIB3431-039-P1-N1-D4

Method BLASTX NCBI GI g4115416

```
BLAST score
E value
                  1.0e-13
                  60
Match length
                  55
% identity
                  (AB021979) farnesyl diphosphate synthase [Oryza sativa]
NCBI Description
                  401059
Seq. No.
                  LIB3431-039-P1-N1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522941
BLAST score
                  231
                  5.0e-19
E value
Match length
                  50
% identity
                  86
                   (AC004411) putative peptide chain release factor
NCBI Description
                   [Arabidopsis thaliana]
                  401060
Seq. No.
                  LIB3431-039-P1-N1-D6
Seq. ID
                  BLASTX
Method
                  g2072555
NCBI GI
                  237
BLAST score
                  1.0e-19
E value
Match length
                   44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   401061
Seq. No.
                  LIB3431-039-P1-N1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3036949
BLAST score
                   276
                   2.0e-24
E value
Match length
                   57
                   93
% identity
                  (AB012638) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
Seq. No.
                   401062
                   LIB3431-039-P1-N1-E4
Seq. ID
Method
                   BLASTX
                   g4455174
NCBI GI
BLAST score
                   256
                   4.0e-22
E value
                   77
Match length
% identity
                   62
                  (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401063
                   LIB3431-039-P1-N1-E6
```

Seq. ID

Method BLASTX NCBI GI g4689380 BLAST score 266 3.0e-23 E value Match length 55



% identity 93

NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein

[Vigna radiata]

Seq. No. 401064

Seq. ID LIB3431-039-P1-N1-E7

Method BLASTX
NCBI GI g671740
BLAST score 433
E value 9.0e-43
Match length 78
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 401065

Seq. ID LIB3431-039-P1-N1-F3

Method BLASTX
NCBI GI g464980
BLAST score 415
E value 1.0e-40
Match length 80
% identity 96

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 166422 (L06967)

ubiquitin carrier protein [Medicago sativa]

Seq. No. 401066

Seq. ID LIB3431-039-P1-N1-F6

Method BLASTX
NCBI GI g2598589
BLAST score 234
E value 2.0e-19
Match length 70
% identity 60

NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 401067

Seq. ID LIB3431-039-P1-N1-F7

Method BLASTX
NCBI GI g5729704
BLAST score 249
E value 3.0e-21
Match length 102
% identity 45

NCBI Description (AC007927) unknown protein, 5' partial [Arabidopsis

thaliana]

Seq. No. 401068

Seq. ID LIB3431-039-P1-N1-F8

Method BLASTN
NCBI GI g2570514
BLAST score 287
E value 1.0e-160
Match length 335
% identity 96

NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

```
401069
Seq. No.
                   LIB3431-039-P1-N1-F9
Seq. ID
Method
                   BLASTN
                   q2073379
NCBI GI
                   168
BLAST score
                   2.0e-89
E value
                   243
Match length
₹ identity
                   92
NCBI Description Rice CP26 mRNA, partial sequence
                   401070
Seq. No.
Seq. ID
                   LIB3431-039-P1-N1-G1
Method
                   BLASTX
                   a1168587
NCBI GI
                   200
BLAST score
                   2.0e-15
E value
                   45
Match length
                   87
% identity
                   ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_1084467_pir__S43728 H+-transporting ATP synthase (EC
                   3.6.1.34) - sorghum >gi_311231_emb_CAA46803_ (X66004)
                   H(+)-transporting ATP synthase [Sorghum bicolor]
Seq. No.
                   401071
                   LIB3431-039-P1-N1-G10
Seq. ID
                   BLASTX
Method
                   g1296955
NCBI GI
BLAST score
                   396
E value
                   2.0e-38
                   76
Match length
                   45
 % identity
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]
                   401072
 Seq. No.
                   LIB3431-039-P1-N1-G11
 Seq. ID
 Method
                   BLASTX
                   g1296955
 NCBI GI
                   320
 BLAST score
 E value
                   2.0e-29
 Match length
                   73
                   39
 % identity
 NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]
 Seq. No.
                   401073
                   LIB3431-039-P1-N1-G12
 Seq. ID
                   BLASTX
 Method
                   q115813
 NCBI GI
 BLAST score
                   257
                   4.0e-22
 E value
 Match length
                   61
                   82
 % identity
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
 NCBI Description
                   CAB-8) >gi_19182_emb CAA33330 (X15258) Type III
                    chlorophyll a/b-binding protein [Lycopersicon esculentum]
```

401074

Seq. No.

Seq. ID

NCBI GI

Method

```
LIB3431-039-P1-N1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1729971
                  296
BLAST score
                  7.0e-27
E value
Match length
                  54
% identity
                  98
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                  sativa]
Seq. No.
                  401075
Seq. ID
                  LIB3431-039-P1-N1-G3
Method
                  BLASTX
NCBI GI
                  g2462750
BLAST score
                  277
E value
                  2.0e-24
Match length
                  72
% identity
                  71
                 (AC002292) Highly similar to auxin-induced protein
NCBI Description
                  (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  401076
Seq. ID
                  LIB3431-039-P1-N1-G4
Method
                  BLASTX
                  g132105
NCBI GI
BLAST score
                  416
                  1.0e-40
E value
Match length
                  75
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401077
Seq. No.
Seq. ID
                  LIB3431-039-P1-N1-G5
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  257
                  4.0e-22
E value
Match length
                  61
% identity
                  82
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  401078
```

51412

LIB3431-039-P1-N1-G6

BLASTX

g115787



```
BLAST score
                  6.0e-40
E value
                  77
Match length
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  401079
Seq. No.
                  LIB3431-039-P1-N1-G7
Seq. ID
Method
                  BLASTX
                  g4206765
NCBI GI
BLAST score
                  180
                  5.0e-13
E value
Match length
                  77
                  52
% identity
                  (AF104329) putative type 1 membrane protein [Arabidopsis
NCBI Description
                  thaliana]
                  401080
Seq. No.
                  LIB3431-039-P1-N1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2464852
BLAST score
                  171
                  5.0e-12
E value
Match length
                  80
                  49
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                  401081
Seq. No.
                  LIB3431-039-P1-N1-H3
Seq. ID
Method
                  BLASTX
                  q1708424
NCBI GI
BLAST score
                  267
E value
                  3.0e-23
Match length
                  61
% identity
                  74
NCBI Description
                  ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590)
                  isoflavone reductase-like protein [Lupinus albus]
                  401082
Seq. No.
                  LIB3431-039-P1-N1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  380
                  2.0e-36
E value
Match length
                  69
                  100
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct
```

Seq. ID LIB3431-039-P1-N1-H8

Method BLASTX NCBI GI g3738261

```
BLAST score
                  1.0e-22
E value
Match length
                  62
% identity
                  89
                  (AB018412) chloroplast phosphoglycerate kinase [Populus
NCBI Description
                  nigra]
                  401084
Seq. No.
                  LIB3431-040-P1-K2-A1
Seq. ID
Method
                  BLASTX
                  g2959781
NCBI GI
                  193
BLAST score
                  3.0e-15
E value
Match length
                  60
% identity
                  65
                  (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                  401085
Seq. No.
                  LIB3431-040-P1-K2-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1370198
BLAST score
                  295
                  8.0e-27
E value
Match length
                  87
% identity
                  67
                  (Z73948) RAB8E [Lotus japonicus]
NCBI Description
Seq. No.
                  401086
                  LIB3431-040-P1-K2-A8
Seq. ID
                  BLASTN
Method
NCBI GI
                  q218184
BLAST score
                  59
                  5.0e-25
E value
                  80
Match length
% identity
                  91
NCBI Description Rice mRNA for oryzain gamma (EC 3.4.22)
                  401087
Seq. No.
                  LIB3431-040-P1-K2-A9
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4138289
BLAST score
                  118
                  9.0e-60
E value
Match length
                  138
                  96
% identity
NCBI Description Oryza sativa mRNA for thioredoxin M
                  401088
Seq. No.
                  LIB3431-040-P1-K2-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3288821
BLAST score
                  436
E value
                   4.0e-43
Match length
                  109
                  76
% identity
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
```

transaminase [Arabidopsis thaliana]

>gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

401089 Seq. No. LIB3431-040-P1-K2-B3 Seq. ID Method BLASTX NCBI GI q871931 BLAST score 415 E value 1.0e-40 Match length 104 84 % identity (D30763) ferredoxin [Oryza sativa] NCBI Description Seq. No. 401090 LIB3431-040-P1-K2-B4 Seq. ID Method BLASTX NCBI GI q2244847 BLAST score 152 E value 3.0e-10 79 Match length 44 % identity (Z97337) hydroxyproline-rich glycoprotein homolog NCBI Description [Arabidopsis thaliana] Seq. No. 401091 LIB3431-040-P1-K2-B5 Seq. ID Method BLASTX q132105 NCBI GI BLAST score 342 2.0e-32 E value 70 Match length % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi 68094 pir_ RKRZS9 ribulose-bisphosphate carboxylase ($\overline{\text{EC 4.1.1.39}}$) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

 Seq. No.
 401092

 Seq. ID
 LIB3431-040-P1-K2-B6

 Method
 BLASTX

 NCBI GI
 g132105

 BLAST score
 339

 E value
 8.0e-32

Match length 133 % identity 47

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor (clone posssilise) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 401093

Seq. ID LIB3431-040-P1-K2-B7

Method BLASTX
NCBI GI g1353352
BLAST score 302
E value 2.0e-27
Match length 94
% identity 66

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

reinhardtii]

Seq. No. 401094

Seq. ID LIB3431-040-P1-K2-C1

Method BLASTX
NCBI GI g114521
BLAST score 520
E value 6.0e-53
Match length 127
% identity 86

NCBI Description ATP SYNTHASE ALPHA CHAIN >gi_67827_pir_PWRZA

H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - rice chloroplast >gi_11979_emb_CAA33993_ (X15901) ATPase alpha subunit [Oryza sativa] >gi_226696_prf__1603356X

ATPase alpha [Oryza sativa]

Seq. No. 401095

Seq. ID LIB3431-040-P1-K2-C11

Method BLASTX
NCBI GI g3126854
BLAST score 520
E value 7.0e-53
Match length 104
% identity 96

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401096

Seq. ID LIB3431-040-P1-K2-C12

Method BLASTX
NCBI GI g231610
BLAST score 193
E value 5.0e-15
Match length 54
% identity 65

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 401097

Seq. ID LIB3431-040-P1-K2-C2

Method BLASTN
NCBI GI g218207
BLAST score 165

```
E value
                  1.0e-87
                  253
Match length
                  91
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
                  401098
Seq. No.
                  LIB3431-040-P1-K2-C3
Seq. ID
                  BLASTX
Method
                  g2130042
NCBI GI
                  486
BLAST score
                  6.0e-56
E value
Match length
                  126
% identity
                  92
                  Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916)
NCBI Description
                  protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                  vulgare]
                  401099
Seq. No.
                  LIB3431-040-P1-K2-C4
Seq. ID
                  BLASTN
Method
                  g5295936
NCBI GI
BLAST score
                  36
                  3.0e-11
E value
                  48
Match length
                  94
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
                  complete sequence
                  401100
Seq. No.
                  LIB3431-040-P1-K2-C5
Seq. ID
                  BLASTX
Method
                  g3559814
NCBI GI
BLAST score
                  658
                   4.0e-69
E value
                  146
Match length
                  86
% identity
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
                   401101
Seq. No.
                  LIB3431-040-P1-K2-C6
Seq. ID
                  BLASTX
Method
                   q2501356
NCBI GI
BLAST score
                   523
                   3.0e-53
E value
                   139
Match length
                   74
% identity
                  TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
NCBI Description
                   >gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor
                   [Solanum tuberosum]
                   401102
Seq. No.
                   LIB3431-040-P1-K2-C7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4995921
```

51417

230

BLAST score

```
E value
                  4.0e-19
Match length
                  56
% identity
                  79
                  (AJ006708) HMG1 protein [Zea mays]
NCBI Description
                  401103
Seq. No.
                  LIB3431-040-P1-K2-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1747294
BLAST score
                  613
                  8.0e-64
E value
                  141
Match length
% identity
                  86
NCBI Description
                 (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
                  401104
Seq. No.
                  LIB3431-040-P1-K2-D1
Seq. ID
Method
                  BLASTN
                  g5042437
NCBI GI
BLAST score
                  199
                  1.0e-108
E value
                  199
Match length
                  100
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                  401105
                  LIB3431-040-P1-K2-D11
Seq. ID
Method
                  BLASTX
                  g2570511
NCBI GI
BLAST score
                  648
E value
                  6.0e-68
Match length
                  127
% identity
                  96
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                  401106
Seq. ID
                  LIB3431-040-P1-K2-D12
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  472
                  2.0e-47
E value
Match length
                  96
% identity
                  95
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
                  401107
Seq. No.
                  LIB3431-040-P1-K2-D2
Seq. ID
                  BLASTX
```

Method NCBI GI q3914587 BLAST score 144 E value 3.0e-09 Match length 30 100 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_1076711_pir__S49992

ribulose-1,5-bisphosphate carboxylase/oxygenase - Aegilops squarrosa >gi_599620_emb_CAA58150_ (X83095) rbcS gene

[Aegilops squarrosa]

401108 Seq. No. LIB3431-040-P1-K2-D4 Seq. ID BLASTX Method NCBI GI q132105 BLAST score 559 1.0e-57 E value 122 Match length 86 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9 ribulose-bisphosphate carboxylase ($\overline{\text{EC}}$ 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 401109 Seq. No. LIB3431-040-P1-K2-D8 Seq. ID Method BLASTX g3345477 NCBI GI BLAST score 218 6.0e-18 E value 58 Match length 69 % identity (AB016283) carbonic anhydrase [Oryza sativa] NCBI Description Seq. No. 401110 LIB3431-040-P1-K2-E1 Seq. ID Method BLASTX q115787 NCBI GI BLAST score 405 1.0e-39 E value Match length 90 91 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 401111 Seq. No. LIB3431-040-P1-K2-E10 Seq. ID Method BLASTX g4490317 NCBI GI BLAST score 364 1.0e-34 E value Match length 133 % identity 52 (AL035678) putative protein [Arabidopsis thaliana] NCBI Description

51419

401112

BLASTX

LIB3431-040-P1-K2-E11

Seq. No. Seq. ID

Method

```
NCBI GI
                  q4490317
BLAST score
                  319
                  3.0e-29
E value
                  158
Match length
% identity
                  42
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  401113
Seq. ID
                  LIB3431-040-P1-K2-E12
Method
                  BLASTX
NCBI GI
                  q729668
BLAST score
                  228
E value
                  1.0e-18
                  66
Match length
% identity
                   61
                  HISTONE H1 >gi_2147479_pir__S65059 histone H1,
NCBI Description
                  drought-inducible - Lycopersicon pennellii >gi_436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.
                   401114
Seq. ID
                  LIB3431-040-P1-K2-E2
Method
                  BLASTX
NCBI GI
                  g120661
BLAST score
                  198
                  1.0e-16
E value
Match length
                  90
% identity
                   60
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                   PRECURSOR >gi 170237 (M14417) glyceraldehyde-3-phosphate
                   dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                   401115
Seq. ID
                  LIB3431-040-P1-K2-E3
Method
                  BLASTX
NCBI GI
                   q132105
BLAST score
                   503
E value
                   3.0e~51
Match length
                   104
% identity
                   88
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   401116
Seq. No.
                  LIB3431-040-P1-K2-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                   254
                   3.0e-22
E value
Match length
                   68
```

51420

75

% identity

```
(AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  401117
Seq. No.
                  LIB3431-040-P1-K2-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3819221
BLAST score
                  84
                  3.0e-39
E value
                  282
Match length
                  83
% identity
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0721
Seq. No.
                  401118
                  LIB3431-040-P1-K2-E8
Seq. ID
Method
                  BLASTX
                  g2407281
NCBI GI
                  455
BLAST score
E value
                  2.0e-45
Match length
                  119
                  77
% identity
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  401119
                  LIB3431-040-P1-K2-E9
Seq. ID
Method
                  BLASTX
                  g1174745
NCBI GI
BLAST score
                  359
E value
                  3.0e-34
Match length
                  80
                  89
% identity
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
                  >gi_1363523_pir__S53761 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - rye
                  >gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
                  [Secale cereale] >gi_1095494_prf__2109226B triosephosphate
                  isomerase [Secale cereale]
Seq. No.
                  401120
                  LIB3431-040-P1-K2-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3885894
BLAST score
                  507
E value
                  2.0e-51
Match length
                  132
                  77
% identity
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                  401121
                  LIB3431-040-P1-K2-F11
Seq. ID
Method
                  BLASTX
                  g2104959
NCBI GI
BLAST score
                  324
E value
                  2.0e-30
                  77
Match length
                  74
% identity
```

```
401122
Seq. No.
                  LIB3431-040-P1-K2-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g120657
BLAST score
                  293
                  2.0e-27
E value
Match length
                  89
                  79
% identity
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi_66024_pir__DEZMG3
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  maize >gi 168479 (M18976) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
                  401123
Seq. No.
                  LIB3431-040-P1-K2-F5
Seq. ID
Method
                  BLASTX
                  g4455158
NCBI GI
BLAST score
                  249
                  4.0e-21
E value
                  71
Match length
% identity
                  63
NCBI Description (AL021687) kinase-like protein [Arabidopsis thaliana]
                  401124
Seq. No.
                  LIB3431-040-P1-K2-F8
Seq. ID
Method
                  BLASTX
                  g3850581
NCBI GI
                  252
BLAST score
                  1.0e-21
E value
Match length
                  84
% identity
                  60
NCBI Description (AC005278) EST gb N96383 comes from this gene. [Arabidopsis
                  thaliana]
                  401125
Seq. No.
                  LIB3431-040-P1-K2-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q596077
BLAST score
                  62
E value
                  1.0e-26
Match length
                  78
                  95
% identity
NCBI Description Zea mays thiamine biosynthetic enzyme (thil-1) mRNA,
                  complete cds
Seq. No.
                  401126
Seq. ID
                  LIB3431-040-P1-K2-G12
Method
                  BLASTX
NCBI GI
                  g2570515
BLAST score
                  456
E value
                  7.0e-49
Match length
                  133
```

NCBI Description (U96925) immunophilin [Vicia faba]

Method BLASIX
NCBI GI g3914603
BLAST score 707
E value 7.0e-75
Match length 146
% identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase [Oryza sativa]

Seq. No. 401128

Seq. ID LIB3431-040-P1-K2-G3

Method BLASTN
NCBI GI g2072554
BLAST score 214
E value 1.0e-117
Match length 309
% identity 92

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 401129

Seq. ID LIB3431-040-P1-K2-G4

Method BLASTX
NCBI GI g461498
BLAST score 248
E value 2.0e-21
Match length 84
% identity 55

NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC

TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)

(ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421)

alanine aminotransferase [Panicum miliaceum]

Seq. No. 401130

Seq. ID LIB3431-040-P1-K2-G5

Method BLASTX
NCBI GI g4138290
BLAST score 360
E value 7.0e-35
Match length 95
% identity 75

NCBI Description (AJ005841) thioredoxin M [Oryza sativa]

Seq. No. 401131

Seq. ID LIB3431-040-P1-K2-G7

Method BLASTX
NCBI GI g3080420
BLAST score 392
E value 6.0e-38



Match length 142 % identity 56

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 401132

Seq. ID LIB3431-040-P1-K2-G8

Method BLASTX
NCBI GI g3080420
BLAST score 389
E value 1.0e-37
Match length 120
% identity 62

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 401133

Seq. ID LIB3431-040-P1-K2-H10

Method BLASTN
NCBI GI g6103440
BLAST score 93
E value 5.0e-45
Match length 149
% identity 91

NCBI Description Oryza sativa metallothionein-like protein (ML2) mRNA,

complete cds

Seq. No. 401134

Seq. ID LIB3431-040-P1-K2-H12

Method BLASTN
NCBI GI g2072554
BLAST score 146
E value 3.0e-76
Match length 186
% identity 95

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 401135

Seq. ID LIB3431-040-P1-K2-H2

Method BLASTN
NCBI GI g3135542
BLAST score 39
E value 8.0e-13
Match length 67
% identity 90

NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds

Seq. No. 401136

Seq. ID LIB3431-040-P1-K2-H5

Method BLASTX
NCBI GI g4584342
BLAST score 221
E value 6.0e-18
Match length 120
% identity 42

NCBI Description (AC007127) putative ubiquitin protein [Arabidopsis

NCBI Description



thaliana]

```
Seq. No.
                  401137
                  LIB3431-040-P1-K2-H6
Seq. ID
                  BLASTX
Method
                  q4079798
NCBI GI
BLAST score
                  540
E value
                  2.0e-55
Match length
                  107
                  99
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
Seq. No.
                  401138
                  LIB3431-040-P1-K2-H8
Seq. ID
                  BLASTX
Method
                  g2407281
NCBI GI
                  616
BLAST score
                  3.0e-64
E value
Match length
                  118
                  97
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  401139
                  LIB3431-040-P1-K2-H9
Seq. ID
Method
                  BLASTX
                  g2072555
NCBI GI
BLAST score
                  348
                  7.0e-33
E value
Match length
                  62
                  98
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  401140
Seq. No.
                  LIB3431-040-P1-N1-A10
Seq. ID
Method
                  BLASTN
                  g2072554
NCBI GI
BLAST score
                  301
E value
                  1.0e-169
Match length
                  333
                   98
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                   401141
Seq. No.
Seq. ID
                  LIB3431-040-P1-N1-B12
Method
                  BLASTX
NCBI GI
                  g2754849
BLAST score
                  169
E value
                   7.0e-12
                   42
Match length
                   79
% identity
```

[Fritillaria agrestis]

(AF039000) putative serine-glyoxylate aminotransferase

BLAST score

E value

218 1.0e-17

401142 Seq. No. Seq. ID LIB3431-040-P1-N1-B6 Method BLASTX g132105 NCBI GI BLAST score 712 2.0e-75 E value Match length 130 100 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 401143 LIB3431-040-P1-N1-B9 Seq. ID Method BLASTX NCBI GI g871931 BLAST score 263 E value 9.0e-23 Match length 80 % identity 70 NCBI Description (D30763) ferredoxin [Oryza sativa] 401144 Seq. No. LIB3431-040-P1-N1-C11 Seq. ID Method BLASTX NCBI GI g517500 BLAST score 333 3.0e-31 E value Match length 81 80 % identity (M87435) precursor of the oxygen evolving complex 17 kDa NCBI Description protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum] Seq. No. 401145 LIB3431-040-P1-N1-C12 Seq. ID BLASTX Method NCBI GI q3126854 BLAST score 324 E value 4.0e-30 67 Match length % identity NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa] 401146 Seq. No. Seq. ID LIB3431-040-P1-N1-C2 Method BLASTX NCBI GI g4995921

```
Match length
% identity
                  75
NCBI Description (AJ006708) HMG1 protein [Zea mays]
                  401147
Seq. No.
                  LIB3431-040-P1-N1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1747294
BLAST score
                  290
                  6.0e-26
E value
Match length
                  55
                  100
% identity
NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.
                  401148
                  LIB3431-040-P1-N1-C5
Seq. ID
Method
                  BLASTN
                  g5295936
NCBI GI
BLAST score
                  56
                  1.0e-22
E value
Match length
                  124
% identity
                  86
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
                  complete sequence
                  401149
Seq. No.
Seq. ID
                  LIB3431-040-P1-N1-C6
Method
                  BLASTX
NCBI GI
                  g2529342
BLAST score
                  157
                  2.0e-10
E value
Match length
                  37
                  84
% identity
NCBI Description (L76554) transketolase [Spinacia oleracea]
                  401150
Seq. No.
                  LIB3431-040-P1-N1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  170
E value
                  1.0e-90
Match length
                  262
                  91
% identity
NCBI Description Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
Seq. No.
                  401151
Seq. ID
                  LIB3431-040-P1-N1-D12
Method
                  BLASTX
NCBI GI
                  g115794
BLAST score
                  446
E value
                  3.0e-44
Match length
                  96
                  89
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
```

III CAB-13) >gi_72748_pir__CDT033 chlorophyll a/b-binding



protein type III precursor (cab-13) - tomato
>gi_19277_emb_CAA42818_ (X60275) LHCII type III
[Lycopersicon esculentum]

 Seq. No.
 401152

 Seq. ID
 LIB3431-040-P1-N1-D3

 Method
 BLASTX

 NCBI GI
 g606817

 BLAST score
 312

BLAST score 312 E value 2.0e-28 Match length 59 % identity 98

NCBI Description (U08404) carbonic anhydrase [Oryza sativa]

>gi 5917783 gb AAD56038.1_AF182806_1 (AF182806) carbonic

anhydrase 3 [Oryza sativa]

Seq. No. 401153

Seq. ID LIB3431-040-P1-N1-D5

Method BLASTX
NCBI GI g132105
BLAST score 609
E value 2.0e-63
Match length 112
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >qi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401154

Seq. ID LIB3431-040-P1-N1-D9

Method BLASTX
NCBI GI g551047
BLAST score 275
E value 3.0e-29
Match length 71
% identity 85

NCBI Description (X79277) type II LHCI [Lolium temulentum]

Seq. No. 401155

Seq. ID LIB3431-040-P1-N1-E3

Method BLASTX
NCBI GI g132105
BLAST score 546
E value 6.0e-56
Match length 99
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

401156 Seq. No. LIB3431-040-P1-N1-E5 Seq. ID BLASTX Method g132105 NCBI GI 512 BLAST score 9.0e-63 E value 120 Match length 97 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi 226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

carboxylase S [Oryza sativa]

Seq. No. 401157

Seq. ID LIB3431-040-P1-N1-E7

Method BLASTN
NCBI GI g20181
BLAST score 127
E value 5.0e-65
Match length 163
% identity 94

NCBI Description Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein

Seq. No. 401158

Seq. ID LIB3431-040-P1-N1-E8

Method BLASTN
NCBI GI g22239
BLAST score 44
E value 2.0e-15
Match length 68
% identity 91

NCBI Description Maize cytosolic mRNA for subunit A of chloroplast GAPDH

(GapA) glyceraldehyde-3-phosphate dehydrogenase

Seq. No. 401159

Seq. ID LIB3431-040-P1-N1-E9

Method BLASTX
NCBI GI g347451
BLAST score 149
E value 2.0e-09
Match length 32
% identity 88

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza

sativa]

Seq. No. 401160

```
LIB3431-040-P1-N1-F1
Seq. ID
                   BLASTX
Method
                   g1174745
NCBI GI
                   355
BLAST score
                   1.0e-33
E value
                   85
Match length
                   84
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                   >gi_1363523_pir__S53761 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - rye
                   >gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
[Secale cereale] >gi_1095494_prf__2109226B triosephosphate
                   isomerase [Secale cereale]
Seq. No.
                   401161
                   LIB3431-040-P1-N1-F11
Seq. ID
                   BLASTX
Method
                   q3885894
NCBI GI
                   233
BLAST score
                   2.0e-19
E value
Match length
                   61
                   79
% identity
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
                   401162
Seq. No.
                   LIB3431-040-P1-N1-F4
Seq. ID
                   BLASTN
Method
                   g3345476
NCBI GI
BLAST score
                   267
                   1.0e-148
E value
Match length
                   315
                   96
% identity
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                   401163
Seq. No.
                   LIB3431-040-P1-N1-G3
Seq. ID
                   BLASTX
Method
                   g167097
NCBI GI
                   179
BLAST score
                   1.0e-25
E value
Match length
                   76
% identity
                   80
NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
                   [Hordeum vulgare]
Seq. No.
                   401164
                   LIB3431-040-P1-N1-G4
Seq. ID
                   BLASTX
Method
                   g3785996
NCBI GI
                   238
BLAST score
E value
                   5.0e-20
Match length
                   97
% identity
                   51
NCBI Description (AC005499) putative annexin [Arabidopsis thaliana]
```

Seq. No. 401165

Seq. ID LIB3431-040-P1-N1-G6

```
BLASTN
Method
                  g4138289
NCBI GI
                  354
BLAST score
                  0.0e+00
E value
                  354
Match length
                  100
% identity
NCBI Description Oryza sativa mRNA for thioredoxin {\tt M}
                  401166
Seq. No.
                  LIB3431-040-P1-N1-G8
Seq. ID
                  BLASTX
Method
                  q3080420
NCBI GI
                  175
BLAST score
                  2.0e-12
E value
Match length
                  43
% identity
                  74
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                   401167
Seq. No.
                  LIB3431-040-P1-N1-H1
Seq. ID
                  BLASTN
Method
                   g2072554
NCBI GI
BLAST score
                  370
                  0.0e + 00
E value
Match length
                   378
                   99
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                   cds
                   401168
Seq. No.
                   LIB3431-040-P1-N1-H12
Seq. ID
Method
                   BLASTX
                   g4079798
NCBI GI
BLAST score
                   392
                   6.0e-38
E value
                   79
Match length
                   96
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   401169
Seq. No.
                   LIB3431-040-P1-N1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2662310
BLAST score
                   158
                   8.0e-21
E value
                   56
Match length
                   90
% identity
```

Seq. No. 401170

Seq. ID LIB3431-040-P1-N1-H4

NCBI Description (AB009307) bpwl [Hordeum vulgare]

Method BLASTX
NCBI GI g3126854
BLAST score 343
E value 2.0e-32



```
Match length
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  401171
Seq. No.
                  LIB3431-040-P1-N1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  376
E value
                  4.0e-36
Match length
                  69
                  99
% identity
NCBI Description
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
Seq. No.
                  401172
                  LIB3431-040-P1-N1-H9
Seq. ID
Method
                  BLASTN
                  g218209
NCBI GI
BLAST score
                  149
                  5.0e-78
E value
                  329
Match length
                  96
% identity
NCBI Description
                 Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  posss2106
                  401173
Seq. No.
                  LIB3431-041-P1-N1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3126853
BLAST score
                  230
E value
                  1.0e-126
Match length
                  249
% identity
                  99
NCBI Description
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
Seq. No.
                  401174
Seq. ID
                  LIB3431-041-P1-N1-A2
Method
                  BLASTX
                  g115787
NCBI GI
                  432
BLAST score
E value
                  1.0e-42
Match length
                  82
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
```

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

401175 Seq. No.

Seq. ID LIB3431-041-P1-N1-A3

Method BLASTX NCBI GI g4079798

```
BLAST score
                  2.0e-24
E value
                  52
Match length
                  100
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  401176
Seq. No.
                  LIB3431-041-P1-N1-A4
Seq. ID
                  BLASTX
Method
                  g2982301
NCBI GI
                  255
BLAST score
                  8.0e-22
E value
                  91
Match length
% identity
                  55
NCBI Description (AF051235) YGL010w-like protein [Picea mariana]
                  401177
Seq. No.
                  LIB3431-041-P1-N1-A6
Seq. ID
                  BLASTX
Method
                  g6093827
NCBI GI
                  169
BLAST score
                  1.0e-11
E value
                  97
Match length
                  41
% identity
                 PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
NCBI Description
                  [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                  PROTEIN PSBY-2] >gi_2956690_emb_CAA11248_ (AJ223306) PSBY
                  [Arabidopsis thaliana] >gi 3414928 (AF079800) PsbY
                  precursor [Arabidopsis thaliana]
                  401178
Seq. No.
                  LIB3431-041-P1-N1-A7
Seq. ID
                  BLASTX
Method
                  g120661
NCBI GI
BLAST score
                  225
                  2.0e-18
E value
                  43
Match length
                  95
% identity
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
                  PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
                  401179
Seq. No.
                  LIB3431-041-P1-N1-A9
Seq. ID
Method
                  BLASTN
                  q11640
NCBI GI
BLAST score
                  45
```

4.0e-16 E value Match length 137 % identity 42

NCBI Description Liverwort Marchantia polymorpha chloroplast genome DNA

401180 Seq. No.

LIB3431-041-P1-N1-B1 Seq. ID

Method BLASTN NCBI GI g2072554

```
BLAST score
E value
                  0.0e + 00
                  403
Match length
                  100
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  401181
Seq. No.
                  LIB3431-041-P1-N1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  300
E value
                  3.0e-27
Match length
                  77
                  75
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  401182
Seq. No.
                  LIB3431-041-P1-N1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6094430
BLAST score
                  191
                  7.0e-19
E value
Match length
                  55
% identity
                  95
                  TUBULIN ALPHA-2 CHAIN (ALPHA-TUBULIN 2) >gi 2511533
NCBI Description
                  (AF008121) alpha-tubulin 2 [Eleusine indica]
Seq. No.
                  401183
                  LIB3431-041-P1-N1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2970051
BLAST score
                  249
E value
                  3.0e-21
Match length
                  60
                  77
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
                  401184
Seq. No.
Seq. ID
                  LIB3431-041-P1-N1-B6
                  BLASTX
Method
NCBI GI
                  q115793
                   309
BLAST score
                  3.0e-28
E value
Match length
                  63
```

% identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR NCBI Description

(CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_

(X63197) type III LHCII CAB precursor protein [Hordeum

vulgare]

Seq. No.

401185

Seq. ID LIB3431-041-P1-N1-B7

Method BLASTX NCBI GI g417260 BLAST score 274

Seq. ID

Method

```
4.0e-24
 E value
 Match length
                   79
 % identity
                   71
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
 NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
                    401186
 Seq. No.
                   LIB3431-041-P1-N1-B8
 Seq. ID
 Method
                   BLASTX
                   g2997591
 NCBI GI
                   238
 BLAST score
                    6.0e-20
 E value
 Match length
                    61
 % identity
                   79
                   (AF020814) glucose-6-phosphate/phosphate-translocator
 NCBI Description
                   precursor [Pisum sativum]
                    401187
 Seq. No.
                   LIB3431-041-P1-N1-C1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g131225
 BLAST score
                    216
                    2.0e-17
E value
                    56
 Match length
                    73
 % identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 NCBI Description
                    V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                    precursor - barley >gi_167087 (M61146) photosystem I
                    hydrophobic protein [Hordeum vulgare]
                    401188
 Seq. No.
                    LIB3431-041-P1-N1-C10
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g131225
 BLAST score
                    327
                    3.0e-30
 E value
 Match length
                    92
                    70
 % identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
 NCBI Description
                    V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                    precursor - barley >gi_167087 (M61146) photosystem I
                    hydrophobic protein [Hordeum vulgare]
                    401189
 Seq. No.
                    LIB3431-041-P1-N1-C11
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g20262
 BLAST score
                    265
                    1.0e-147
 E value
 Match length
                    272
                    99
 % identity
 NCBI Description O.sativa light-induced mRNA
 Seq. No.
                    401190
```

51435

LIB3431-041-P1-N1-C12

BLASTX

```
NCBI GI
                  a2570511
BLAST score
                  163
                  2.0e-26
E value
Match length
                  74
% identity
                  80
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  401191
                  LIB3431-041-P1-N1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6015059
BLAST score
                  422
E value
                  2.0e-41
Match length
                  83
% identity
                  100
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
                  (AF030517) translation elongation factor-1 alpha; EF-1
                  alpha [Oryza sativa]
Seq. No.
                  401192
                  LIB3431-041-P1-N1-C8
```

Seq. ID Method BLASTX NCBI GI g730510 BLAST score 150 E value 1.0e-09 Match length 45 % identity 67

NCBI Description RAS-RELATED PROTEIN RIC1 >gi_542150_pir__S38740 GTP-binding

protein - rice >gi_432607 gb_AAB28535 (S66160) ras-related GTP binding protein possessing GTPase activity=ric1 [Oryza sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]

[Oryza sativa]

Seq. No. 401193

Seq. ID LIB3431-041-P1-N1-D2

Method BLASTN NCBI GI q6006355 BLAST score 88 E value 1.0e-41 Match length 130 % identity

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401194

Seq. ID LIB3431-041-P1-N1-D3

Method BLASTX NCBI GI q4877984 BLAST score 262 E value 1.0e-22 Match length 53 % identity 96

NCBI Description (AF145755) THA4 [Zea mays]

Seq. No. 401195

Seq. ID LIB3431-041-P1-N1-D7

Method BLASTN NCBI GI g218154

```
BLAST score
                  1.0e-16
E value
Match length
                  46
% identity
                  100
NCBI Description Oryza sativa gene for cytoplasmic aldolase, complete cds,
                  clone:Aldp
                  401196
Seq. No.
                  LIB3431-041-P1-N1-E10
Seq. ID
Method
                  BLASTX
                  g3582335
NCBI GI
                  493
BLAST score
                  1.0e-49
E value
Match length
                  105
% identity
                  84
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                  401197
Seq. No.
                  LIB3431-041-P1-N1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738261
BLAST score
                  171
E value
                  3.0e-12
Match length
                  58
% identity
                  67
                 (AB018412) chloroplast phosphoglycerate kinase [Populus
NCBI Description
                  nigra]
Seq. No.
                  401198
                  LIB3431-041-P1-N1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g416266
BLAST score
                  44
                  2.0e-15
E value
Match length
                  126
% identity
                  83
NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence
                  401199
Seq. No.
                  LIB3431-041-P1-N1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3075487
BLAST score
                  308
E value
                  1.0e-173
Match length
                  315
% identity
                  99
NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                  mRNA, complete cds
Seq. No.
                  401200
Seq. ID
                  LIB3431-041-P1-N1-E7
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                  465
```

51437

0.0e+00

465 100

E value Match length

% identity



NCBI Description Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No. 401201
Seq. ID LIB3431-041-P1-N1-E8
Method BLASTX
NCBI GI q3386621

Method BLASTX
NCBI GI g3386621
BLAST score 157
E value 2.0e-10
Match length 36
% identity 81

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 401202

Seq. ID LIB3431-041-P1-N1-E9

Method BLASTX
NCBI GI g3980406
BLAST score 360
E value 4.0e-34
Match length 105
% identity 63

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 401203

Seq. ID LIB3431-041-P1-N1-F1

Method BLASTX
NCBI GI g3377797
BLAST score 225
E value 2.0e-18
Match length 68
% identity 66

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 401204

Seq. ID LIB3431-041-P1-N1-F12

Method BLASTN
NCBI GI g1835730
BLAST score 123
E value 7.0e-63
Match length 147
% identity 96

NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,

complete cds

Seq. No. 401205

Seq. ID LIB3431-041-P1-N1-F2

Method BLASTX
NCBI GI g131225
BLAST score 364
E value 1.0e-34
Match length 99
% identity 72

% identity

82

```
PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  401206
Seq. No.
                  LIB3431-041-P1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  143
                  6.0e-09
E value
Match length
                  53
                  49
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  401207
Seq. No.
Seq. ID
                  LIB3431-041-P1-N1-F5
                  BLASTN
Method
NCBI GI
                  q2293567
BLAST score
                  79
                  2.0e-36
E value
                  181
Match length
                  84
% identity
NCBI Description Oryza sativa HvB12D homolog mRNA, complete cds
                  401208
Seq. No.
                  LIB3431-041-P1-N1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2980805
                  322
BLAST score
                  1.0e-29
E value
                  80
Match length
                  84
% identity
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
                  401209
Seq. No.
                  LIB3431-041-P1-N1-F9
Seq. ID
Method
                  BLASTX
                  g1084455
NCBI GI
BLAST score
                  362
                  2.0e-34
E value
Match length
                  69
                  100
% identity
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                   401210
Seq. No.
                  LIB3431-041-P1-N1-G12
Seq. ID
Method
                  BLASTX
                  g82080
NCBI GI
                  145
BLAST score
                  1.0e-09
E value
Match length
                   33
```

% identity

91

NCBI Description (AF124045) unknown [Sorghum bicolor]

```
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  401211
Seq. No.
                  LIB3431-041-P1-N1-G3
Seq. ID
Method
                  BLASTX
                  g517500
NCBI GI
BLAST score
                  251
                  1.0e-21
E value
Match length
                  73
                  70
% identity
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  401212
                  LIB3431-041-P1-N1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2696804
BLAST score
                  152
                  5.0e-10
E value
Match length
                  28
                  100
% identity
NCBI Description
                 (AB009665) water channel protein [Oryza sativa]
Seq. No.
                  401213
                  LIB3431-041-P1-N1-H3
Seq. ID
Method
                  BLASTX
                  g347451
NCBI GI
BLAST score
                  351
                  4.0e-33
E value
Match length
                  69
                  96
% identity
NCBI Description
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
Seq. No.
                  401214
                  LIB3431-041-P1-N1-H6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2570512
BLAST score
                  48
E value
                  2.0e-18
Match length
                  48
% identity
                  100
                  Oryza sativa chlorophyll a-b binding protein mRNA, complete
NCBI Description
                  cds
Seq. No.
                  401215
Seq. ID
                  LIB3431-041-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  q5410350
BLAST score
                  216
E value
                  3.0e-17
Match length
                  45
```

BLAST score

313

```
401216
Seq. No.
                  LIB3431-041-P1-N1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  235
E value
                  1.0e-19
Match length
                  55
                  84
% identity
                 (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  401217
Seq. No.
                  LIB3431-041-P2-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  380
                  3.0e-59
E value
Match length
                  135
% identity
                  87
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  401218
Seq. No.
                  LIB3431-041-P2-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  218
                  3.0e-18
E value
                  50
Match length
                  90
% identity
NCBI Description
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
                  401219
Seq. No.
                  LIB3431-041-P2-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  a120657
BLAST score
                  575
                  2.0e-59
E value
Match length
                  136
% identity
                  85
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi_66024_pir__DEZMG3
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                  401220
Seq. ID
                  LIB3431-041-P2-K1-B1
Method
                  BLASTN
NCBI GI
                  g6103440
```

```
E value
                  1.0e-176
                  332
Match length
                  99
% identity
                  Oryza sativa metallothionein-like protein (ML2) mRNA,
NCBI Description
                  complete cds
                  401221
Seq. No.
                  LIB3431-041-P2-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
                  297
BLAST score
                  4.0e-31
E value
                  90
Match length
% identity
                  80
                 (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  401222
Seq. No.
                  LIB3431-041-P2-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4958922
BLAST score
                  219
                  1.0e-17
E value
                  88
Match length
                  53
% identity
NCBI Description (AB027757) NADPH oxidoreductase homolog [Cicer arietinum]
                  401223
Seq. No.
                  LIB3431-041-P2-K1-B12
Seq. ID
                  BLASTX
Method
                  g6094430
NCBI GI
                  200
BLAST score
                  6.0e-16
E value
                  70
Match length
                  60
% identity
NCBI Description TUBULIN ALPHA-2 CHAIN (ALPHA-TUBULIN 2) >gi 2511533
                   (AF008121) alpha-tubulin 2 [Eleusine indica]
Seq. No.
                  401224
                  LIB3431-041-P2-K1-B6
Seq. ID
Method
                  BLASTX
                  q2570511
NCBI GI
                  494
BLAST score
                  5.0e-50
E value
Match length
                  95
                  98
% identity
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
                   401225
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-B7
```

Method BLASTN
NCBI GI g20262
BLAST score 296
E value 1.0e-166
Match length 328
% identity 98

NCBI Description O.sativa light-induced mRNA

Seq. ID

Method

```
Seq. No.
                  401226
                  LIB3431-041-P2-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1652217
BLAST score
                  269
                  1.0e-23
E value
Match length
                  107
                  54
% identity
NCBI Description
                 (D90903) hypothetical protein [Synechocystis sp.]
                  401227
Seq. No.
                  LIB3431-041-P2-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  322
E value
                  1.0e-29
Match length
                  80
% identity
                  75
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir $33632
NCBI Description
                  lir1 protein - rice >gi_20263_emb CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
                  401228
Seq. No.
                  LIB3431-041-P2-K1-C12
Seq. ID
Method
                  BLASTX
                  g4689380
NCBI GI
BLAST score
                  402
E value
                  2.0e-39
Match length
                  78
                  95
% identity
NCBI Description
                 (AF139465) LHCII type III chlorophyll a/b binding protein
                  [Vigna radiata]
                  401229
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-C2
Method
                  BLASTX
NCBI GI
                  g4582455
BLAST score
                  185
                  9.0e-14
E value
Match length
                  99
% identity
                  36
                  (AC007071) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  401230
Seq. No.
                  LIB3431-041-P2-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  711
                  2.0e-75
E value
Match length
                  140
% identity
                  99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  401231
Seq. No.
```

51443

LIB3431-041-P2-K1-C7

BLASTX

```
g3551954
NCBI GI
BLAST score
                  349
                  9.0e-33
E value
Match length
                  137
% identity
                  51
                  (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                  hybrid cultivar]
Seq. No.
                  401232
                  LIB3431-041-P2-K1-C8
Seq. ID
Method
                  BLASTN
                  g432606
NCBI GI
BLAST score
                  75
E value
                  4.0e-34
Match length
                  154
% identity
                  99
                  ric1=ras-related GTP binding protein possessing GTPase
NCBI Description
                  activity [Oryza sativa=rice, Yamahoushi, callus, mRNA, 955
Seq. No.
                  401233
                  LIB3431-041-P2-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707998
BLAST score
                  612
E value
                  1.0e-63
Match length
                  150
% identity
                  80
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                  (SHMT) >gi 481944 pir S40218 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - potato
                  >gi 438247 emb CAA81082 (Z25863) glycine
                  hydroxymethyltransferase [Solanum tuberosum]
Seq. No.
                  401234
                  LIB3431-041-P2-K1-D2
Seq. ID
                  BLASTN
Method
                  g6006355
NCBI GI
                  132
BLAST score
E value
                  6.0e-68
                  197
Match length
                  46
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  401235
Seq. No.
                  LIB3431-041-P2-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4877984
BLAST score
                  369
E value
                  3.0e-35
                  143
```

Match length % identity 57

NCBI Description (AF145755) THA4 [Zea mays]

Seq. No. 401236

LIB3431-041-P2-K1-D6 Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g5903095
BLAST score
                  159
                  2.0e-10
E value
                  49
Match length
                  61
% identity
                  (AC008017) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  401237
Seq. No.
                  LIB3431-041-P2-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218154
BLAST score
                  46
E value
                  1.0e-16
Match length
                  46
                  100
% identity
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
NCBI Description
                  clone:Aldp
Seq. No.
                  401238
                  LIB3431-041-P2-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3582335
BLAST score
                  745
E value
                  3.0e-88
                  165
Match length
% identity
                  95
                  (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                  401239
Seq. No.
                  LIB3431-041-P2-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q129915
BLAST score
                  493
E value
                  9.0e-50
Match length
                  131
% identity
                  78
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 66912 pir__TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
                  precursor, chloroplast - wheat >gi_21833 emb_CAA33303_
                   (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum
                  aestivum] >gi 3293043 emb CAA51931 (X73528)
                  phosphoglycerate kinase [Triticum aestivum]
Seq. No.
                  401240
                  LIB3431-041-P2-K1-E12
Seq. ID
Method
                  BLASTX
                  g3128167
NCBI GI
BLAST score
                  202
                  2.0e-15
E value
Match length
                  155
% identity
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3212874 (AC004005) hypothetical protein [Arabidopsis
```

Seq. No. 401241

thaliana]

```
LIB3431-041-P2-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6015437
                  36
BLAST score
                  3.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  401242
Seq. No.
                  LIB3431-041-P2-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3986695
BLAST score
                  519
E value
                  7.0e-53
Match length
                  122
% identity
                  86
                 (AF101423) ribosomal protein L12 [Cichorium intybus]
NCBI Description
Seq. No.
                  401243
                  LIB3431-041-P2-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131388
BLAST score
                  188
E value
                  4.0e-14
Match length
                  87
                  56
% identity
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
Seq. No.
                  401244
Seq. ID
                  LIB3431-041-P2-K1-E6
Method
                  BLASTX
NCBI GI
                  q3075488
BLAST score
                  426
E value
                  2.0e-51
Match length
                  126
% identity
NCBI Description
                 (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  401245
Seq. ID
                  LIB3431-041-P2-K1-E7
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                  355
E value
                  0.0e + 00
Match length
                  363
% identity
                  100
```

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 401246

Seq. ID

```
LIB3431-041-P2-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3386621
BLAST score
                  511
                  7.0e-52
E value
Match length
                  117
% identity
                  85
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                  401247
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-E9
Method
                  BLASTX
NCBI GI
                  q3980400
                  487
BLAST score
                  5.0e-49
E value
                  166
Match length
% identity
                  58
NCBI Description
                  (AC004561) putative tropinone reductase [Arabidopsis
                  thaliana]
                  401248
Seq. No.
                  LIB3431-041-P2-K1-F1
Seq. ID
Method
                  BLASTX
                  q3377797
NCBI GI
                  295
BLAST score
                  1.0e-26
E value
Match length
                  116
% identity
                  53
NCBI Description
                  (AF075597) Similar to 60S ribosome protein L19; coded for
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                  401249
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-F11
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  307
E value
                  1.0e-172
Match length
                  319
                  99
% identity
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                  401250
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-F12
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  537
                  7.0e-55
E value
Match length
                  114
% identity
                  90
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  401251
Seq. No.
```

51447

LIB3431-041-P2-K1-F2

```
Method BLASTX
NCBI GI g131225
BLAST score 386
E value 1.0e-37
Match length 83
% identity 90
```

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi 167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

```
      Seq. No.
      401252

      Seq. ID
      LIB3431-041-P2-K1-F4

      Method
      BLASTX

      NCBI GI
      g2660677

      BLAST score
      418

      E value
      4.0e-41
```

E value 4.00 Match length 124 % identity 62

NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]

 Seq. No.
 401253

 Seq. ID
 LIB3431-041-P2-K1-F5

 Method
 BLASTN

 NCBI GI
 g2293567

 BLAST score
 165

 E value
 6.0e-88

E value 6.0 Match length 197 % identity 96

NCBI Description Oryza sativa HvB12D homolog mRNA, complete cds

Seq. No. 401254

Seq. ID LIB3431-041-P2-K1-F6

Method BLASTN

NCBI GI g3821780

BLAST score 36

E value 8.0e-11

Match length 36

% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 401255

Seq. ID LIB3431-041-P2-K1-F7

Method BLASTX
NCBI GI g2980805
BLAST score 596
E value 8.0e-62
Match length 145
% identity 77

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 401256

Seq. ID LIB3431-041-P2-K1-F8

Method BLASTX
NCBI GI g4007792
BLAST score 316
E value 6.0e-29

E value

3.0e-18

```
Match length
                  148
% identity
                  43
                  (AL034463) Xenopus 14s cohesin smc1 subunit homolog
NCBI Description
                  [Schizosaccharomyces pombe]
                  401257
Seq. No.
                  LIB3431-041-P2-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1084455
BLAST score
                  565
                  3.0e-58
E value
                  125
Match length
                  86
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                  401258
Seq. No.
                  LIB3431-041-P2-K1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1168537
BLAST score
                  532
                  2.0e-54
E value
                  125
Match length
                  75
% identity
                  ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
NCBI Description
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi 218143 dbj BAA02242_ (D12777) aspartic proteinase
                  [Oryza sativa]
                  401259
Seq. No.
                  LIB3431-041-P2-K1-G12
Seq. ID
                  BLASTX
Method
                  g82080
NCBI GI
BLAST score
                  154
                  3.0e-10
E value
Match length
                  57
                  56
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  401260
Seq. No.
                  LIB3431-041-P2-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  228
                  4.0e-19
E value
Match length
                  51
% identity
                  86
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                  401261
Seq. No.
                  LIB3431-041-P2-K1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3819215
BLAST score
                  49
```

```
Match length
                  93
% identity
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0706
Seq. No.
                  401262
                  LIB3431-041-P2-K1-G9
Seq. ID
                  BLASTX
Method
                  g119958
NCBI GI
BLAST score
                  428
                  4.0e-42
E value
                  123
Match length
% identity
                  70
                 FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831)
NCBI Description
                  ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387)
                  Fd III [Zea mays] >gi_444686_prf 1907324C
                  ferredoxin:ISOTYPE=III [Zea mays]
                  401263
Seq. No.
                  LIB3431-041-P2-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570510
                  102
BLAST score
                  2.0e-50
E value
Match length
                  149
% identity
                  92
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete
                  cds
Seq. No.
                  401264
                  LIB3431-041-P2-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q542200
BLAST score
                  143
                  7.0e-09
E value
                  55
Match length
% identity
                  53
NCBI Description hypothetical protein - garden asparagus
                  >gi 452714 emb CAA54526 (X77320) unknown [Asparagus
                  officinalis]
Seq. No.
                  401265
                  LIB3431-041-P2-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  682
E value
                  6.0e-72
Match length
                  148
```

88 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone posss1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf _1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

401266 Seq. No. Seq. ID LIB3431-041-P2-K1-H7 Method BLASTN NCBI GI g5410347 90 BLAST score 6.0e-43 E value Match length 258 % identity 84 NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence 401267 Seq. No. LIB3431-041-P2-K1-H8 Seq. ID Method BLASTX NCBI GI g3126854 BLAST score 634 2.0e-66 E value Match length 122 % identity 98 (AF061577) chlorophyll a/b binding protein [Oryza sativa] NCBI Description 401268 Seq. No. LIB3431-042-P1-K1-A1 Seq. ID Method BLASTX NCBI GI g2407281 BLAST score 662 1.0e-69 E value Match length 129 % identity 95 (AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description subunit [Oryza sativa] 401269 Seq. No. Seq. ID LIB3431-042-P1-K1-A2 Method BLASTX NCBI GI g4733937 BLAST score 343 E value 3.0e - 32Match length 142 % identity 46 NCBI Description (AF080245) sesquiterpene synthase [Elaeis oleifera] 401270 Seq. No. LIB3431-042-P1-K1-A3 Seq. ID Method BLASTX q3183079 NCBI GI BLAST score 620 1.0e-64 E value Match length 141

% identity 84

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi 1375075 dbj BAA12870.1_ (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

Seq. No. 401271

Seq. ID LIB3431-042-P1-K1-A4

Method BLASTX

```
NCBI GI
                  q1261917
BLAST score
                  318
E value
                  3.0e-29
Match length
                  98
                  59
% identity
                 (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
NCBI Description
Seq. No.
                  401272
                  LIB3431-042-P1-K1-A5
Seq. ID
```

Method BLASTX NCBI GI g2129608 BLAST score 594 E value 1.0e-61 Match length 138 % identity 81

NCBI Description GTP-binding protein, 68K - Arabidopsis thaliana >gi 807577

(L38614) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 401273 LIB3431-042-P1-K1-A8 Seq. ID Method BLASTX

NCBI GI g6056199 BLAST score 281 E value 6.0e-25 Match length 116 % identity 46

NCBI Description (AC009400) unknown protein [Arabidopsis thaliana]

401274 Seq. No.

LIB3431-042-P1-K1-A9 Seq. ID

Method BLASTX NCBI GI g347451 BLAST score 255 E value 6.0e-22 Match length 99 % identity 54

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza

sativa]

Seq. No. 401275

Seq. ID LIB3431-042-P1-K1-B1

Method BLASTX NCBI GI g4972067 BLAST score 247 E value 6.0e-21 Match length 106 % identity

NCBI Description (AL078467) putative protei [Arabidopsis thaliana]

Seq. No. 401276

Seq. ID LIB3431-042-P1-K1-B11

Method BLASTN NCBI GI q4959460 BLAST score 36 E value 1.0e-10 Match length 36 % identity 100

```
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
                  401277
Seq. No.
                  LIB3431-042-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  q729135
NCBI GI
BLAST score
                  584
                  2.0e-60
E value
Match length
                  144
% identity
                  76
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                  3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612
                  catechol O-methyltransferase (EC \overline{2}.1.1.6) - \overline{\text{maize}}
                  >gi_168532 (M73235) O-methyltransferase [Zea mays]
Seq. No.
                  401278
                  LIB3431-042-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5733882
BLAST score
                  299
E value
                  5.0e-27
Match length
                  136
                  52
% identity
                  (AC007932) Similar to gb_Y12465 serine/threonine,kinase
NCBI Description
                  from Sorghum bicolor and contains a PF_00069 Eukaryotic
                  protein kinase domain. [Arabidopsis thaliana]
Seq. No.
                  401279
                  LIB3431-042-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2065017
                  290
BLAST score
                  5.0e-26
E value
                  115
Match length
% identity
                   46
                  (Y09822) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   401280
Seq. No.
                  LIB3431-042-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g871931
BLAST score
                   416
                   9.0e-41
E value
Match length
                  111
                   78
% identity
                  (D30763) ferredoxin [Oryza sativa]
NCBI Description
                   401281
Seq. No.
                  LIB3431-042-P1-K1-B6
Seq. ID
                  BLASTX
Method
                   g133936
NCBI GI
BLAST score
                   221
                   6.0e-18
E value
Match length
                   70
                   67
% identity
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir__R3RZ3
```



ribosomal protein S3 - rice chloroplast
>gi_12025_emb_CAA33934_ (X15901) ribosomal protein S3
[Oryza sativa] >gi_226646_prf__1603356BW ribosomal protein
S3 [Oryza sativa]

Seq. No. 401282

Seq. ID LIB3431-042-P1-K1-B9

Method BLASTN
NCBI GI g2286152
BLAST score 53
E value 8.0e-21
Match length 73

% identity 93 NCBI Description Zea mays cytoplasmic malate dehydrogenase mRNA, complete

cds

Seq. No. 401283

Seq. ID LIB3431-042-P1-K1-C10

Method BLASTX
NCBI GI g2754849
BLAST score 574
E value 3.0e-59
Match length 124
% identity 89

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase

[Fritillaria agrestis]

Seq. No. 401284

Seq. ID LIB3431-042-P1-K1-C11

Method BLASTX
NCBI GI g132105
BLAST score 525
E value 1.0e-53
Match length 115
% identity 86

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401285

Seq. ID LIB3431-042-P1-K1-C2

Method BLASTX
NCBI GI g4567284
BLAST score 162
E value 5.0e-11
Match length 51
% identity 63

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 401286

Seq. ID LIB3431-042-P1-K1-C4



```
Method BLASTX
NCBI GI g1483563
BLAST score 676
E value 3.0e-71
Match length 139
% identity 91
```

NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No. 401287

Seq. ID LIB3431-042-P1-K1-C5

Method BLASTX
NCBI GI g132105
BLAST score 546
E value 5.0e-56
Match length 129
% identity 82

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401288

Seq. ID LIB3431-042-P1-K1-C6

Method BLASTX
NCBI GI g3915131
BLAST score 613
E value 7.0e-64
Match length 119
% identity 100

NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)

>gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza
sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin
h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza

sativa]

Seq. No. 401289

Seq. ID LIB3431-042-P1-K1-C7

Method BLASTX
NCBI GI g417260
BLAST score 412
E value 2.0e-40
Match length 126
% identity 66

NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632

lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)

light-regulated gene [Oryza sativa]

Seq. No. 401290

Seq. ID LIB3431-042-P1-K1-C8

Method BLASTX
NCBI GI g4079798
BLAST score 335



```
3.0e-31
E value
Match length
                  111
% identity
                  62
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  401291
Seq. No.
                  LIB3431-042-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  g2911068
NCBI GI
BLAST score
                  199
                  2.0e-15
E value
Match length
                  43
% identity
                  79
                  (AL021960) G10-like protein [Arabidopsis thaliana]
NCBI Description
                  401292
Seq. No.
                  LIB3431-042-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q322867
BLAST score
                  520
                  5.0e-53
E value
Match length
                  135
% identity
                  75
NCBI Description
                  translation initiation factor eIF-4F isozyme form subunit
                  p82 - wheat
                  401293
Seq. No.
                  LIB3431-042-P1-K1-D3
Seq. ID
Method
                  BLASTX
                  g3914603
NCBI GI
BLAST score
                  287
E value
                  1.0e-25
Match length
                  134
% identity
                  51
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  401294
                  LIB3431-042-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  503
                  6.0e-51
E value
Match length
                  118
% identity
                  81
```

(U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description

[Zea mays]

Seq. No. 401295

Seq. ID LIB3431-042-P1-K1-D6

Method BLASTX NCBI GI q3913018 BLAST score 740 E value 9.0e-79

Match length 99
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 401296
Seq. ID LIB3431-042-P1-K1-D7
Method BLASTX
NCBI GI 9320618

Method BLASTX
NCBI GI g320618
BLAST score 565
E value 3.0e-58
Match length 124
% identity 86
NCBI Description chlorophy

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 401297

Seq. ID LIB3431-042-P1-K1-D8

Method BLASTX
NCBI GI g320618
BLAST score 652
E value 2.0e-68
Match length 122
% identity 99

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 401298

Seq. ID LIB3431-042-P1-K1-D9

Method BLASTX
NCBI GI g320618
BLAST score 536
E value 7.0e-55
Match length 118
% identity 86

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

 $>gi_227611_prf_1707316A$ chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 401299

Seq. ID LIB3431-042-P1-K1-E1

Method BLASTN
NCBI GI g6016845
BLAST score 89
E value 3.0e-42
Match length 146
% identity 92

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.

Seq. ID

401305

LIB3431-042-P1-K1-E8



```
401300
Seq. No.
                  LIB3431-042-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  g100796
NCBI GI
BLAST score
                  712
                  2.0e-75
E value
Match length
                  143
                  93
% identity
NCBI Description phosphoribulokinase (EC 2.7.1.19) - wheat
                  401301
Seq. No.
                  LIB3431-042-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g902200
                  296
BLAST score
                  1.0e-166
E value
                  388
Match length
                  49
% identity
NCBI Description Z.mays complete chloroplast genome
                  401302
Seq. No.
                  LIB3431-042-P1-K1-E5
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
BLAST score
                  472
                  2.0e-47
E value
                  105
Match length
                  85
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  401303
Seq. No.
Seq. ID
                  LIB3431-042-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g3582335
BLAST score
                  728
                  2.0e-77
E value
Match length
                  141
% identity
                  92
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                  401304
Seq. No.
                  LIB3431-042-P1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2072724
BLAST score
                  384
E value
                  0.0e + 00
                  403
Match length
                  99
% identity
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog1
```

```
BLASTX
Method
                   g132105
NCBI GI
BLAST score
                   657
E value
                   5.0e-69
                   140
Match length
                   89
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4\overline{.1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375_prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401306
                   LIB3431-042-P1-K1-E9
Seq. ID
                   BLASTX
Method
                   g2570515
NCBI GI
BLAST score
                   640
E value
                   5.0e-67
                   134
Match length
                   96
% identity
                   (AF022740) glycolate oxidase [Oryza sativa]
NCBI Description
Seq. No.
                   401307
                   LIB3431-042-P1-K1-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   677
```

2.0e-71 E value 132 Match length 95 % identity NCBI Description

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase ($\overline{\text{EC}}$ 4.1.1.39) small chain precursor (clone posss1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

401308 Seq. No. LIB3431-042-P1-K1-F10 Seq. ID BLASTX Method g82080 NCBI GI 432 BLAST score 1.0e-42 E value 122 Match length

% identity chlorophyll a/b-binding protein type III precursor - tomato NCBI Description >gi 226872_prf__1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 401309



```
LIB3431-042-P1-K1-F11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2407280
                  44
BLAST score
                  4.0e-16
E value
                  56
Match length
                  95
% identity
NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
                  401310
Seq. No.
                  LIB3431-042-P1-K1-F5
Seq. ID
                  BLASTN
Method
                  g6015437
NCBI GI
                  36
BLAST score
                  1.0e-10
E value
                  36
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  401311
Seq. No.
                  LIB3431-042-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3868756
BLAST score
                  699
E value
                  5.0e-74
Match length
                  136
% identity
                  93
NCBI Description (D86611) catalase [Oryza sativa]
                  401312
Seq. No.
                  LIB3431-042-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  g548603
NCBI GI
                  372
BLAST score
E value
                  1.0e-35
Match length
                  113
% identity
                  69
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
                  401313
Seq. No.
Seq. ID
                  LIB3431-042-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q1353352
                  197
BLAST score
E value
                  4.0e-15
Match length
                  54
% identity
                  72
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
```

Seq. No. 401314

Seq. ID LIB3431-042-P1-K1-G10

Method BLASTX

Method

BLASTX

```
q3789954
NCBI GI
BLAST score
                  667
E value
                  3.0e-70
Match length
                  124
                  100
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  401315
Seq. No.
                  LIB3431-042-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5803242
BLAST score
                  86
E value
                  2.0e-40
                  157
Match length
                  20
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                  401316
Seq. No.
                  LIB3431-042-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  711
E value
                  2.0e-75
Match length
                  141
% identity
                  94
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  401317
Seq. ID
                  LIB3431-042-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q1708424
                  408
BLAST score
                  8.0e-40
E value
Match length
                  112
% identity
                  65
                  ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590)
NCBI Description
                  isoflavone reductase-like protein [Lupinus albus]
Seq. No.
                  401318
                  LIB3431-042-P1-K1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1658312
BLAST score
                  104
E value
                  3.0e-51
Match length
                  104
                  50
% identity
NCBI Description O.sativa osr40g2 gene
Seq. No.
                  401319
Seq. ID
                  LIB3431-042-P1-K1-G4
```



NCBI GI g132105 BLAST score 632 E value 4.0e-66 Match length 135 % identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi 226375 prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401320

Seq. ID LIB3431-042-P1-K1-G5

Method BLASTX
NCBI GI g3426051
BLAST score 577
E value 1.0e-59
Match length 135
% identity 84

NCBI Description (AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401321

Seq. ID LIB3431-042-P1-K1-G6

Method BLASTX
NCBI GI g3915096
BLAST score 507
E value 6.0e-58
Match length 137
% identity 85

NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73) >gi_1574976 (U47293) trans-cinnamate 4-hydroxylase [Populus

tremuloides]

Seq. No. 401322

Seq. ID LIB3431-042-P1-K1-G8

Method BLASTX
NCBI GI g1617197
BLAST score 304
E value 1.0e-27
Match length 76
% identity 76

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 401323

Seq. ID LIB3431-042-P1-K1-G9

Method BLASTX
NCBI GI g2190992
BLAST score 301
E value 3.0e-27
Match length 117
% identity 51

NCBI Description (AF004358) glutathione S-transferase TSI-1 [Aegilops



tauschii]

401324 Seq. No. LIB3431-042-P1-K1-H1 Seq. ID Method BLASTX q128191 NCBI GI BLAST score 480 3.0e-48 E value 134 Match length % identity 77 NITRATE REDUCTASE [NAD(P)H] >gi_66210_pir__RDBHNP nitrate NCBI Description reductase (NAD(P)H) (EC 1.6.6.2) - barley >gi 19065 emb_CAA42739_ (X60173) nitrate reductase (NAD(P)H) [Hordeum vulgare] Seq. No. 401325 LIB3431-042-P1-K1-H10 Seq. ID BLASTX Method q3789954 NCBI GI 615 BLAST score E value 4.0e-64 115 Match length % identity 99 (AF094776) chlorophyll a/b-binding protein precursor [Oryza NCBI Description sativa] 401326 Seq. No. LIB3431-042-P1-K1-H12 Seq. ID Method BLASTX q1173347 NCBI GI BLAST score 201 1.0e-15 E value Match length 66 % identity 64 SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR NCBI Description (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum] 401327 Seq. No. LIB3431-042-P1-K1-H2 Seq. ID Method BLASTX NCBI GI g6093778 BLAST score 370 2.0e-35 E value 103 Match length % identity 75 NCBI Description PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3) >gi_2511574_emb_CAA73619.1_ (Y13176) multicatalytic
endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana] >gi 4966368 gb AAD34699.1 AC006341 27 (AC006341) Identical

to gb Y13176 Arabidopsis thaliana mRNA for proteasome

subunit prc3. ESTs gb H36972, gb T22551 and gb_T13800 come

Method

NCBI GI

BLAST score



from this gene

```
401328
Seq. No.
                  LIB3431-042-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3420052
BLAST score
                  485
E value
                  8.0e-51
Match length
                  137
                  77
% identity
                  (AC004680) putative ubiqinone reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  401329
                  LIB3431-042-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3288821
BLAST score
                  666
                  4.0e-70
E value
Match length
                  138
% identity
                  90
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                  401330
                  LIB3431-042-P1-K1-H5
Seq. ID
Method
                  BLASTX
                  g82080
NCBI GI
BLAST score
                  455
                  2.0e-45
E value
Match length
                  131
                  67
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  401331
Seq. ID
                  LIB3431-042-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q115815
BLAST score
                  275
                  1.0e-24
E value
Match length
                  57
% identity
                  91
                  CHLOROPHYLL A-B BINDING PROTEIN M9 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi_22355_emb_CAA39376_ (X55892) light-harvesting
                  chlorophyll a/b binding protein [Zea mays]
Seq. No.
                  401332
Seq. ID
                  LIB3431-042-P1-K1-H7
```

51464

BLASTX

366

g3914466

E value 5.0e-35
Match length 67
% identity 97

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN

subunit precursor [Zea mays]

Seq. No. 401333

Seq. ID LIB3431-042-P1-K1-H9

Method BLASTN
NCBI GI g3885887
BLAST score 371
E value 0.0e+00
Match length 378
% identity 100

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 401334

Seq. ID LIB3431-042-P1-N1-A3

Method BLASTX
NCBI GI g3183079
BLAST score 210
E value 1.0e-16
Match length 58
% identity 74

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi 1375075 dbj BAA12870.1 (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

Seq. No. 401335

Seq. ID LIB3431-042-P1-N1-A4

Method BLASTX
NCBI GI g1071925
BLAST score 194
E value 9.0e-15
Match length 51
% identity 65

NCBI Description Cw-19 peptide, non specific lipid transfer protein,

precursor - barley >gi 510528 emb CAA48623_ (X68656) Cw-19

peptide, non specific lipid transfer protein [Hordeum

vulgare]

Seq. No. 401336

Seq. ID LIB3431-042-P1-N1-A5

Method BLASTX
NCBI GI g2129825
BLAST score 391
E value 1.0e-37
Match length 93
% identity 83

NCBI Description dynamin-like protein phragmoplastin 12 - soybean

>gi 1217994 (U25547) SDL [Glycine max]

Seq. No. 401337

Seq. ID LIB3431-042-P1-N1-A8

Method BLASTX

NCBI GI

E value

BLAST score

g871931

8.0e-11

161

```
q6056199
NCBI GI
BLAST score
                  149
E value
                  2.0e-09
Match length
                  80
                  39
% identity
                 (AC009400) unknown protein [Arabidopsis thaliana]
NCBI Description
                  401338
Seq. No.
                  LIB3431-042-P1-N1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4972067
                  195
BLAST score
E value
                  2.0e-15
Match length
                  107
% identity
                  50
                 (AL078467) putative protei [Arabidopsis thaliana]
NCBI Description
                  401339
Seq. No.
                  LIB3431-042-P1-N1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729135
BLAST score
                  315
                  7.0e-29
E value
Match length
                  74
% identity
                  78
NCBI Description
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
                  (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                  3-O-METHYLTRANSFERASE) (COMT) >gi 283034 pir S28612
                  catechol O-methyltransferase (EC 2.1.1.6) - maize
                  >gi 168532 (M73235) O-methyltransferase [Zea mays]
                  401340
Seq. No.
                  LIB3431-042-P1-N1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3158476
BLAST score
                  270
E value
                  2.0e-23
Match length
                  65
                  75
% identity
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  401341
                  LIB3431-042-P1-N1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2065019
                  258
BLAST score
                  3.0e-22
E value
Match length
                  95
% identity
                  25
                  (Y09823) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  401342
Seq. No.
Sea. ID
                  LIB3431-042-P1-N1-B5
Method
                  BLASTX
```

```
Match length
                  75
% identity
NCBI Description
                  (D30763) ferredoxin [Oryza sativa]
                  401343
Seq. No.
Seq. ID
                  LIB3431-042-P1-N1-B6
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  368
                  0.0e+00
E value
Match length
                  492
                  95
% identity
NCBI Description
                  Rice complete chloroplast genome
Seq. No.
                  401344
                  LIB3431-042-P1-N1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  393
                  4.0e-38
E value
Match length
                  94
% identity
                  82
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  401345
                  LIB3431-042-P1-N1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  421
E value
                  2.0e-41
Match length
                  112
                  76
% identity
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  401346
Seq. No.
                  LIB3431-042-P1-N1-C1
Seq. ID
Method
                  BLASTX
                  g131225
NCBI GI
BLAST score
                  311
E value
                  1.0e-28
Match length
                  76
% identity
                  76
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >g\overline{i}_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  401347
Seq. No.
Seq. ID
                  LIB3431-042-P1-N1-C10
```

Method BLASTX NCBI GI g2754849 BLAST score 394 E value 4.0e-38

Match length % identity 86 (AF039000) putative serine-glyoxylate aminotransferase NCBI Description [Fritillaria agrestis] 401348 Seq. No. LIB3431-042-P1-N1-C11 Seq. ID Method BLASTX NCBI GI g132105 BLAST score 421 3.0e-41 E value Match length 76 100 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 401349 Seq. No. LIB3431-042-P1-N1-C4 Seq. ID Method BLASTX NCBI GI q1483563 BLAST score 265 6.0e-23 E value Match length 53 % identity 92 (X99825) leucine aminopeptidase [Petroselinum crispum] NCBI Description 401350 Seq. No. LIB3431-042-P1-N1-C5 Seq. ID Method BLASTX NCBI GI g671740 BLAST score 227 1.0e-18 E value Match length 56 % identity 79 (X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description construct] 401351 Seq. No.

Seq. ID LIB3431-042-P1-N1-C6

Method BLASTN
NCBI GI g454881
BLAST score 207
E value 1.0e-113
Match length 234
% identity 97

NCBI Description Rice gene for thioredoxin h, complete cds

Seq. No. 401352

Seq. ID LIB3431-042-P1-N1-C7

Method BLASTX

NCBI GI g417260 BLAST score 406 E value 2.0e-39 Match length 128 % identity 65

NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632

lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)

light-regulated gene [Oryza sativa]

Seq. No. 401353

Seq. ID LIB3431-042-P1-N1-C9

Method BLASTN
NCBI GI g4079797
BLAST score 66
E value 1.0e-28
Match length 246
% identity 81

NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA,

complete cds

Seq. No. 401354

Seq. ID LIB3431-042-P1-N1-D10

Method BLASTX
NCBI GI g132105
BLAST score 522
E value 4.0e-53
Match length 94
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone posss1139) - rice >gi 218208 dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401355

Seq. ID LIB3431-042-P1-N1-D11

Method BLASTX
NCBI GI g115787
BLAST score 402
E value 5.0e-39
Match length 77
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 401356

Seq. ID LIB3431-042-P1-N1-D12

Method BLASTN NCBI GI g452439 BLAST score 68



E value 1.0e-29 Match length 201 % identity 87 Wheat (clone p80k-34) initiation factor isozyme 4F p82 NCBI Description subunit mRNA, complete cds 401357 Seq. No. Seq. ID LIB3431-042-P1-N1-D6 Method BLASTX g2407279 NCBI GI BLAST score 188 4.0e-14 E value Match length 40 % identity 95 NCBI Description (AF017362) aldolase [Oryza sativa] 401358 Seq. No. LIB3431-042-P1-N1-D7 Seq. ID Method BLASTX NCBI GI g115787 BLAST score 417 6.0e-41 E value Match length 79 100 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 401359 Seq. No. LIB3431-042-P1-N1-D8 Seq. ID Method BLASTX NCBI GI g3036951 BLAST score 341 E value 6.0e-32 Match length 66 % identity 98 (AB012639) light harvesting chlorophyll a/b-binding protein NCBI Description [Nicotiana sylvestris] 401360 Seq. No. LIB3431-042-P1-N1-D9 Seq. ID Method BLASTX NCBI GI q3036951 BLAST score 334 E value 4.0e-31

Match length 66 % identity 97

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No. 401361

Seq. ID LIB3431-042-P1-N1-E10

Method BLASTX NCBI GI g6041819 BLAST score 220

E value 1.0e-17 Match length 95 % identity 47 NCBI Description (AC009918) unknown protein [Arabidopsis thaliana] 401362 Seq. No. Seq. ID LIB3431-042-P1-N1-E2 Method BLASTX NCBI GI q21839 BLAST score 361 E value 3.0e-34 Match length 74 % identity 96 (X57952) phosphoribulokinase [Triticum aestivum] NCBI Description 401363 Seq. No. Seq. ID LIB3431-042-P1-N1-E3 Method BLASTX NCBI GI q1173275 BLAST score 653 E value 2.0e-68 Match length 147 % identity 91 NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_2119068_pir__S58630 ribosomal protein S7 - maize
chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal protein S7 [Zea mays] >gi 902298 emb CAA60362 (X86563) ribosomal protein S7 [Zea mays] Seq. No. 401364 Seq. ID LIB3431-042-P1-N1-E5 Method BLASTX NCBI GI g115787 BLAST score 578 E value 1.0e-59 Match length 111 % identity 100 CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 401365 Seq. ID LIB3431-042-P1-N1-E6 Method BLASTX NCBI GI q3582335 BLAST score 191 E value 2.0e-14 62 Match length 60 % identity (AC005496) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 401366 Seq. ID LIB3431-042-P1-N1-E7 Method BLASTN NCBI GI g2072726

```
BLAST score
                  0.0e+00
E value
Match length
                  455
                  97
% identity
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
Seq. No.
                  401367
Seq. ID
                  LIB3431-042-P1-N1-E8
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  320
E value
                  1.0e-29
Match length
                  61
% identity
                  98
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  401368
Seq. No.
                  LIB3431-042-P1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  326
E value
                  3.0e-30
Match length
                  61
% identity
                  100
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401369
Seq. ID
                  LIB3431-042-P1-N1-F1
Method
                  BLASTX
NCBI GI
                  a671740
BLAST score
                  233
                  3.0e-19
E value
Match length
                  47
% identity
                  96
```

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 401370

Seq. ID LIB3431-042-P1-N1-F10

Method BLASTX
NCBI GI g115813
BLAST score 233
E value 2.0e-19
Match length 53
% identity 85

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi 19182 emb CAA33330 (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

```
Seq. No.
                  401371
                  LIB3431-042-P1-N1-F11
Seq. ID
Method
                  BLASTN
                  g2407280
NCBI GI
                  44
BLAST score
                  4.0e-16
E value
                  56
Match length
                  95
% identity
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  401372
Seq. No.
                  LIB3431-042-P1-N1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g733456
BLAST score
                  306
                  6.0e-28
E value
Match length
                  67
                  91
% identity
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  401373
Seq. No.
                  LIB3431-042-P1-N1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  204
                  2.0e-16
E value
Match length
                  42
% identity
                  93
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  401374
                  LIB3431-042-P1-N1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3929924
BLAST score
                  298
E value
                  6.0e-27
Match length
                  56
                  100
% identity
NCBI Description
                  (AB020502) catalase [Oryza sativa]
                  401375
Seq. No.
                  LIB3431-042-P1-N1-F7
Seq. ID
Method
                  BLASTX
                  g548603
NCBI GI
BLAST score
                  562
                  7.0e-58
E value
Match length
                  110
                  97
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi 478404 pir JQ2247 photosystem I chain D precursor -
```

Match length

% identity

103 50

NCBI Description O.sativa osr40g2 gene



barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 401376 LIB3431-042-P1-N1-G1 Seq. ID Method BLASTX q1353352 NCBI GI 197 BLAST score 4.0e-15 E value Match length 54 % identity 72 (U31975) alanine aminotransferase [Chlamydomonas NCBI Description reinhardtii] 401377 Seq. No. Seq. ID LIB3431-042-P1-N1-G10 Method BLASTX g3789954 NCBI GI BLAST score 174 E value 2.0e-12 Match length 31 % identity 100 (AF094776) chlorophyll a/b-binding protein precursor [Oryza NCBI Description sativa] 401378 Seq. No. Seq. ID LIB3431-042-P1-N1-G11 Method BLASTN NCBI GI g4680189 BLAST score 84 E value 3.0e-39 Match length 148 % identity 23 Oryza sativa subsp. indica putative dnaJ-like protein, NCBI Description putative myb-related protein, putative farnesyl pyrophosphate synthase, and hypothetical protein genes, complete cds 401379 Seq. No. LIB3431-042-P1-N1-G2 Seq. ID Method BLASTX g1708424 NCBI GI BLAST score 274 4.0e-24 E value 92 Match length 57 % identity ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590) NCBI Description isoflavone reductase-like protein [Lupinus albus] 401380 Seq. No. LIB3431-042-P1-N1-G3 Seq. ID Method BLASTN NCBI GI q1658312 BLAST score 100 E value 9.0e-49

NCBI GI

BLAST score

g128191

343

401381 Seq. No. LIB3431-042-P1-N1-G4 Seq. ID Method BLASTX NCBI GI g132105 BLAST score 295 1.0e-26 E value 57 Match length 98 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 401382 Seq. No. LIB3431-042-P1-N1-G6 Seq. ID Method BLASTX NCBI GI g3915088 BLAST score 254 9.0e-22 E value Match length 75 % identity 63 TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID NCBI Description 4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73) >gi 903872 (L38898) trans-cinnamate 4-monooxygenase [Petroselinum crispum] 401383 Seq. No. LIB3431-042-P1-N1-G8 Seq. ID Method BLASTX g1617197 NCBI GI BLAST score 276 E value 3.0e-24 Match length 71 % identity 70 NCBI Description (Z72488) CP12 [Nicotiana tabacum] 401384 Seq. No. LIB3431-042-P1-N1-G9 Seq. ID Method BLASTX NCBI GI q1617197 189 BLAST score 3.0e-14 E value Match length 39 % identity 90 NCBI Description (Z72488) CP12 [Nicotiana tabacum] 401385 Seq. No. LIB3431-042-P1-N1-H1 Seq. ID Method BLASTX



```
4.0e-32
E value
Match length
                   73
                   88
% identity
                   NITRATE REDUCTASE [NAD(P)H] >gi_66210_pir__RDBHNP nitrate reductase (NAD(P)H) (EC 1.6.6.2) - barley
NCBI Description
                   >gi_19065_emb_CAA42739_ (X60173) nitrate reductase
                   (NAD(P)H) [Hordeum vulgare]
Seq. No.
                   401386
                   LIB3431-042-P1-N1-H10
Seq. ID
                   BLASTN
Method
                   g3789953
NCBI GI
BLAST score
                   68
                   3.0e-30
E value
Match length
                   100
% identity
                   92
                   Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   401387
Seq. No.
                   LIB3431-042-P1-N1-H12
Seq. ID
                   BLASTN
Method
                   g5852077
NCBI GI
BLAST score
                   179
                   3.0e-96
E value
                   218
Match length
                   96
% identity
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                   clone: b6015
                   401388
Seq. No.
                   LIB3431-042-P1-N1-H2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g169820
                   90
BLAST score
                   7.0e-43
E value
Match length
                   373
% identity
                   82
NCBI Description Oryza sativa triosephosphate isomerase (Rictpi) mRNA,
                   complete cds
                   401389
Seq. No.
                   LIB3431-042-P1-N1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5734585
                   307
BLAST score
                   5.0e-28
E value
Match length
                   82
                   73
% identity
NCBI Description
                   (AJ245861) putative internal rotenone-insensitive NADH
```

Seq. No. 401390

Seq. ID LIB3431-042-P1-N1-H7

Method BLASTX NCBI GI g3914466

dehydrogenase [Solanum tuberosum]



BLAST score 366 E value 5.0e-35 Match length 67 % identity 97

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN

subunit precursor [Zea mays]

Seq. No. 401391

Seq. ID LIB3431-043-P1-K1-A1

Method BLASTX
NCBI GI g132105
BLAST score 735
E value 4.0e-78
Match length 156
% identity 90

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone posssilas) - rice >gi 218208 dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401392

Seq. ID LIB3431-043-P1-K1-A11

Method BLASTX
NCBI GI g3126854
BLAST score 628
E value 1.0e-65
Match length 119
% identity 99

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401393

Seq. ID LIB3431-043-P1-K1-A12

Method BLASTN
NCBI GI g3885887
BLAST score 112
E value 2.0e-56
Match length 143
% identity 96

NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,

complete cds

Seq. No. 401394

Seq. ID LIB3431-043-P1-K1-A2

Method BLASTX
NCBI GI g3150410
BLAST score 277
E value 2.0e-24
Match length 96
% identity 60

NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

```
401395
Seq. No.
                  LIB3431-043-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3004555
BLAST score
                  220
E value
                  1.0e-17
Match length
                  164
% identity
                  12
                  (AC003673) similar to salt inducible protein [Arabidopsis
NCBI Description
                  thaliana]
                  401396
Seq. No.
                  LIB3431-043-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4959460
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
                  100
% identity
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
                  401397
                  LIB3431-043-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g125606
BLAST score
                  184
E value
                   2.0e-13
Match length
                   59
% identity
                   61
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463 pir S12248
NCBI Description
                   pyruvate kinase (EC 2.7.1.40) - potato
                   >qi 22576 emb CAA37727 (X53688) pyruvate kinase [Solanum
                   tuberosum]
                   401398
Seq. No.
                   LIB3431-043-P1-K1-A8
Seq. ID
Method
                   BLASTX
                   g3551954
NCBI GI
BLAST score
                   468
                   8.0e-47
E value
Match length
                   145
                   57
% identity
                  (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                  hybrid cultivar]
                   401399
Seq. No.
                   LIB3431-043-P1-K1-A9
Seq. ID
Method
                  BLASTX
                   g2570499
NCBI GI
                   191
BLAST score
E value
                   1.0e-14
Match length
                   38
```

Seq. No. 401400

100

sativa]

% identity

NCBI Description

(AF022732) 23kDa polypeptide of photosystem II [Oryza



```
LIB3431-043-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  690
                  8.0e-73
E value
                  147
Match length
% identity
                  89
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375_prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401401
Seq. No.
                  LIB3431-043-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499417
BLAST score
                  499
                  2.0e-50
E value
Match length
                  120
% identity
                  78
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
NCBI Description
                  >gi_1085826_pir__S49248 H-protein - Flaveria anomala
                  >gi 547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
                  anomala]
                  401402
Seq. No.
                  LIB3431-043-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4079798
                  537
BLAST score
E value
                  7.0e-55
Match length
                  104
% identity
                  100
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  401403
Seq. No.
                  LIB3431-043-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  584
                  2.0e-60
E value
                  110
Match length
                  97
% identity
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
```

NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401404 LIB3431-043-P1-K1-B4 Seq. ID Method BLASTX q3258238 NCBI GI BLAST score 157 E value 2.0e-10 108 Match length 30 % identity (AP000007) 224aa long hypothetical protein [Pyrococcus NCBI Description horikoshii] Seq. No. 401405 LIB3431-043-P1-K1-B5 Seq. ID BLASTX Method g2982453 NCBI GI BLAST score 224 E value 3.0e-22 Match length 72 78 % identity (AL022223) fructose-bisphosphate aldolase-like protein NCBI Description [Arabidopsis thaliana] Seq. No. 401406 LIB3431-043-P1-K1-B6 Seq. ID Method BLASTX g132105 NCBI GI BLAST score 839 E value 3.0e-90 175 Match length 91 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxy \overline{l} ase (\overline{E} C $4.\overline{1}.1.39$) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 401407 LIB3431-043-P1-K1-B9 Seq. ID Method BLASTX g732174 NCBI GI BLAST score 531 3.0e-54 E value Match length 144 % identity 67 NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE KO3H1.2 >gi_3878176_emb_CAA82662.1_ (Z29560) similar to DEAH subfamily RNA helicases, especially yeast pre-mRNA splicing factors 22 and 16; cDNA EST EMBL:D27770 comes from this gene; cDNA EST EMBL: D27769 comes from this

gene; cDNA EST EMBL: D36247 comes from thi...

>gi 4249768 gb AAD13795 (AF120269) sex determination

protein MOG-1 [Caenorhabditis elegans]

Seq. No. 401408 LIB3431-043-P1-K1-C1 Seq. ID BLASTX Method g320618 NCBI GI BLAST score 521 E value 4.0e-53 115 Match length 86 % identity chlorophyll a/b-binding protein I precursor - rice NCBI Description >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa] 401409 Seq. No. LIB3431-043-P1-K1-C10 Seq. ID Method BLASTN NCBI GI q21832 BLAST score 39 1.0e-12 E value Match length 43 % identity 98 Wheat mRNA for chloroplast phosphoglycerate kinase (EC NCBI Description 2.7.2.3) 401410 Seq. No. LIB3431-043-P1-K1-C12 Seq. ID BLASTX Method NCBI GI q5360230 BLAST score 1053 1.0e-115 E value 204 Match length % identity 96 NCBI Description (AB015287) Ran [Oryza sativa] 401411 Seq. No. LIB3431-043-P1-K1-C2 Seq. ID BLASTX Method NCBI GI q115787 489 BLAST score 2.0e-49 E value 117 Match length 85 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 401412

Seq. ID LIB3431-043-P1-K1-C4

MethodBLASTXNCBI GIg2072555BLAST score175E value2.0e-12

NCBI GI

BLAST score

```
Match length
                  32
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  401413
Seq. No.
Seq. ID
                  LIB3431-043-P1-K1-C5
Method
                  BLASTX
                  g676884
NCBI GI
BLAST score
                  289
                  9.0e-26
E value
Match length
                  77
% identity
                  71
                  (D29681) The expression is induced by Pi starvation.
NCBI Description
                  [Nicotiana tabacum] >gi 1094819 prf 2106387C Al-induced
                  protein [Nicotiana tabacum]
                  401414
Seq. No.
                  LIB3431-043-P1-K1-C6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1661159
BLAST score
                  81
E value
                  5.0e-38
Match length
                  85
                  99
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b binding protein (kcdl895)
                  mRNA, complete cds
Seq. No.
                  401415
                  LIB3431-043-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  507
E value
                  2.0e-51
Match length
                  123
% identity
                  81
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  401416
Seq. ID
                  LIB3431-043-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q4587556
BLAST score
                  433
E value
                  1.0e-42
Match length
                  140
% identity
                  61
                  (AC006577) Similar to gi_1653162 (p)ppGpp
NCBI Description
                  3-pyrophosphohydrolase from Synechocystis sp genome
                  gb D90911. EST gb W43807 comes from this gene.
                   [Arabidopsis thaliana]
                  401417
Seq. No.
Seq. ID
                  LIB3431-043-P1-K1-D1
Method
                  BLASTX
```

51482

g2618686



E value 5.0e-39
Match length 163
% identity 48

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 401418

Seq. ID LIB3431-043-P1-K1-D10

Method BLASTN
NCBI GI g3618309
BLAST score 157
E value 3.0e-83
Match length 173
% identity 97

NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds,

clone:E10707

Seq. No. 401419

Seq. ID LIB3431-043-P1-K1-D12

Method BLASTX
NCBI GI g1718097
BLAST score 448
E value 2.0e-44
Match length 125
% identity 62

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)

(41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir_A55016

lysosomal membrane protein DVA41 - slime mold

(Dictyostelium discoideum) >gi_532733 (U13150) vacuolar

ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No. 401420

Seq. ID LIB3431-043-P1-K1-D2

Method BLASTX
NCBI GI g671740
BLAST score 486
E value 6.0e-49
Match length 88
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 401421

Seq. ID LIB3431-043-P1-K1-D3

Method BLASTX
NCBI GI g115787
BLAST score 515
E value 2.0e-52
Match length 121
% identity 86

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182_emb_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 401422

Seq. ID LIB3431-043-P1-K1-D5

```
Method
                  BLASTX
NCBI GI
                  q417260
BLAST score
                  407
                  1.0e-39
E value
                  128
Match length
                  65
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632
NCBI Description
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
                  401423
Seq. No.
                  LIB3431-043-P1-K1-D7
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
                  530
BLAST score
                  4.0e-54
E value
                  121
Match length
% identity
                  83
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  401424
Seq. No.
                  LIB3431-043-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4583548
                  723
BLAST score
E value
                  1.0e-76
                  183
Match length
                  78
% identity
                  (AJ010820) chloroplast FtsY homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  401425
                  LIB3431-043-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  q1749676
NCBI GI
BLAST score
                  147
E value
                  3.0e-09
Match length
                  82
% identity
                  44
                  (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
NCBI Description
                  EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
                  401426
Seq. No.
                  LIB3431-043-P1-K1-E1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2773153
BLAST score
                  489
```

E value 0.0e + 00Match length 496 100 % identity

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 401427



```
LIB3431-043-P1-K1-E10
Seq. ID
Method
                  BLASTX
                  q82080
NCBI GI
                  378
BLAST score
                  3.0e-36
E value
                  112
Match length
                  66
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  401428
Seq. No.
                  LIB3431-043-P1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q115787
BLAST score
                  741
                  1.0e-78
E value
                  169
Match length
% identity
                  88
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  401429
Seq. No.
                  LIB3431-043-P1-K1-E3
Seq. ID
Method
                  BLASTN
                  q6006355
NCBI GI
                  221
BLAST score
E value
                  1.0e-121
                  297
Match length
                  100
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  401430
                  LIB3431-043-P1-K1-E5
Seq. ID
Method
                  BLASTX
                  g3256035
NCBI GI
                  238
BLAST score
E value
                  9.0e-20
                  135
Match length
                  39
% identity
                  (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                  bicolor]
                  401431
Seq. No.
                  LIB3431-043-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
```

Method BLASTX
NCBI GI g3789954
BLAST score 465
E value 2.0e-46
Match length 87
% identity 98

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]



```
Seq. No.
                   401432
Seq. ID
                  LIB3431-043-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q729478
BLAST score
                  413
E value
                  2.0e-40
                  158
Match length
                  53
% identity
NCBI Description
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                  >gi 442481 dbj BAA04616 (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa] >gi 6069649 dbj BAA85425.1
                   (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                  a region of the predicted gene.; similar to
                  ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
Seq. No.
                  401433
                  LIB3431-043-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4585882
BLAST score
                  721
                  2.0e-76
E value
                  159
Match length
% identity
                  81
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  401434
Seq. ID
                  LIB3431-043-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  688
                  2.0e-72
E value
Match length
                  133
                  97
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  401435
Seq. ID
                  LIB3431-043-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2443402
BLAST score
                  824
E value
                  2.0e-88
Match length
                  162
% identity
                  100
NCBI Description
                  (D87745) orthophosphate dikinase [Oryza sativa]
                  >gi 2443405 dbj BAA22420 (D87952) orthophosphate dikinase
                   [Oryza sativa]
Seq. No.
                  401436
Seq. ID
                  LIB3431-043-P1-K1-F8
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2739375
BLAST score 150
E value 2.0e-09
Match length 95
% identity 41



NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 401437

Seq. ID LIB3431-043-P1-K1-G1

Method BLASTX
NCBI GI g417488
BLAST score 580
E value 3.0e-72
Match length 155
% identity 85

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi_169473 (M69038) alpha-glucan phosphorylase

type H isozyme [Solanum tuberosum]

Seq. No. 401438

Seq. ID LIB3431-043-P1-K1-G11

Method BLASTX
NCBI GI g3126854
BLAST score 581
E value 3.0e-60
Match length 109
% identity 100

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401439

Seq. ID LIB3431-043-P1-K1-G12

Method BLASTX
NCBI GI g131388
BLAST score 469
E value 7.0e-47
Match length 145
% identity 69

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 401440

Seq. ID LIB3431-043-P1-K1-G3

Method BLASTX
NCBI GI g3126854
BLAST score 671
E value 2.0e-76
Match length 144
% identity 99

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401441

Seq. ID LIB3431-043-P1-K1-G4

Method BLASTX
NCBI GI g5596468
BLAST score 266
E value 4.0e-23



Match length 59 % identity

(AL096882) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

401442

Seq. ID

LIB3431-043-P1-K1-G5

Method NCBI GI BLASTX g4454459 564

BLAST score E value Match length

5.0e-58 133

82

% identity NCBI Description

(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.

401443

Seq. ID Method

LIB3431-043-P1-K1-G7

NCBI GI BLAST score BLASTX g5091616 643

E value Match length

3.0e-67 202 65

% identity NCBI Description

(AC007454) F23M19.3 [Arabidopsis thaliana]

Seq. No.

401444

Seq. ID

LIB3431-043-P1-K1-G8

Method BLASTX g115787 NCBI GI 586 BLAST score 1.0e-60 E value Match length 133

% identity 88

NCBI Description

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No.

401445

Seq. ID

LIB3431-043-P1-K1-G9

Method BLASTX NCBI GI q115787 BLAST score 554 E value 5.0e-57 Match length 126 % identity 87

NCBI Description

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No.

401446

Seq. ID

LIB3431-043-P1-K1-H1

Method BLASTX NCBI GI g5926718 BLAST score 544

```
E value
                  1.0e-55
                  154
Match length
                  69
% identity
                  (AB007911) PRA2 [Pisum sativum]
NCBI Description
                  401447
Seq. No.
                  LIB3431-043-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g3914603
NCBI GI
                  728
BLAST score
                  3.0e-77
E value
                  144
Match length
                  97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                  401448
Seq. No.
                  LIB3431-043-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  g2146745
NCBI GI
                  493
BLAST score
                  9.0e-53
E value
                  168
Match length
% identity
                  67
                  protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                  >qi 642132 dbj BAA08215 (D45354) protein kinase
                  [Arabidopsis thaliana]
                  401449
Seq. No.
                  LIB3431-043-P1-K1-H12
Seq. ID
                  BLASTX
Method
                  g115802
NCBI GI
BLAST score
                  195
                  8.0e-15
E value
                  36
Match length
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                  a/b-binding protein (cab-\overline{3}6) - common tobacco
                  >qi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
                  401450
Seq. No.
                  LIB3431-043-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132096
BLAST score
                   922
                  1.0e-100
E value
Match length
                  175
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
                   (RUBISCO SMALL SUBUNIT A) >gi 68095 pir RKRZS6
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS2106) - rice >gi 218210_dbj_BAA00539_
```

(D00644) small subunit of ribulose-1,5-bisphosphate

Method

NCBI GI

BLASTX

g4079798



carboxylase (RuBPC) [Oryza sativa]

```
Seq. No.
                  401451
                  LIB3431-043-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3986110
BLAST score
                  431
E value
                  2.0e-42
                  121
Match length
                   69
% identity
                  (AB012716) heat shock protein 70 cognate [Salix gilgiana]
NCBI Description
                  401452
Seq. No.
Seq. ID
                  LIB3431-043-P1-K1-H8
Method
                  BLASTX
                   g5669656
NCBI GI
BLAST score
                   273
                   6.0e-24
E value
Match length
                   98
% identity
                   56
                  (AF096263) ER33 protein [Lycopersicon esculentum]
NCBI Description
                   401453
Seq. No.
                  LIB3431-043-P1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3126854
                   300
BLAST score
                   3.0e-27
E value
Match length
                  57
% identity
                  100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                   401454
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-A12
Method
                   BLASTN
NCBI GI
                   q3885887
BLAST score
                   389
                   0.0e + 00
E value
                   397
Match length
% identity
                   99
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
                   401455
Seq. No.
Seq. ID
                   LIB3431-043-P1-N1-A4
Method
                   BLASTN
NCBI GI
                   q11957
BLAST score
                   98
E value
                   1.0e-47
Match length
                   340
% identity
                   41
NCBI Description Rice complete chloroplast genome
                   401456
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-A9
```

51490

BLAST score E value 9.0e-32 Match length 66 98 % identity (AF052203) 23 kDa polypeptide of photosystem II [Oryza NCBI Description sativa] 401457

Seq. No. Seq. ID

LIB3431-043-P1-N1-B10

Method BLASTX NCBI GI g132105 BLAST score 508 E value 1.0e-51 Match length 91 % identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401458

LIB3431-043-P1-N1-B11 Seq. ID

Method BLASTX NCBI GI g2499417 BLAST score 309 E value 3.0e-28 Match length 71 % identity 82

NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR

> >gi_1085826_pir__S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria

anomala]

Seq. No. 401459

Seq. ID LIB3431-043-P1-N1-B2

Method BLASTX NCBI GI q4079798 BLAST score 183 E value 2.0e-13 Match length 34 100 % identity

NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza

sativa]

Seq. No. 401460

Seq. ID LIB3431-043-P1-N1-B3

Method BLASTX NCBI GI g347451 BLAST score 248 E value 4.0e-21 Match length 48 % identity 100



(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza NCBI Description sativa]

Seq. No. 401461

LIB3431-043-P1-N1-B4 Seq. ID

Method BLASTN NCBI GI g20262 BLAST score 191 E value 1.0e-103 Match length 379 % identity 88

NCBI Description O.sativa light-induced mRNA

Seq. No. 401462

LIB3431-043-P1-N1-B6 Seq. ID

Method BLASTX NCBI GI q132105 BLAST score 165 E value 2.0e-11 Match length 32 % identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401463

Seq. ID LIB3431-043-P1-N1-C1

Method BLASTX NCBI GI q115787 BLAST score 409 E value 6.0e-40 Match length 77 % identity 100

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 401464

Seq. ID LIB3431-043-P1-N1-C12

Method BLASTN NCBI GI q5360229 BLAST score 397 0.0e + 00E value Match length 401 100 % identity

NCBI Description Oryza sativa mRNA for Ran, complete cds

Seq. No. 401465

LIB3431-043-P1-N1-C2 Seq. ID

```
Method
                   BLASTX
NCBI GI
                   g226263
BLAST score
                   213
E value
                   5.0e-17
Match length
                   47
                   85
% identity
NCBI Description
                   401466
```

chlorophyll a/b binding protein [Glycine max]

Seq. No. Seq. ID

LIB3431-043-P1-N1-C7

Method BLASTX NCBI GI g1835731 BLAST score 314 8.0e-29 E value Match length 80 % identity 79

(U86018) photosystem II 10 kDa polypeptide [Oryza sativa] NCBI Description

Seq. No.

401467

LIB3431-043-P1-N1-D1 Seq. ID

Method BLASTX NCBI GI g1661160 BLAST score 185 7.0e-14 E value Match length 54 % identity 69

(U74295) chlorophyll a/b binding protein [Oryza sativa] NCBI Description

Seq. No. 401468

LIB3431-043-P1-N1-D10 Seq. ID

Method BLASTX NCBI GI q3618310 367 BLAST score 4.0e-35 E value Match length 70 % identity 100

(AB001883) zinc finger protein [Oryza sativa] NCBI Description

Seq. No.

401469 LIB3431-043-P1-N1-D2 Seq. ID

Method BLASTX NCBI GI g671740 BLAST score 383 5.0e-37 E value Match length 71

% identity 99

(X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description

construct]

Seq. No. 401470

Seq. ID LIB3431-043-P1-N1-D3

Method BLASTX NCBI GI q4512125 BLAST score 243 E value 1.0e-20 Match length 45 % identity 100



(AF133340) putative chlorophyll a/b-binding protein NCBI Description [Phalaenopsis sp. 'KCbutterfly'] 401471 Seq. No. LIB3431-043-P1-N1-D5 Seq. ID BLASTX Method g417260 NCBI GI BLAST score 300 3.0e-27 E value 76 Match length 75 % identity LIGHT REGULATED PROTEIN PRECURSOR >gi_422003 pir__\$33632 NCBI Description lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa] 401472 Seq. No. LIB3431-043-P1-N1-D7 Seq. ID BLASTX Method q115787 NCBI GI BLAST score 428 3.0e-42 E value Match length 81 100 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 401473 Seq. No. LIB3431-043-P1-N1-D8 Seq. ID BLASTX Method g4583548 NCBI GI BLAST score 346 E value 1.0e-32 Match length 79 85 % identity NCBI Description (AJ010820) chloroplast FtsY homolog [Arabidopsis thaliana] 401474 Seq. No. LIB3431-043-P1-N1-D9 Seq. ID Method BLASTX g1749676 NCBI GI 143 BLAST score E value 9.0e-09 76 Match length % identity 45 (D89234) similar to Saccharomyces cerevisiae ORF YGR205W, NCBI Description EMBL Accession Number Z72990 [Schizosaccharomyces pombe]

Seq. No. 401475

Seq. ID LIB3431-043-P1-N1-E10

Method BLASTX
NCBI GI g115813
BLAST score 253
E value 1.0e-21
Match length 61

```
80
on CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
```

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 401476

% identity

Seq. ID LIB3431-043-P1-N1-E12

Method BLASTX
NCBI GI g3036946
BLAST score 271
E value 8.0e-24
Match length 52
% identity 98

NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No. 401477

Seq. ID LIB3431-043-P1-N1-E3

Method BLASTN
NCBI GI g6006355
BLAST score 43
E value 7.0e-15
Match length 123
% identity 84

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401478

Seq. ID LIB3431-043-P1-N1-E5

Method BLASTX
NCBI GI g3256035
BLAST score 195
E value 7.0e-15
Match length 67
% identity 55

NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum

bicolor]

Seq. No. 401479

Seq. ID LIB3431-043-P1-N1-E7

Method BLASTX
NCBI GI g128690
BLAST score 535
E value 1.0e-54
Match length 118
% identity 89

NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST

>gi_66161_pir__DERZN3 NADH dehydrogenase (ubiquinone) (EC
1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_

(X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa] >gi_226610_prf__1603356AG NADH dehydrogenase ND3 [Oryza

sativa]

Seq. No. 401480

Seq. ID LIB3431-043-P1-N1-E8

Method BLASTN NCBI GI g3819688 BLAST score 41

```
1.0e-13
E value
Match length
                  49
% identity
                  96
NCBI Description
                  Hordeum vulgare genomic DNA fragment; clone MWG2318.uni
                  401481
Seq. No.
                  LIB3431-043-P1-N1-E9
Seq. ID
Method
                  BLASTX
                  g693920
NCBI GI
BLAST score
                  325
                  3.0e-30
E value
Match length
                  64
% identity
                  98
                  (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                  tuberosum]
Seq. No.
                  401482
Seq. ID
                  LIB3431-043-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  299
E value
                  3.0e-27
Match length
                  76
                  80
% identity
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  401483
Seq. ID
                  LIB3431-043-P1-N1-F2
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  181
E value
                  3.0e-13
Match length
                  35
% identity
                  97
NCBI Description
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
                  401484
Seq. No.
                  LIB3431-043-P1-N1-F6
Seq. ID
Method
                  BLASTX
                  g2443402
NCBI GI
BLAST score
                  174
                  2.0e-12
E value
Match length
                  32
% identity
                  100
                  (D87745) orthophosphate dikinase [Oryza sativa]
NCBI Description
                  >gi_2443405_dbj_BAA22420_ (D87952) orthophosphate dikinase
                  [Oryza sativa]
Seq. No.
                  401485
                  LIB3431-043-P1-N1-F7
Seq. ID
Method
                  BLASTX
```

51496

g2754849

8.0e-26

288

NCBI GI BLAST score

E value

% identity

```
Match length
                  63
                  89
% identity
NCBI Description
                  (AF039000) putative serine-glyoxylate aminotransferase
                  [Fritillaria agrestis]
                  401486
Seq. No.
                  LIB3431-043-P1-N1-G1
Seq. ID
Method
                  BLASTX
                  g417488
NCBI GI
BLAST score
                  152
E value
                  4.0e-16
Match length
                  51
% identity
                  81
NCBI Description
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
                  H) >gi 100452 pir A40995 starch phosphorylase (EC 2.4.1.1)
                  H - potato >gi 169473 (M69038) alpha-glucan phosphorylase
                  type H isozyme [Solanum tuberosum]
Seq. No.
                  401487
                  LIB3431-043-P1-N1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006895
BLAST score
                  158
                  3.0e-10
E value
Match length
                  51
                  49
% identity
NCBI Description
                 (Z99708) putative protein [Arabidopsis thaliana]
                  401488
Seq. No.
                  LIB3431-043-P1-N1-G11
Seq. ID
Method
                  BLASTX
                  g3126854
NCBI GI
BLAST score
                  277
E value
                  2.0e-24
Match length
                  52
                  100
% identity
NCBI Description
                 (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  401489
Seq. ID
                  LIB3431-043-P1-N1-G3
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  200
E value
                  2.0e-19
Match length
                  53
                  98
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  401490
Seq. ID
                  LIB3431-043-P1-N1-G4
Method
                  BLASTX
NCBI GI
                  q5596468
BLAST score
                  145
E value
                  5.0e-09
Match length
                  43
```

NCBI Description (AL096882) putative protein [Arabidopsis thaliana]

65

```
401491
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-G8
                  BLASTX
Method
NCBI GI
                  g3036942
BLAST score
                  247
                  5.0e-21
E value
                  46
Match length
% identity
                  100
                  (AB012636) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
                  401492
Seq. No.
                  LIB3431-043-P1-N1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  52
                  3.0e-20
E value
                  72
Match length
% identity
                  93
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  401493
                  LIB3431-043-P1-N1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q303736
BLAST score
                  152
                  7.0e-10
E value
                  80
Match length
% identity
                  49
                  (D12541) GTP-binding protein [Pisum sativum]
NCBI Description
                  >gi 738934 prf 2001457B GTP-binding protein [Pisum
                  sativum]
                  401494
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-H10
Method
                  BLASTX
NCBI GI
                  g167097
BLAST score
                  151
                  5.0e-17
E value
                  52
Match length
                  88
% identity
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
                   401495
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-H11
                  BLASTN
Method
NCBI GI
                  q3377792
BLAST score
                  131
                  2.0e-67
E value
Match length
                  284
                  87
% identity
NCBI Description Oryza sativa ribulose-1,5-bisphosphate
```

carboxylase/oxygenase activase (rca) mRNA, complete cds



```
401496
Seq. No.
                  LIB3431-043-P1-N1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  163
                  4.0e-11
E value
Match length
                  31
                  100
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  401497
Seq. No.
                  LIB3431-043-P1-N1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  301
E value
                  3.0e-27
Match length
                  57
% identity
                  100
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  401498
                  LIB3431-043-P1-N1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3218542
BLAST score
                  36
                  1.0e-10
E value
Match length
                  119
                  82
% identity
NCBI Description Oryza sativa AOX1b and AOX1a genes, complete cds
                   401499
Seq. No.
                  LIB3431-043-P1-N1-H6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g473216
BLAST score
                   36
                   1.0e-10
E value
                   44
Match length
                   95
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
                   401500
Seq. No.
                  LIB3431-044-P1-K1-A1
Seq. ID
                   BLASTX
Method
                   g320618
NCBI GI
                   457
BLAST score
                   1.0e-45
E value
                   106
Match length
% identity
                   83
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
```

Seq. No. 401501

[Oryza sativa]



```
LIB3431-044-P1-K1-A10
Seq. ID
Method
                  BLASTX
                  q3647283
NCBI GI
BLAST score
                  278
                  1.0e-45
E value
                  147
Match length
                  63
% identity
                  (AJ011418) ubiquitin activating enzyme [Lycopersicon
NCBI Description
                  esculentum]
                  401502
Seq. No.
                  LIB3431-044-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
                  237
BLAST score
                  8.0e-20
E value
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  401503
Seq. No.
                  LIB3431-044-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  815
                  2.0e-87
E value
Match length
                  159
                  98
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  401504
Seq. No.
                  LIB3431-044-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1173275
BLAST score
                  653
E value
                  3.0e-74
Match length
                  150
                  96
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
NCBI Description
                  >gi_2119068_pir__S58630 ribosomal protein S7 - maize
                  chloroplast >gi 902274 emb CAA60339 (X86563) ribosomal
                  protein S7 [Zea mays] >gi 902298 emb CAA60362 (X86563)
                  ribosomal protein S7 [Zea mays]
                  401505
Seq. No.
                  LIB3431-044-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  656
E value
                  5.0e-69
Match length
                  123
                  100
% identity
                 (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
```

Seq. No. 401506

```
LIB3431-044-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   a1835731
BLAST score
                   594
E value
                   2.0e-61
Match length
                   126
% identity
                   91
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  401507
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g729477
BLAST score
                   603
E value
                  1.0e-62
Match lèngth
                  126
% identity
                  87
NCBI Description
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
                  >gi 320548 pir A44974 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - common ice plant >gi 167256 (M25528)
                  ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                   [Mesembryanthemum crystallinum] >qi 226768 prf 1604475A
                  ferredoxin NADP reductase [Mesembryanthemum crystallinum]
Seq. No.
                  401508
Seq. ID
                  LIB3431-044-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3402711
BLAST score
                  349
E value
                  5.0e-33
Match length
                  120
% identity
                  57
NCBI Description
                  (AC004261) putative RNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  401509
Seq. ID
                  LIB3431-044-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  a3789954
BLAST score
                  240
E value
                  2.0e-20
Match length
                  60
% identity
                  77
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
Seq. No.
                  401510
Seq. ID
                  LIB3431-044-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  6.0e-20
E value
Match length
                  44
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
```

51501

protein [Oryza sativa]

>gi_6103441 gb AAF03603.1 (AF147786) metallothionein-like

Seq. No. 401511

Seq. ID LIB3431-044-P1-K1-B10

Method BLASTX
NCBI GI g1731181
BLAST score 195
E value 7.0e-15
Match length 136
% identity 38

NCBI Description HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II

>gi_3874230_emb_CAA90107.1_ (Z49909) weak similarity with a
B. Flavum translocation protein (Swiss Prot accession
number P38376); cDNA EST yk220e10.5 comes from this gene;

cDNA EST yk549e12.3 comes from this gene; cDNA EST

yk618d6.3 comes from this gene

Seq. No. 401512

Seq. ID LIB3431-044-P1-K1-B11

Method BLASTX
NCBI GI g3126854
BLAST score 717
E value 5.0e-76
Match length 137
% identity 99

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401513

Seq. ID LIB3431-044-P1-K1-B12

Method BLASTX
NCBI GI g548605
BLAST score 513
E value 4.0e-52
Match length 131
% identity 80

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 401514

Seq. ID LIB3431-044-P1-K1-B3

Method BLASTX
NCBI GI g4972093
BLAST score 227
E value 1.0e-18
Match length 131
% identity 40

NCBI Description (AL078468) putative protein [Arabidopsis thaliana]

Seq. No. 401515

Seq. ID LIB3431-044-P1-K1-B4

Method BLASTX
NCBI GI g3063524
BLAST score 183
E value 2.0e-13
Match length 37

```
% identity
NCBI Description
                  (AF052305) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  401516
Seq. ID
                  LIB3431-044-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
                  6.0e-10
E value
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  401517
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2827150
BLAST score
                  559
E value
                  2.0e-57
Match length
                  148
                  76
% identity
NCBI Description
                  (AF029895) acetyl-coenzyme A carboxylase [Triticum
                  aestivum]
Seq. No.
                  401518
Seq. ID
                  LIB3431-044-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g2344892
BLAST score
                  213
E value
                  7.0e-17
Match length
                  68
% identity
                  69
NCBI Description
                  (AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.
                  401519
Seq. ID
                  LIB3431-044-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q1495768
BLAST score
                  152
E value
                  8.0e-10
Match length
                  144
% identity
                  45
NCBI Description
                  (Z68506) chloroplast inner envelope protein, 110 kD
                  (IEP110) [Pisum sativum]
Seq. No.
                  401520
Seq. ID
                  LIB3431-044-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q2130082
```

NCBI GI g213008:
BLAST score 442
E value 1.0e-43
Match length 169
% identity 51

NCBI Description protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443 (U37133) receptor kinase-like protein [Oryza sativa] >gi_2586085 (U72723) receptor kinase-like protein [Oryza





longistaminata] >gi_1586408_prf__2203451A receptor kinase-like protein [Oryza sativa]

Seq. No. 401521

Seq. ID LIB3431-044-P1-K1-C2

Method BLASTX
NCBI GI g2688824
BLAST score 181
E value 3.0e-13
Match length 111
% identity 41

NCBI Description (U93273) putative auxin-repressed protein [Prunus

armeniaca]

Seq. No. 401522

Seq. ID LIB3431-044-P1-K1-C3

Method BLASTX
NCBI GI g548603
BLAST score 295
E value 1.0e-26
Match length 56
% identity 98

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

>gi_478404_pir__JQ2247 photosystem I chain D precursor barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 401523

Seq. ID LIB3431-044-P1-K1-C9

Method BLASTX
NCBI GI g3789952
BLAST score 651
E value 2.0e-68
Match length 128
% identity 98

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No. 401524

Seq. ID LIB3431-044-P1-K1-D1

Method BLASTX
NCBI GI g399213
BLAST score 877
E value 1.0e-94
Match length 181
% identity 96

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato

>gi 170435 (M32604) ATP-dependent protease (CD4B)

[Lycopersicon esculentum]

Seq. No. 401525

Seq. ID LIB3431-044-P1-K1-D12

Method BLASTN
NCBI GI g5295936
BLAST score 46
E value 2.0e-16

```
Match length
% identity
                  85
NCBI Description
                  Oryza sativa genomic DNA, chromosome 6, clone: P0681F10,
                  complete sequence
Seq. No.
                  401526
Seq. ID
                  LIB3431-044-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q2492515
BLAST score
                  662
E value
                  2.0e-69
Match length
                  155
% identity
                  86
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >gi_2129924_pir__S58298 ATPase - pepper (fragment)
                  >gi_929013_emb_CAA62084 (X90472) ATPase [Capsicum annuum]
Seq. No.
                  401527
                  LIB3431-044-P1-K1-D6
Seq. ID
Method
                  BLASTX .
NCBI GI
                  q1652164
BLAST score
                  490
E value
                  3.0e-49
Match length
                  167
% identity
                  61
NCBI Description (D90903) hypothetical protein [Synechocystis sp.]
Seq. No.
                  401528
Seq. ID
                  LIB3431-044-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3618310
BLAST score
                  439
E value
                  3.0e-43
Match length
                  132
% identity
                  69
NCBI Description
                  (AB001883) zinc finger protein [Oryza sativa]
Seq. No.
                  401529
Seq. ID
                  LIB3431-044-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  784
E value
                  8.0e-84
Match length
                  151
% identity
                  97
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  401530
Seq. ID
                  LIB3431-044-P1-K1-E12
```

Method BLASTX
NCBI GI g131225
BLAST score 670
E value 2.0e-70
Match length 151
% identity 88

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein





precursor - barley >gi_167087 (M61146) photosystem I
hydrophobic protein [Hordeum vulgare]

Seq. No. 401531

Seq. ID LIB3431-044-P1-K1-E5

Method BLASTX
NCBI GI g115787
BLAST score 762
E value 3.0e-81
Match length 149
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 401532

Seq. ID LIB3431-044-P1-K1-E6

Method BLASTX
NCBI GI g5042409
BLAST score 442
E value 1.0e-43
Match length 136
% identity 64

NCBI Description (AC006193) Putative membrane related protein [Arabidopsis

thaliana]

Seq. No. 401533

Seq. ID LIB3431-044-P1-K1-E7

Method BLASTX
NCBI GI g5702231
BLAST score 190
E value 3.0e-14
Match length 108
% identity 44

NCBI Description (AF145386) hypersensitive reaction associated Ca2+-binding

protein [Phaseolus vulgaris]

Seq. No. 401534

Seq. ID LIB3431-044-P1-K1-E8

Method BLASTX
NCBI GI g548605
BLAST score 590
E value 5.0e-61
Match length 130
% identity 90

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi 304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 401535

Seq. ID LIB3431-044-P1-K1-E9

Method BLASTN NCBI GI g3821780



BLAST score 36 E value 1.0e-10 Match length 47 % identity 66

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

401536

Seq. ID Method LIB3431-044-P1-K1-F1

Method BLASTX
NCBI GI g2827665
BLAST score 605
E value 6.0e-63
Match length 141
% identity 73

NCBI Description (AL021637) vacuolar sorting receptor-like protein

[Arabidopsis thaliana]

Seq. No.

401537

Seq. ID

LIB3431-044-P1-K1-F12

Method BLASTX
NCBI GI g6091733
BLAST score 219
E value 2.0e-17
Match length 65
% identity 62

NCBI Description (ACO10797) unknown protein [Arabidopsis thaliana]

Seq. No.

401538

Seq. ID

LIB3431-044-P1-K1-F2

Method BLASTX
NCBI GI g2982453
BLAST score 636
E value 2.0e-66
Match length 157
% identity 82

NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein

[Arabidopsis thaliana]

Seq. No.

401539

Seq. ID

LIB3431-044-P1-K1-F3

Method BLASTX
NCBI GI g115787
BLAST score 720
E value 3.0e-76
Match length 157
% identity 90

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No.

401540

Seq. ID

LIB3431-044-P1-K1-F5

Method BLASTX NCBI GI g2147484 BLAST score 766

```
E value
                  1.0e-81
Match length
                  170
% identity
                  85
                 homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
NCBI Description
                  homeobox protein [Phalaenopsis sp. 'hybrid SM9108']
                  401541
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1644427
BLAST score
                  452
E value
                  7.0e-45
Match length
                  130
% identity
                  66
NCBI Description
                 (U74610) glyoxalase II [Arabidopsis thaliana]
                  401542
Seq. No.
                  LIB3431-044-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  301
                  3.0e-27
E value
Match length
                  76
                  75
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  401543
Seq. No.
                  LIB3431-044-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g2072555
NCBI GI
BLAST score
                  218
                  2.0e-17
E value
Match length
                  44
% identity
                  93
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  401544
Seq. ID
                  LIB3431-044-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q1352461
BLAST score
                  388
E value
                  2.0e-37
Match length
                  90
                  83
% identity
NCBI Description IN2-2 PROTEIN
```

Seq. No. 401545

Seq. ID LIB3431-044-P1-K1-G1

Method BLASTX
NCBI GI g4972067
BLAST score 287
E value 2.0e-27
Match length 166
% identity 44

NCBI Description (AL078467) putative protei [Arabidopsis thaliana]

Seq. No.

Seq. ID

401551

LIB3431-044-P1-K1-G6

```
Seq. No.
                  401546
Seq. ID
                  LIB3431-044-P1-K1-G10
Method
                  BLASTX
                  q3132476
NCBI GI
                  579
BLAST score
E value
                  9.0e-60
Match length
                  167
% identity
                  66
NCBI Description
                  (AC003096) unknown protein [Arabidopsis thaliana]
                  401547
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  616
E value
                  4.0e-64
Match length
                  134
% identity
                  87
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  401548
Seq. ID
                  LIB3431-044-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q4490728
BLAST score
                  290
                  6.0e-26
E value
Match length
                  65
% identity
                  75
NCBI Description
                  (AL035709) putative protein [Arabidopsis thaliana]
Seq. No.
                  401549
Seq. ID
                  LIB3431-044-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  q19094
BLAST score
                  48
E value
                  4.0e-18
Match length
                  64
% identity
                  94
NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N
Seq. No.
                  401550
Seq. ID
                  LIB3431-044-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q1684851
BLAST score
                  212
E value
                  6.0e-17
Match length
                  62
% identity
                  68
NCBI Description
                  (U77935) DnaJ-like protein [Phaseolus vulgaris]
```

51509

```
Method BLASTX
NCBI GI g1052960
BLAST score 848
E value 3.0e-91
Match length 172
% identity 91
```

NCBI Description (U37437) PNIL34 [Ipomoea nil]

Seq. No. 401552

Seq. ID LIB3431-044-P1-K1-G9

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 401553

Seq. ID LIB3431-044-P1-K1-H10

Method BLASTX
NCBI GI g2129675
BLAST score 218
E value 1.0e-17
Match length 84
% identity 67

NCBI Description probable chlorophyll synthetase G4 - Arabidopsis thaliana

>gi_972938 (U19382) putative chlorophyll synthetase
[Arabidopsis thaliana] >gi 3068709 (AF049236) putative

chlorophyll synthetase [Arabidopsis thaliana]

Seq. No. 401554

Seq. ID LIB3431-044-P1-K1-H11

Method BLASTX
NCBI GI 94531444
BLAST score 320
E value 1.0e-44
Match length 151
% identity 62

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 401555

Seq. ID LIB3431-044-P1-K1-H12

Method BLASTX
NCBI GI g3202024
BLAST score 743
E value 6.0e-79
Match length 159
% identity 86

NCBI Description (AF069315) thylakoid-bound L-ascorbate peroxidase precursor

[Mesembryanthemum crystallinum]

Seq. No. 401556

Seq. ID LIB3431-044-P1-K1-H2

Method BLASTN



NCBI GI g2072726 BLAST score 542 E value 0.0e+00 Match length 557 % identity 99

NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No.

401557

Seq. ID

LIB3431-044-P1-K1-H3

Method BLASTX
NCBI GI g2554675
BLAST score 745
E value 3.0e-79
Match length 166
% identity 90

NCBI Description Three-Dimensional Structure Of Glycolate Oxidase With Bound

Active-Site Inhibitors >gi 2624594 pdb 1AL7

Three-Dimensional Structures Of Glycolate Oxidase With

Bound Active-Site Inhibitors

Seq. No. 401558

Seq. ID LIB3431-044-P1-K1-H4

Method BLASTX
NCBI GI g132105
BLAST score 731
E value 1.0e-77
Match length 155
% identity 90

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401559

Seq. ID LIB3431-044-P1-K1-H5

Method BLASTX
NCBI GI g3126854
BLAST score 756
E value 1.0e-80
Match length 144
% identity 99

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.

401560

Seq. ID LIB3431-044-P1-K1-H6

Method BLASTX
NCBI GI g132105
BLAST score 776
E value 7.0e-83
Match length 168
% identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR





(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_ RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_ 1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 401561

Seq. ID LIB3431-044-P1-K1-H9

Method BLASTX
NCBI GI g132105
BLAST score 830
E value 4.0e-89
Match length 173
% identity 91

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401562

Seq. ID LIB3431-044-P1-N1-A1

Method BLASTN
NCBI GI g218171
BLAST score 58
E value 2.0e-24
Match length 84
% identity 93

NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll

a/b binding protein of photosystem II (LHCPII), complete

cds

Seq. No. 401563

Seq. ID LIB3431-044-P1-N1-A10

Method BLASTX
NCBI GI g2982309
BLAST score 194
E value 8.0e-15
Match length 46
% identity 78

NCBI Description (AF051239) probable ubiquitin activating enzyme 2 [Picea

mariana]

Seq. No. 401564

Seq. ID LIB3431-044-P1-N1-A11

Method BLASTN
NCBI GI g2072554
BLAST score 240
E value 1.0e-132
Match length 248

```
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  401565
Seq. No.
                  LIB3431-044-P1-N1-A12
Seq. ID
Method
                  BLASTN
                  g2662340
NCBI GI
BLAST score
                  59
E value
                  8.0e-25
Match length
                  91
                  91
% identity
NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds
Seq. No.
                  401566
                  LIB3431-044-P1-N1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173275
BLAST score
                  640
                  7.0e-67
E value
Match length
                  149
                  89
% identity
                 CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
NCBI Description
                  >gi_2119068_pir__S58630 ribosomal protein S7 - maize
                  chloroplast >gi 902274 emb CAA60339 (X86563) ribosomal
                  protein S7 [Zea mays] >gi 902298 emb CAA60362 (X86563)
                  ribosomal protein S7 [Zea mays]
Seq. No.
                  401567
Seq. ID
                  LIB3431-044-P1-N1-A5
Method
                  BLASTN
NCBI GI
                  g2570512
BLAST score
                  88
E value
                  8.0e-42
Match length
                  195
% identity
                  96
NCBI Description
                  Oryza sativa chlorophyll a-b binding protein mRNA, complete
Seq. No.
                  401568
                  LIB3431-044-P1-N1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  436
E value
                  4.0e-43
Match length
                  94
                  89
% identity
NCBI Description
                 (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

Seq. No. 401569

Seq. ID LIB3431-044-P1-N1-A7

Method BLASTN
NCBI GI g1835730
BLAST score 51
E value 3.0e-20
Match length 59
% identity 97





NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 401570

Seq. ID LIB3431-044-P1-N1-A9

Method BLASTN
NCBI GI g3789953
BLAST score 267
E value 1.0e-148
Match length 275
% identity 99

NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor

(Cab26) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 401571

Seq. ID LIB3431-044-P1-N1-B1

Method BLASTN
NCBI GI g2072554
BLAST score 113
E value 5.0e-57
Match length 164
% identity 93

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 401572

Seq. ID LIB3431-044-P1-N1-B11

Method BLASTX
NCBI GI g3126854
BLAST score 410
E value 4.0e-40
Match length 78
% identity 99

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 401573

Seq. ID LIB3431-044-P1-N1-B12

Method BLASTX
NCBI GI g548605
BLAST score 187
E value 2.0e-14
Match length 38
% identity 95

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 401574

Seq. ID LIB3431-044-P1-N1-B2

Method BLASTN
NCBI GI g19086
BLAST score 56
E value 1.0e-22
Match length 100

```
% identity
NCBI Description Hordeum vulgare pot. psaE mRNA
                  401575
Seq. No.
                  LIB3431-044-P1-N1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2344892
BLAST score
                  182
                  2.0e-13
E value
Match length
                  41
                  80
% identity
NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.
                  401576
                  LIB3431-044-P1-N1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1777706
BLAST score
                  59
E value
                  1.0e-24
Match length
                  71
                  96
% identity
NCBI Description Zea mays 18S ribosomal RNA gene, partial sequence
                  401577
Seq. No.
                  LIB3431-044-P1-N1-C4
Seq. ID
Method
                  BLASTX
                  g2829916
NCBI GI
BLAST score
                  297
E value
                  7.0e-27
Match length
                  72
                  78
% identity
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  401578
                  LIB3431-044-P1-N1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3789951
BLAST score
                  157
E value
                  6.0e-83
Match length
                  300
% identity
                  93
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  401579
Seq. No.
Seq. ID
                  LIB3431-044-P1-N1-D6
Method
                  BLASTX
NCBI GI
                  g1652164
```

Method BLASTX
NCBI GI g1652164
BLAST score 145
E value 6.0e-09
Match length 59
% identity 51

NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 401580

Seq. ID LIB3431-044-P1-N1-E10

```
Method
NCBI GI
                  q3618310
BLAST score
                  308
                  4.0e-28
E value
Match length
                  67
                  91
% identity
NCBI Description (AB001883) zinc finger protein [Oryza sativa]
                  401581
Seq. No.
                  LIB3431-044-P1-N1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115802
BLAST score
                  170
E value
                  3.0e-12
Match length
                  32
% identity
                  97
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                  CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
                  401582
Seq. No.
                  LIB3431-044-P1-N1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20177
BLAST score
                  150
                  5.0e-79
E value
                  176
Match length
% identity
                  97
NCBI Description Rice cablR gene for light harvesting chlorophyll
                  a/b-binding protein
                  401583
Seq. No.
                  LIB3431-044-P1-N1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548605
                  198
BLAST score
E value
                  1.0e-15
Match length
                  44
% identity
                  89
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  401584
Seq. No.
```

Seq. ID LIB3431-044-P1-N1-F11

Method BLASTX
NCBI GI g3126854
BLAST score 376
E value 4.0e-36
Match length 71
% identity 100

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

```
401585
Seq. No.
Seq. ID
                   LIB3431-044-P1-N1-F3
Method
                   BLASTN
NCBI GI
                   q20181
BLAST score
                   76
                   1.0e-34
E value
Match length
                   118
% identity
                   94
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                   a/b-binding protein
Seq. No.
                   401586
Seq. ID
                   LIB3431-044-P1-N1-F6
Method
                   BLASTX
NCBI GI
                   q1644427
BLAST score
                   343
E value
                   3.0e-32
Match length
                   79
% identity
                   80
NCBI Description
                  (U74610) glyoxalase II [Arabidopsis thaliana]
                   401587
Seq. No.
                   LIB3431-044-P1-N1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1617197
BLAST score
                   148
E value
                   2.0e-09
Match length
                   30
                   87
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                   401588
Seq. No.
                  LIB3431-044-P1-N1-F8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   209
E value
                   1.0e-114
Match length
                   265
% identity
                   97
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                   cds
Seq. No.
                   401589
Seq. ID
                  LIB3431-044-P1-N1-F9
Method
                  BLASTX
NCBI GI
                  g2462750
BLAST score
                   204
E value
                   6.0e-16
Match length
                   58
                   67
% identity
```

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3431-044-P1-N1-G11

401590

Method BLASTX NCBI GI g115787



BLAST score 389
E value 1.0e-37
Match length 75
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 401591

Seq. ID LIB3431-044-P1-N1-G6

Method BLASTX
NCBI GI g1052960
BLAST score 224
E value 3.0e-18
Match length 54
% identity 81

NCBI Description (U37437) PNIL34 [Ipomoea nil]

Seq. No. 401592

Seq. ID LIB3431-044-P1-N1-G9

Method BLASTX
NCBI GI g2072555
BLAST score 307
E value 5.0e-28
Match length 55
% identity 98

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 401593

Seq. ID LIB3431-044-P1-N1-H12

Method BLASTX
NCBI GI g4996602
BLAST score 268
E value 2.0e-23
Match length 71
% identity 75

NCBI Description (AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana

tabacum]

Seq. No. 401594

Seq. ID LIB3431-044-P1-N1-H2

Method BLASTN
NCBI GI g2072726
BLAST score 430
E value 0.0e+00
Match length 468
% identity 98

NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 401595

Seq. ID LIB3431-044-P1-N1-H3

Method BLASTN NCBI GI g2570514



BLAST score 250 E value 1.0e-138 Match length 281 % identity 98

NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.

401596

Seq. ID

LIB3431-044-P1-N1-H4

Method BLASTN
NCBI GI g218207
BLAST score 255
E value 1.0e-141
Match length 278
% identity 98

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS1139

Seq. No.

401597

Seq. ID

LIB3431-044-P1-N1-H5

Method BLASTN
NCBI GI g3126853
BLAST score 89
E value 1.0e-42
Match length 116
% identity 95

NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89)

mRNA, nuclear gene encoding chloroplast protein, complete

cds

Seq. No.

401598

Seq. ID LIB3431-044-P1-N1-H6

Method BLASTX
NCBI GI g132105
BLAST score 293
E value 2.0e-26
Match length 57
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No.

401599

Seq. ID

LIB3431-045-P1-K1-A1

Method BLASTX
NCBI GI g4680340
BLAST score 429
E value 3.0e-42
Match length 134
% identity 68

NCBI Description (AF128457) putative nucleolysin [Oryza sativa subsp.



indical

```
401600
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-A10
```

Method BLASTN

NCBI GI g5441876 BLAST score 106 E value 2.0e-52 Match length 327 35 % identity

Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 NCBI Description

(contig b)

Seq. No. 401601

Seq. ID LIB3431-045-P1-K1-A12

Method BLASTX NCBI GI q4689380 BLAST score 640 E value 5.0e-67 Match length 139 % identity 83

NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein

[Vigna radiata]

Seq. No. 401602

Seq. ID LIB3431-045-P1-K1-A3

Method BLASTX NCBI GI q132105 BLAST score 752 E value 4.0e-80 Match length 160 % identity 90

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401603

Seq. ID LIB3431-045-P1-K1-A4

Method BLASTX NCBI GI g132105 BLAST score 794 5.0e-85 E value Match length 168 % identity 90

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

NCBI GI

E value

BLAST score

Match length

% identity

q3885886

8.0e-51

502

120

80

```
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401604
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q4581146
BLAST score
                  587
E value
                  7.0e-61
                  142
Match length
% identity
                  82
NCBI Description
                 (AC006919) putative fructose-bisphosphate aldolase,
                  cytoplasmic [Arabidopsis thaliana]
Seq. No.
                  401605
                  LIB3431-045-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  814
                  2.0e-87
E value
Match length
                  154
                  99
% identity
NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  401606
                  LIB3431-045-P1-K1-A7
Seq. ID
Method
                  BLASTX
                  g871931
NCBI GI
BLAST score
                  517
E value
                  2.0e-52
Match length
                  131
% identity
                  80
NCBI Description (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  401607
Seq. ID
                  LIB3431-045-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  654
E value
                  1.0e-68
Match length
                  127
% identity
NCBI Description
                 CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182 emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  401608
Seq. ID
                  LIB3431-045-P1-K1-B1
Method
                  BLASTX
```

51521





```
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
                  401609
Seq. No.
                  LIB3431-045-P1-K1-B10
Seq. ID
Method
                  BLASTX
                  g3549656
NCBI GI
BLAST score
                  258
E value
                  3.0e-22
Match length
                  91
                  58
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                  401610
Seq. No.
                  LIB3431-045-P1-K1-B2
Seq. ID
Method
                  BLASTX
                  g2662343
NCBI GI
BLAST score
                  464
                  1.0e-58
E value
Match length
                  140
% identity
                  97
                 (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  401611
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4914330
                  488
BLAST score
                  4.0e-49
E value
Match length
                  121
% identity
                  67
NCBI Description (AC005489) F14N23.16 [Arabidopsis thaliana]
                  401612
Seq. No.
                  LIB3431-045-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  302
                  2.0e-27
E value
Match length
                  58
% identity
                  98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

 Seq. No.
 401613

 Seq. ID
 LIB3431-045-P1-K1-B5

 Method
 BLASTX

 NCBI GI
 g6056413

 BLAST score
 595

 E value
 9.0e-62

 Match length
 144

51522



% identity 81 NCBI Description (AC009525) Unknown protein [Arabidopsis thaliana]

Seq. No. 401614

Seq. ID LIB3431-045-P1-K1-B6

Method BLASTX
NCBI GI g2191152
BLAST score 222
E value 8.0e-18
Match length 117
% identity 50

NCBI Description (AF007269) A IG002N01.31 gene product [Arabidopsis

thaliana]

Seq. No. 401615

Seq. ID LIB3431-045-P1-K1-B7

Method BLASTX
NCBI GI g1495768
BLAST score 329
E value 2.0e-30
Match length 149
% identity 46

NCBI Description (Z68506) chloroplast inner envelope protein, 110 kD

(IEP110) [Pisum sativum]

Seq. No. 401616

Seq. ID LIB3431-045-P1-K1-B8

Method BLASTX
NCBI GI g132105
BLAST score 690
E value 8.0e-73
Match length 147
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401617

Seq. ID LIB3431-045-P1-K1-B9

Method BLASTX
NCBI GI g3169012
BLAST score 485
E value 1.0e-48
Match length 123
% identity 76

NCBI Description (AJ002610) putative calmodulin binding transporter protein

[Hordeum vulgare]

Seq. No. 401618

Seq. ID LIB3431-045-P1-K1-C1

Method BLASTX



NCBI GI q320618 BLAST score 356 8.0e-34 E value Match length 84 % identity 81

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 401619

Seq. ID LIB3431-045-P1-K1-C10

Method BLASTX NCBI GI a3885894 BLAST score 551 E value 1.0e-56 Match length 136 % identity 80

(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa] NCBI Description

Seq. No. 401620

Seq. ID LIB3431-045-P1-K1-C2

Method BLASTX NCBI GI q444790 BLAST score 255 E value 7.0e-22 Match length 124 % identity 52

NCBI Description nucleotide translocator [Arabidopsis thaliana]

Seq. No. 401621

Seq. ID LIB3431-045-P1-K1-C9

Method BLASTN NCBI GI q2306980 BLAST score 37 E value 7.0e-12 Match length 41 % identity 98

NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,

complete cds

Seq. No. 401622

Seq. ID LIB3431-045-P1-K1-D11

Method BLASTX NCBI GI q2497903 BLAST score 220 9.0e-18 E value Match length 59 % identity 68

METALLOTHIONEIN-LIKE PROTEIN TYPE 2 NCBI Description

>gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like protein [Oryza sativa] >gi_1815628 (U43530) metallothionein-like type 2 [Oryza sativa]

401623 Seq. No.

LIB3431-045-P1-K1-D12 Seq. ID



Method BLASTX
NCBI GI g1174780
BLAST score 534
E value 1.0e-54
Match length 113
% identity 88

NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR (ORANGE PERICARP

2) >gi_320135_pir__PQ0450 tryptophan synthase (EC 4.2.1.20) beta-2 chain precursor - maize (fragment) >gi 168574

beta-2 chain precursor - maize (fragment) >gi_168574
(M76685) tryptophan synthase beta-subunit [Zea mays]

Seq. No. 401624

Seq. ID LIB3431-045-P1-K1-D3

Method BLASTX
NCBI GI g5051771
BLAST score 293
E value 3.0e-26
Match length 96
% identity 66

NCBI Description (AL078637) putative protein [Arabidopsis thaliana]

Seq. No. 401625

Seq. ID LIB3431-045-P1-K1-D5

Method BLASTX
NCBI GI g132105
BLAST score 511
E value 6.0e-52
Match length 115
% identity 85

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401626

Seq. ID LIB3431-045-P1-K1-D6

Method BLASTX
NCBI GI g2072555
BLAST score 175
E value 2.0e-12
Match length 32
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441 gb_AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 401627

Seq. ID LIB3431-045-P1-K1-D8

Method BLASTX
NCBI GI g115787
BLAST score 717
E value 4.0e-76

```
Match length
% identity
                  96
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  401628
                  LIB3431-045-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5803254
BLAST score
                  223
E value
                  4.0e-18
Match length
                  104
% identity
                  49
                  (AP000399) ESTs C97429(C60159), D22427(C11106),
NCBI Description
                  AU078031(E31854), D15683(C1084) correspond to a region of
                  the predicted gene; hypothetical protein [Oryza sativa]
Seq. No.
                  401629
                  LIB3431-045-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1651828
BLAST score
                  222
E value
                  5.0e-18
Match length
                  150
% identity
                  40
                  (D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]
NCBI Description
Seq. No.
                  401630
                  LIB3431-045-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244749
BLAST score
                  724
                  8.0e-77
E value
Match length
                  161
% identity
                  82
                 (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  401631
                  LIB3431-045-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  g21839
NCBI GI
BLAST score
                  319
E value
                  2.0e-29
Match length
                  139
                  59
% identity
NCBI Description
                 (X57952) phosphoribulokinase [Triticum aestivum]
```

Seq. No. 401632

LIB3431-045-P1-K1-E3 Seq. ID

Method BLASTX NCBI GI q4741942 BLAST score 409 E value 8.0e-40 Match length 120

```
% identity
NCBI Description
                  (AF134121) Lhca5 protein [Arabidopsis thaliana]
                  401633
Seq. No.
                  LIB3431-045-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  429
E value
                  2.0e-42
Match length
                  107
% identity
                  79
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  401634
Seq. ID
                  LIB3431-045-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q5042437
BLAST score
                  58
E value
                  1.0e-23
Match length
                  97
                  90
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                  401635
Seq. ID
                  LIB3431-045-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  609
E value
                  3.0e-63
Match length
                  148
% identity
                  79
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  401636
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3212852
BLAST score
                  523
E value
                  4.0e-53
Match length
                  174
% identity
                  60
```

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 401637

Seq. ID LIB3431-045-P1-K1-F11

Method BLASTX NCBI GI q5733866 BLAST score 514 E value 3.0e-52 Match length 153 % identity 63

(AC007932) Contains similarity to gb M73488 NCBI Description

1-aminocyclopropane-1-carboxylate deaminase from

Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from



this gene. [Arabidopsis thaliana]

```
Seq. No.
                  401638
Seq. ID
                  LIB3431-045-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g2073379
BLAST score
                  165
E value
                  9.0e-88
Match length
                  203
% identity
                  95
NCBI Description Rice CP26 mRNA, partial sequence
                  401639
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  751
                  8.0e-82
E value
Match length
                  156
% identity
                  97
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  401640
                  LIB3431-045-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  613
E value
                  7.0e-64
Match length
                  117
% identity
                  99
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  401641
Seq. No.
                  LIB3431-045-P1-K1-F6
Seq. ID
Method
                  BLASTN
                  g3618309
NCBI GI
BLAST score
                  45
E value
                  3.0e-16
Match length
                  65
                  94
% identity
NCBI Description
                  Oryza sativa mRNA for zinc finger protein, complete cds,
                  clone:E10707
Seq. No.
                  401642
Seq. ID
                  LIB3431-045-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g4587556
BLAST score
                  168
E value
                  8.0e-12
Match length
                  44
% identity
                  75
NCBI Description
                  (AC006577) Similar to gi_1653162 (p)ppGpp
                  3-pyrophosphohydrolase from Synechocystis sp genome
                  gb_D90911. EST gb_W43807 comes from this gene.
```

Seq. No. 401643

[Arabidopsis thaliana]



```
Seq. ID
                  LIB3431-045-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  a5734636
BLAST score
                  385
                  5.0e-37
E value
Match length
                  138
% identity
                  51
NCBI Description
                 (AP000391) Similar to putative lipase (AC006232) [Oryza
                  sativa]
Seq. No.
                  401644
Seq. ID
                  LIB3431-045-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q2129538
BLAST score
                  618
                  2.0e-64
E value
Match length
                  132
                  89
% identity
NCBI Description AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
Seq. No.
                  401645
Seq. ID
                  LIB3431-045-P1-K1-G12
Method
                  BLASTX
                  g3914603
NCBI GI
BLAST score
                  836
E value
                  6.0e-90
Match length
                  161
% identity
                  98
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                  401646
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                  881
E value
                  4.0e-95
Match length
                  169
% identity
                  99
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  401647
Seq. ID
                  LIB3431-045-P1-K1-G3
```

Method BLASTX NCBI GI g3928083 BLAST score 522 4.0e-53 E value Match length 138 % identity 70

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

```
401648
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-G5
Method
                  BLASTX
                  g4006881
NCBI GI
BLAST score
                  312
                  7.0e-37
E value
Match length
                  120
% identity
                  67
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                  401649
Seq. No.
                  LIB3431-045-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914005
BLAST score
                  470
E value
                  5.0e-47
                  105
Match length
% identity
                  90
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586
                  (U85494) LON1 protease [Zea mays]
                  401650
Seq. No.
                  LIB3431-045-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570515
BLAST score
                  244
                  2.0e-21
E value
Match length
                  92
% identity
                  68
NCBI Description (AF022740) glycolate oxidase [Oryza sativa]
                  401651
Seq. No.
                  LIB3431-045-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789952
                  207
BLAST score
                  2.0e-16
E value
Match length
                  41
% identity
                  95
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  401652
Seq. No.
                  LIB3431-045-P1-K1-H11
Seq. ID
Method
                  BLASTN
                  g2331130
NCBI GI
BLAST score
                  222
E value
                  1.0e-121
                  226
```

Match length % identity 100

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

Seq. No.

401653

Seq. ID

LIB3431-045-P1-K1-H12

Method BLASTX NCBI GI g3510256

```
BLAST score 282
E value 5.0e-25
Match length 96
```

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 401654

% identity

Seq. ID LIB3431-045-P1-K1-H2

58

Method BLASTN
NCBI GI 94097337
BLAST score 335
E value 0.0e+00
Match length 406
% identity 100

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 401655

Seq. ID LIB3431-045-P1-K1-H3
Method BLASTX
NCBI GI q5912299

NCBI GI g5912299
BLAST score 354
E value 2.0e-33
Match length 83
% identity 84

NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

Seq. No. 401656

Seq. ID LIB3431-045-P1-K1-H4

Method BLASTX
NCBI GI g1172977
BLAST score 311
E value 6.0e-56
Match length 145
% identity 80

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 401657

Seq. ID LIB3431-045-P1-K1-H5

Method BLASTX
NCBI GI g1170871
BLAST score 854
E value 5.0e-92
Match length 166
% identity 99

NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)

(ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)

>gi_1076749_pir__S46499 NADP-dependent malic enzyme - rice >gi_415315_dbj_BAA03949_ (D16499) NADP-dependent malic

enzyme [Oryza sativa]

Seq. No. 401658

Seq. ID LIB3431-045-P1-K1-H6

Method BLASTX NCBI GI g3036949 BLAST score 301



E value 2.0e-27
Match length 58
% identity 100

NCBI Description (AB012638) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No. 401659

Seq. ID LIB3431-045-P1-N1-A10

Method BLASTN
NCBI GI g5441876
BLAST score 390
E value 0.0e+00
Match length 454
% identity 96

NCBI Description Oryza sativa genomic DNA, chromosome 2, clone:P0437H03

(contig b)

Seq. No. 401660

Seq. ID LIB3431-045-P1-N1-A2

Method BLASTX
NCBI GI g1070408
BLAST score 174
E value 2.0e-12
Match length 47
% identity 77

NCBI Description ferredoxin [2Fe-2S] I - rice

Seq. No. 401661

Seq. ID LIB3431-045-P1-N1-A3

Method BLASTX
NCBI GI g347451
BLAST score 326
E value 3.0e-30
Match length 61
% identity 100

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza

sativa]

Seq. No. 401662

Seq. ID LIB3431-045-P1-N1-A4

Method BLASTX
NCBI GI g671740
BLAST score 301
E value 2.0e-27
Match length 57
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 401663

Seq. ID LIB3431-045-P1-N1-A5

Method BLASTX
NCBI GI g5419990
BLAST score 204
E value 5.0e-16
Match length 66
% identity 62

```
(AJ243524) putative fructose-bisphosphate aldolase [Phleum
NCBI Description
                  pratense]
Seq. No.
                  401664
                  LIB3431-045-P1-N1-A6
Seq. ID
Method
                  BLASTX
                  g347451
NCBI GI
BLAST score
                  207
                  3.0e-16
E value
Match length
                  39
% identity
                  100
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  401665
Seq. ID
                  LIB3431-045-P1-N1-A7
Method
                  BLASTN
NCBI GI
                  q5670155
BLAST score
                  113
                  1.0e-56
E value
Match length
                  353
% identity
                  88
                  Oryza sativa subsp. japonica BAC clone 34K24, complete
NCBI Description
                  sequence
Seq. No.
                  401666
                  LIB3431-045-P1-N1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115791
BLAST score
                  194
                  8.0e-15
E value
Match length
                   44
% identity
                  82
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 81770 pir S01961 chlorophyll a/b-binding
                  protein 2 precursor - soybean >gi 18548 emb_CAA31418
                   (X12980) chlorophyll a/b binding preprotein (AA -33 to 223)
                   [Glycine max]
                   401667
Seq. No.
                  LIB3431-045-P1-N1-B1
Seq. ID
                   BLASTX
Method
                   q3885886
NCBI GI
BLAST score
                   163
                   4.0e-11
E value
Match length
                   32
% identity
                   84
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
```

Seq. No. 401668

Seq. ID LIB3431-045-P1-N1-B10

Method BLASTX
NCBI GI g3549656
BLAST score 177
E value 9.0e-13
Match length 75
% identity 45





NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 401669

Seq. ID LIB3431-045-P1-N1-B12

Method BLASTX
NCBI GI g3892058
BLAST score 267
E value 3.0e-23
Match length 82
% identity 56

NCBI Description (AC002330) putative glutamate-/aspartate-binding peptide

[Arabidopsis thaliana]

Seq. No. 401670

Seq. ID LIB3431-045-P1-N1-B2

Method BLASTN
NCBI GI g2662342
BLAST score 58
E value 7.0e-24
Match length 89
% identity 95

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 401671

Seq. ID LIB3431-045-P1-N1-B4

Method BLASTX
NCBI GI g132105
BLAST score 302
E value 2.0e-27
Match length 58
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401672

Seq. ID LIB3431-045-P1-N1-B8

Method BLASTX
NCBI GI g671740
BLAST score 277
E value 2.0e-24
Match length 53
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 401673

Seq. ID LIB3431-045-P1-N1-C1

Method BLASTN NCBI GI g2306980

BLAST score 50

```
E value 3.0e-19
Match length 70
% identity 93
NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds
```

Seq. No. 401674

Seq. ID LIB3431-045-P1-N1-C10

Method BLASTX
NCBI GI g3885894
BLAST score 213
E value 5.0e-17
Match length 66
% identity 65

NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No. 401675

Seq. ID LIB3431-045-P1-N1-C12

Method BLASTN
NCBI GI g20181
BLAST score 79
E value 3.0e-36
Match length 107
% identity 93

NCBI Description Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein

Seq. No. 401676

Seq. ID LIB3431-045-P1-N1-C9

Method BLASTN
NCBI GI g2306980
BLAST score 87
E value 4.0e-41
Match length 175
% identity 86

NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,

complete cds

Seq. No. 401677

Seq. ID LIB3431-045-P1-N1-D10

Method BLASTX
NCBI GI g1835731
BLAST score 359
E value 4.0e-34
Match length 80
% identity 88

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 401678

Seq. ID LIB3431-045-P1-N1-D11

Method BLASTN
NCBI GI g1815627
BLAST score 137
E value 7.0e-71
Match length 137
% identity 100

NCBI Description Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA,



complete cds

401679 Seq. No. LIB3431-045-P1-N1-D3 Seq. ID BLASTN Method NCBI GI g3789953 BLAST score 228 E value 1.0e-125 268 Match length

96

% identity Oryza sativa chlorophyll a/b-binding protein precursor NCBI Description (Cab26) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 401680

LIB3431-045-P1-N1-D5 Seq. ID

BLASTX Method g671740 NCBI GI BLAST score 326 3.0e-30 E value Match length 61 100 % identity

(X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description

construct]

Seq. No. 401681

LIB3431-045-P1-N1-D6 Seq. ID

Method BLASTN g2072554 NCBI GI 392 BLAST score E value 0.0e + 00407 Match length 99 % identity

Oryza sativa metallothionein-like protein mRNA, complete NCBI Description

cds

401682 Seq. No.

LIB3431-045-P1-N1-D8 Seq. ID

Method BLASTX NCBI GI g115787 BLAST score 403 3.0e-39 E value 76 Match length 100 % identity

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description

CAB-2) (LHCP) $>gi_82461_pir_S03706$ chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 401683

LIB3431-045-P1-N1-E11 Seq. ID

Method BLASTX NCBI GI q2274988 BLAST score 291 E value 4.0e-26 Match length 74



% identity NCBI Description (AJ000226) partial sequence, homology to serine hydroxymethyltransferases [Hordeum vulgare] 401684 Seq. No. LIB3431-045-P1-N1-E3 Seq. ID Method BLASTX g4741942 NCBI GI BLAST score 439 2.0e-43 E value Match length 111 76 % identity NCBI Description (AF134121) Lhca5 protein [Arabidopsis thaliana] 401685 Seq. No. LIB3431-045-P1-N1-E4 Seq. ID BLASTN Method g3075487 NCBI GI BLAST score 314 E value 1.0e-176 314 Match length % identity 100 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds 401686 Seq. No. LIB3431-045-P1-N1-E5 Seq. ID Method BLASTX g461812 NCBI GI BLAST score 298 6.0e-27 E value 88 Match length 56 % identity CYTOCHROME P450 72A1 (CYPLXXII) (PROBABLE NCBI Description GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus] 401687 Seq. No. LIB3431-045-P1-N1-E6 Seq. ID Method BLASTN NCBI GI g5042437 BLAST score 135 E value 1.0e-69 Match length 196 % identity 92 NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence Seq. No. 401688

Seq. ID LIB3431-045-P1-N1-E7

BLASTX Method NCBI GI g115813 BLAST score 257 4.0e-22 E value Match length 61 % identity 82



NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi 19182 emb_CAA33330_ (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 401689

Seq. ID LIB3431-045-P1-N1-E8

Method BLASTX
NCBI GI g3789954
BLAST score 357
E value 7.0e-34
Match length 66
% identity 100

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 401690

Seq. ID LIB3431-045-P1-N1-E9

Method BLASTX
NCBI GI g131225
BLAST score 256
E value 4.0e-22
Match length 56
% identity 82

% identity 82 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 401691

Seq. ID LIB3431-045-P1-N1-F1

Method BLASTX
NCBI GI g3212852
BLAST score 309
E value 3.0e-28
Match length 80
% identity 66

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 401692

Seq. ID LIB3431-045-P1-N1-F11

Method BLASTX
NCBI GI g5733866
BLAST score 343
E value 3.0e-32
Match length 86
% identity 69

NCBI Description (AC007932) Contains similarity to gb_M73488

1-aminocyclopropane-1-carboxylate deaminase from

Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from

this gene. [Arabidopsis thaliana]

Seq. No. 401693

Seq. ID LIB3431-045-P1-N1-F12

Method BLASTN
NCBI GI g2073379
BLAST score 184
E value 4.0e-99

```
Match length
% identity
                   98
                  Rice CP26 mRNA, partial sequence
NCBI Description
Seq. No.
                   401694
                  LIB3431-045-P1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3126854
BLAST score
                   294
E value
                   2.0e-26
Match length
                   57
                   98
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   401695
Seq. No.
Seq. ID
                   LIB3431-045-P1-N1-F4
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   192
                   5.0e-19
E value
Match length
                   61
% identity
                   89
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   401696
Seq. No.
                   LIB3431-045-P1-N1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5734636
BLAST score
                   180
                   4.0e-13
E value
Match length
                   48
% identity
                   65
                   (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
                   401697
Seq. No.
                   LIB3431-045-P1-N1-G1
Seq. ID
                   BLASTX
Method
                   g1052960
NCBI GI
                   348
BLAST score
                   8.0e-33
E value
Match length
                   79
                   86
% identity
                  (U37437) PNIL34 [Ipomoea nil]
NCBI Description
                   401698
Seq. No.
                   LIB3431-045-P1-N1-G12
Seq. ID
                   BLASTX
Method
                   g167097
NCBI GI
BLAST score
                   151
                   6.0e-17
E value
Match length
                   52
% identity
                   88
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
```

401699

Seq. No.

```
LIB3431-045-P1-N1-G2
Seq. ID
                  BLASTX
Method
                  q167097
NCBI GI
BLAST score
                  151
                  7.0e-15
E value
                  47
Match length
                  91
% identity
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                  [Hordeum vulgare]
                  401700
Seq. No.
                  LIB3431-045-P1-N1-G6
Seq. ID
                  BLASTX
Method
                  q3914005
NCBI GI
BLAST score
                  328
E value
                  2.0e-30
Match length
                  73
                  89
% identity
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586
NCBI Description
                  (U85494) LON1 protease [Zea mays]
                  401701
Seq. No.
                  LIB3431-045-P1-N1-G8
Seq. ID
                  BLASTN
Method
                  g2570514
NCBI GI
BLAST score
                  206
                  1.0e-112
E value
Match length
                  326
% identity
                  91
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
                  401702
Seq. No.
                  LIB3431-045-P1-N1-H10
Seq. ID
                  BLASTN
Method
                  g3789951
NCBI GI
BLAST score
                  77
                  2.0e-35
E value
                  105
Match length
% identity
                  93
                 Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  401703
Seq. No.
                  LIB3431-045-P1-N1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4105602
                  343
```

BLAST score 0.0e + 00E value Match length 371 % identity 98

NCBI Description Oryza sativa metallothionein (MTe) gene, complete cds

401704 Seq. No.

Seq. ID LIB3431-045-P1-N1-H3

Method BLASTN NCBI GI g5912298

```
BLAST score
                  5.0e-16
E value
                  59
Match length
                  95
% identity
NCBI Description Oryza sativa mRNA for gigantea homologue, partial
                  401705
Seq. No.
                  LIB3431-045-P1-N1-H4
Seq. ID
                  BLASTX
Method
                  g1172977
NCBI GI
BLAST score
                  327
                  2.0e-30
E value
                  69
Match length
                  87
% identity
                  60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                  401706
Seq. No.
                  LIB3431-045-P1-N1-H6
Seq. ID
Method
                  BLASTX
                  g3036951
NCBI GI
                  301
BLAST score
                  2.0e-27
E value
Match length
                  58
% identity
                  100
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
                  401707
Seq. No.
                  LIB3431-046-P1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1353352
BLAST score
                  483
                  1.0e-48
E value
Match length
                  149
                   57
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                   401708
Seq. No.
                  LIB3431-046-P1-K1-A10
Seq. ID
                   BLASTX
Method
                   q6006363
NCBI GI
                   288
BLAST score
E value
                   7.0e-26
Match length
                   58
                   98
% identity
                  (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
NCBI Description
                   to a region of the predicted gene.; Similar to water stress
                   inducible protein (U74296) [Oryza sativa]
                   401709
Seq. No.
```

Seq. ID LIB3431-046-P1-K1-A11

Method BLASTX
NCBI GI g4105561
BLAST score 684
E value 3.0e-72

```
Match length
                   97
 % identity
                   (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
NCBI Description
                   401710
Seq. No.
                   LIB3431-046-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   q115787
NCBI GI
                   438
BLAST score
                   3.0e-43
E value
                   106
Match length
                   85
 % identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   401711
 Seq. No.
                   LIB3431-046-P1-K1-A3
 Seq. ID
                   BLASTX
 Method
NCBI GI
                   a320618
                   465
 BLAST score
                   1.0e-46
 E value
                   108
 Match length
 % identity
                   chlorophyll a/b-binding protein I precursor - rice
 NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
 Seq. No.
                   401712
                   LIB3431-046-P1-K1-A4
 Seq. ID
                   BLASTX
 Method
                   q2288969
 NCBI GI
 BLAST score
                   422
                   2.0e-41
 E value
                   122
 Match length
                   70
 % identity
                   (Y12862) glutathione transferase [Zea mays]
 NCBI Description
 Seq. No.
                    401713
                   LIB3431-046-P1-K1-A6
 Seq. ID
                   BLASTX
 Method
                    g320618
 NCBI GI
                    712
 BLAST score
                    2.0e-75
 E value
                    159
 Match length
                    86
 % identity
                   chlorophyll a/b-binding protein I precursor - rice
 NCBI Description
                    >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                    chlorophyll a/b-binding protein [Oryza sativa]
                    >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza satīva]
```

Seq. No.

```
LIB3431-046-P1-K1-A7
Seq. ID
                  BLASTX
Method
                  q3075488
NCBI GI
BLAST score
                  545
E value
                  5.0e-56
                  107
Match length
                  98
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  401715
Seq. No.
                  LIB3431-046-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  q100454
NCBI GI
BLAST score
                  627
                  2.0e-65
E value
Match length
                  154
% identity
                  77
                  photosystem II oxygen-evolving complex protein 1 - potato
NCBI Description
                   >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein
                  of oxygen-evolving complex [Solanum tuberosum]
                   401716
Seq. No.
                   LIB3431-046-P1-K1-B10
Seq. ID
                   BLASTX
Method
                   q6093830
NCBI GI
BLAST score
                   155
                   2.0e-10
E value
Match length
                   37
% identity
                   81
                   PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
NCBI Description
                   [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                   PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
                   putative photosytem II peptide [Spinacia oleracea]
                   401717
Seq. No.
                   LIB3431-046-P1-K1-B11
Seq. ID
                   BLASTX
Method
                   g82080
NCBI GI
BLAST score
                   433
                   9.0e-43
E value
                   124
Match length
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi_226872_prf _1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   401718
Seq. No.
                   LIB3431-046-P1-K1-B12
Seq. ID
                   BLASTX
Method
                   g3395439
NCBI GI
                   266
BLAST score
E value
                   4.0e-23
Match length
                   81
% identity
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
```

401719

Seq. No.

```
LIB3431-046-P1-K1-B3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4959460
BLAST score
                   37
                   2.0e-11
E value
Match length
                   37
                   100
% identity
                   Zea mays RACB small GTP binding protein mRNA, complete cds
NCBI Description
                   401720
Seq. No.
                   LIB3431-046-P1-K1-B6
Seq. ID
Method
                   BLASTX
                   g4138290
NCBI GI
BLAST score
                   582
                   3.0e-60
E value
Match length
                   128
% identity
                   85
                   (AJ005841) thioredoxin M [Oryza sativa]
NCBI Description
                   401721
Seq. No.
                   LIB3431-046-P1-K1-B8
Seq. ID
Method
                   BLASTX
                   g629864
NCBI GI
                   410
BLAST score
                   6.0e-40
E value
                   86
Match length
% identity
                   97
NCBI Description histone H2B - garden asparagus >gi_563329_emb_CAA57778_
                   (X82362) histone 2B [Asparagus officinalis]
                   401722
Seq. No.
                   LIB3431-046-P1-K1-B9
Seq. ID
                   BLASTX
Method
                   q4680212
NCBI GI
                   163
BLAST score
                   3.0e-11
E value
Match length
                   52
% identity
                   62
NCBI Description (AF114171) hypothetical protein [Sorghum bicolor]
Seq. No.
                   401723
                 LIB3431-046-P1-K1-C12
Seq. ID
                   BLASTX
Method
                   q131225
NCBI GI
BLAST score
                    565
                   3.0e-58
E value
                   119
Match length
                    91
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir_ A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I
                    hydrophobic protein [Hordeum vulgare]
                    401724
 Seq. No.
                    LIB3431-046-P1-K1-C2
 Seq. ID
```

BLASTX

g671740

Method

NCBI GI

```
BLAST score 583
E value 2.0e-60
Match length 109
% identity 98
```

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct]

Seq. No. 401725

Seq. ID LIB3431-046-P1-K1-C4

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 9.0e-20
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 401726

Seq. ID LIB3431-046-P1-K1-C6

Method BLASTN
NCBI GI g3377792
BLAST score 76
E value 4.0e-35
Match length 95
% identity 96

NCBI Description Oryza sativa ribulose-1,5-bisphosphate

carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 401727

Seq. ID LIB3431-046-P1-K1-C7

Method BLASTX
NCBI GI g132105
BLAST score 632
E value 4.0e-66
Match length 137
% identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401728

Seq. ID LIB3431-046-P1-K1-C8

Method BLASTX
NCBI GI g1617197
BLAST score 293
E value 2.0e-26
Match length 76
% identity 74

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

```
401729
Seq. No.
Seq. ID
                  LIB3431-046-P1-K1-C9
                  BLASTN
Method
                  g11957
NCBI GI
BLAST score
                  83
                  3.0e-39
E value
                  127
Match length
                  46
% identity
NCBI Description Rice complete chloroplast genome
                  401730
Seq. No.
                  LIB3431-046-P1-K1-D11
Seq. ID
                  BLASTX
Method
                  g115794
NCBI GI
                  826
BLAST score
                  9.0e-89
E value
                  161
Match length
                  95
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
NCBI Description
                  III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi 19277 emb CAA42818 (X60275) LHCII type III
                   [Lycopersicon esculentum]
                  401731
Seq. No.
                  LIB3431-046-P1-K1-D12
Seq. ID
                  BLASTX
Method
                  g3377841
NCBI GI
                   453
BLAST score
                   3.0e-45
E value
                  107
Match length
                   82
% identity
                  (AF075598) contains similarity to phosphofructokinases
NCBI Description
                   (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]
                   401732
Seq. No.
Seq. ID
                   LIB3431-046-P1-K1-D2
                   BLASTX
Method
                   q4099148
NCBI GI
                   551
BLAST score
E value
                   1.0e-56
Match length
                   140
% identity
NCBI Description (U84268) YLP [Hordeum vulgare]
                   401733
Seq. No.
                   LIB3431-046-P1-K1-D3
Seq. ID
Method
                   BLASTX
                   g5668608
NCBI GI
BLAST score
                   362
                   2.0e-34
E value
                   148
Match length
 % identity
                   48
                  (AF115334) MenG [Pseudomonas fluorescens]
NCBI Description
```

401734

Seq. No.

```
LIB3431-046-P1-K1-D6
Seq. ID
                  BLASTX
Method
                  g2072555
NCBI GI
                  175
BLAST score
E value
                  1.0e-12
Match length
                  32
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >qi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  401735
Seq. No.
                  LIB3431-046-P1-K1-D8
Seq. ID
                  BLASTX
Method
                  q1519249
NCBI GI
BLAST score
                  697
E value
                  1.0e-73
Match length
                  146
% identity
                  95
                  (U65956) GF14-b protein [Oryza sativa]
NCBI Description
                  401736
Seq. No.
                  LIB3431-046-P1-K1-D9
Seq. ID
                  BLASTX
Method
                  g5738522
NCBI GI
BLAST score
                  180
                  2.0e-13
E value
                   50
Match length
                   72
% identity
                  (AL109846) putative pre-mrna splicing factor atp-dependent
NCBI Description
                   rna helicase [Schizosaccharomyces pombe]
Seq. No.
                   401737
                   LIB3431-046-P1-K1-E1
Seq. ID
                   BLASTX
Method
                   g417260
NCBI GI
BLAST score
                   381
                   1.0e-36
E value
Match length
                   121
                   64
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003_pir __S33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
                   401738
Seq. No.
                   LIB3431-046-P1-K1-E12
Seq. ID
                   BLASTX
Method
                   g115787
NCBI GI
                   540
BLAST score
                   2.0e-55
E value
                   123
Match length
                   88
 % identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
```

[Oryza sativa]

BLAST score

E value

422

1.0e-41

```
401739
Seq. No.
                  LIB3431-046-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131225
BLAST score
                  607
                  4.0e-63
E value
                  127
Match length
                  92
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  401740
Seq. No.
Seq. ID
                  LIB3431-046-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q6063542
BLAST score
                  681
                  8.0e-72
E value
                  135
Match length
% identity
                  100
                   (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
Seq. No.
                  401741
                  LIB3431-046-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q131205
BLAST score
                  178
E value
                   9.0e-13
Match length
                   36
                  100
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I)
NCBI Description
                   >gi 72677_pir__A1RZI photosystem I protein psaI - rice
                   chloroplast >gi_11996_emb_CAA33957_ (X15901) ORF36 [Oryza
                   sativa] >gi_226617_prf__1603356AP photosystem I small
                   peptide [Oryza sativa]
Seq. No.
                   401742
                  LIB3431-046-P1-K1-E6
Seq. ID
Method
                   BLASTX
                   q4530126
NCBI GI
BLAST score
                   236
                   2.0e-19
E value
                   90
Match length
                   51
% identity
                  (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
                   401743
Seq. No.
                   LIB3431-046-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   g3334333
NCBI GI
```



Match length 103 % identity 76

NCBI Description SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi_2660798 (AF034832)

cytosolic copper/zinc superoxide dismutase

[Mesembryanthemum crystallinum]

Seq. No. 401744

Seq. ID LIB3431-046-P1-K1-E8

Method BLASTX
NCBI GI g3789954
BLAST score 563
E value 4.0e-58
Match length 120
% identity 88

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 401745

Seq. ID LIB3431-046-P1-K1-E9

Method BLASTX
NCBI GI 94587556
BLAST score 284
E value 2.0e-25
Match length 103
% identity 53

NCBI Description (AC006577) Similar to gi_1653162 (p)ppGpp

3-pyrophosphohydrolase from Synechocystis sp genome

gb_D90911. EST gb_W43807 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 401746

Seq. ID LIB3431-046-P1-K1-F1

Method BLASTX
NCBI GI g115787
BLAST score 529
E value 5.0e-54
Match length 121
% identity 88

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 401747

Seq. ID LIB3431-046-P1-K1-F11

Method BLASTX
NCBI GI g3345477
BLAST score 707
E value 7.0e-75
Match length 151
% identity 90

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 401748

Seq. ID LIB3431-046-P1-K1-F3

Method BLASTX

```
q4415940
NCBI GI
BLAST score
                  249
                  3.0e-21
E value
                  103
Match length
% identity
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  401749
Seq. No.
Seq. ID
                  LIB3431-046-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  q82080
                  412
BLAST score
                  3.0e-40
E value
                  117
Match length
                  68
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  401750
Seq. No.
                  LIB3431-046-P1-K1-F5
Seq. ID
                  BLASTX
Method
                  q1835731
NCBI GI
                  507
BLAST score
E value
                  2.0e-51
                  123
Match length
                  81
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  401751
Seq. No.
                  LIB3431-046-P1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4512125
BLAST score
                  178
                   6.0e-13
E value
                   32
Match length
                   100
% identity
                  (AF133340) putative chlorophyll a/b-binding protein
NCBI Description
                   [Phalaenopsis sp. 'KCbutterfly']
                   401752
Seq. No.
                   LIB3431-046-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914603
BLAST score
                   680
E value
                   1.0e-71
Match length
                   131
                   99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                   CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                   activase [Oryza sativa]
```

Seq. No. 401753

Seq. ID LIB3431-046-P1-K1-G1

Method BLASTX NCBI GI g3789952

```
BLAST score
                  1.0e-63
E value
Match length
                  121
                  93
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  401754
Seq. No.
                  LIB3431-046-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q132105
BLAST score
                  660
                  2.0e-69
E value
                  141
Match length
                  89
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401755
Seq. No.
                  LIB3431-046-P1-K1-G11
Seq. ID
                  {\tt BLASTX}
Method
                  g3914470
NCBI GI
                  311
BLAST score
                   6.0e-37
E value
                  115
Match length
                   71
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi 1321868 emb CAA66373 (X97771) 10kD PSII protein
                   [Hordeum vulgare]
                   401756
Seq. No.
                   LIB3431-046-P1-K1-G12
Seq. ID
                   BLASTX
Method
                   q82080
NCBI GI
BLAST score
                   438
E value
                   2.0e-44
Match length
                   138
% identity
                   68
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872 prf 1609235A chlorophyll a/b binding protein
```

[Lycopersicon esculentum]

Seq. No. 401757

Seq. ID LIB3431-046-P1-K1-G3

Method BLASTX
NCBI GI g131388
BLAST score 352
E value 3.0e-33
Match length 120
% identity 65



NCBI Description

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 401758

Seq. No. 401758
Seq. ID LIB3431-046-P1-K1-G6
Method BLASTN
NCBI GI g6006355

NCBI GI g6006353
BLAST score 108
E value 8.0e-54
Match length 164
% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

 Seq. No.
 401759

 Seq. ID
 LIB3431-046-P1-K1-G8

 Method
 BLASTX

 NCBI GI
 g2499417

 BLAST score
 467

 E value
 1.0e-46

BLAST score 467
E value 1.0e-4
Match length 111
% identity 80

NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR

>gi_1085826_pir__S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria

anomala]

Seq. No. 401760

Seq. ID LIB3431-046-P1-K1-G9

Method BLASTX
NCBI GI g4469020
BLAST score 602
E value 2.0e-62
Match length 132
% identity 86

NCBI Description (AL035602) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 401761

Seq. ID LIB3431-046-P1-K1-H1

Method BLASTX
NCBI GI g115787
BLAST score 544
E value 9.0e-56
Match length 124
% identity 88

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

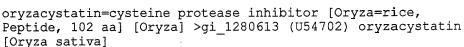
Seq. No. 401762



```
LIB3431-046-P1-K1-H10
Seq. ID
                   BLASTX
Method
                   g3345477
NCBI GI
BLAST score
                   564
                   5.0e-58
E value
                   106
Match length
                   100
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                   401763
                   LIB3431-046-P1-K1-H2
Seq. ID
                   BLASTX
Method
                   q2072555
NCBI GI
                   237
BLAST score
E value
                   9.0e-20
Match length
                   44
% identity
                   100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   401764
Seq. No.
                   LIB3431-046-P1-K1-H3
Seq. ID
Method
                   BLASTX
                   q399213
NCBI GI
BLAST score
                   781
E value
                   2.0e-83
Match length
                   170
                   91
% identity
                   ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                   CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato
                   >qi 170435 (M32604) ATP-dependent protease (CD4B)
                   [Lycopersicon esculentum]
                   401765
Seq. No.
                   LIB3431-046-P1-K1-H4
Seq. ID
                   BLASTX
Method
                   g4079798
NCBI GI
                   408
BLAST score
                   8.0e-40
E value
                   112
Match length
% identity
                   72
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   401766
Seq. No.
                   LIB3431-046-P1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q118170
BLAST score
                    429
E value
                    4.0e-42
Match length
                   102
                    85
% identity
                   CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
NCBI Description
                   >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784 (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
```

oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967)





 Seq. No.
 401767

 Seq. ID
 LIB3431-046-P1-K1-H7

 Method
 BLASTX

 NCBI GI
 g1173347

 RIAST score
 883

BLAST score 883 E value 2.0e-95 Match length 173 % identity 93

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265 emb_CAA46507_

(X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 401768

Seq. ID LIB3431-046-P1-K1-H9
Method BLASTX

Method BLASTX
NCBI GI g2495180
BLAST score 396
E value 2.0e-38
Match length 94
% identity 83

NCBI Description PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)

(HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN

SYNTHASE) >gi_421882_pir__S35873 hydroxymethylbilane synthase (EC 4.3.1.8) - garden pea >gi_541971_pir__JQ2278 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - garden pea chloroplast >gi_313724_emb_CAA51820_ (X73418)

hydroxymethylbilane synthase [Pisum sativum]

Seq. No. 401769

Seq. ID LIB3431-046-P1-N1-A1

Method BLASTX
NCBI GI g1353352
BLAST score 233
E value 2.0e-19
Match length 62
% identity 73

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

reinhardtii]

Seq. No. 401770

Seq. ID LIB3431-046-P1-N1-A10

Method BLASTN
NCBI GI g6006355
BLAST score 214
E value 1.0e-117
Match length 353
% identity 99

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401771

% identity

NCBI Description

96



```
LIB3431-046-P1-N1-A11
Seq. ID
                  BLASTN
Method
                  g4105560
NCBI GI
BLAST score
                  101
E value
                  2.0e-49
                  164
Match length
                  90
% identity
                  Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA,
NCBI Description
                  complete cds
                  401772
Seq. No.
                  LIB3431-046-P1-N1-A4
Seq. ID
Method
                  BLASTX
                  q2288969
NCBI GI
BLAST score
                  205
E value
                  5.0e-16
Match length
                  68
% identity
                  54
                  (Y12862) glutathione transferase [Zea mays]
NCBI Description
Seq. No.
                  401773
                  LIB3431-046-P1-N1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  409
E value
                   6.0e-40
Match length
                  77
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   401774
Seq. No.
                  LIB3431-046-P1-N1-A7
Seq. ID
Method
                  BLASTX
                  g2326947
NCBI GI
BLAST score
                   224
                   3.0e-18
E value
Match length
                   44
% identity
                   98
                   (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
                   401775
Seq. No.
                  LIB3431-046-P1-N1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g482311
BLAST score
                   244
                   9.0e-21
E value
Match length
                   50
```

51555

complex protein 1 [Oryza sativa]

photosystem II oxygen-evolving complex protein 1 - rice

(strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving

Method

NCBI GI

BLASTX

g2072555

```
401776
Seq. No.
                  LIB3431-046-P1-N1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4158219
BLAST score
                  554
E value
                  6.0e-57
Match length
                  108
                  100
% identity
NCBI Description
                  (Y18623) amylogenin [Oryza sativa]
                  401777
Seq. No.
                  LIB3431-046-P1-N1-B5
Seq. ID
Method
                  BLASTX
                  g5932555
NCBI GI
BLAST score
                  423
E value
                  1.0e-41
Match length
                  104
% identity
                  76
                  (AC009465) putative ribose 5-phosphate isomerase
NCBI Description
                  [Arabidopsis thaliana]
                  401778
Seq. No.
                  LIB3431-046-P1-N1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4138290
BLAST score
                  239
E value
                  5.0e-20
Match length
                  48
% identity
                  100
                  (AJ005841) thioredoxin M [Oryza sativa]
NCBI Description
                  401779
Seq. No.
                  LIB3431-046-P1-N1-C10
Seq. ID
Method
                  BLASTN
                  g1398998
NCBI GI
BLAST score
                  52
                  3.0e-20
E value
Match length
                  192
% identity
                  82
                  Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II,
NCBI Description
                  complete cds
                  401780
Seq. No.
                  LIB3431-046-P1-N1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3063523
BLAST score
                  59
                  2.0e-24
E value
Match length
                  166
                  83
% identity
NCBI Description
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
                  401781
Seq. No.
                  LIB3431-046-P1-N1-C4
Seq. ID
```



7.0e-15

BLAST score E value

```
BLAST score
                  9.0e-20
E value
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  401782
Seq. ID
                  LIB3431-046-P1-N1-C6
Method
                  BLASTX
NCBI GI
                  g167097
BLAST score
                  165
E value
                  4.0e-24
Match length
                  70
% identity
                  83
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                  [Hordeum vulgare]
                  401783
Seq. No.
Seq. ID
                  LIB3431-046-P1-N1-C7
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  299
E value
                  4.0e-27
Match length
                  61
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  401784
                  LIB3431-046-P1-N1-D11
Seq. ID
Method
                  BLASTX
                  g829283
NCBI GI
                  203
BLAST score
                  6.0e-16
E value
Match length
                  48
% identity
                  83
                  (Z15018) heat shock protein hsp82 [Oryza sativa]
NCBI Description
Seq. No.
                  401785
                  LIB3431-046-P1-N1-D12
Seq. ID
Method
                  BLASTX
                  q3377841
NCBI GI
                  182
BLAST score
                  1.0e-13
E value
Match length
                  47
                  74
% identity
                  (AF075598) contains similarity to phosphofructokinases
NCBI Description
                   (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]
Seq. No.
                   401786
                  LIB3431-046-P1-N1-D2
Seq. ID
                  BLASTN
Method
                  g4099149
NCBI GI
```

```
Match length
                  87
% identity
                  Hordeum vulgare vacuolar proton-translocating ATPase
NCBI Description
                  subunit E (Ylp) mRNA, complete cds
Seq. No.
                  401787
Seq. ID
                  LIB3431-046-P1-N1-D3
Method
                  BLASTX
NCBI GI
                  q5668608
BLAST score
                  192
E value
                  1.0e-14
Match length
                  83
                   42
% identity
                  (AF115334) MenG [Pseudomonas fluorescens]
NCBI Description
Seq. No.
                  401788
Seq. ID
                  LIB3431-046-P1-N1-D4
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  340
                   6.0e-32
E value
Match length
                  80
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   401789
Seq. No.
Seq. ID
                  LIB3431-046-P1-N1-D5
                  BLASTX
Method
                   q829283
NCBI GI
BLAST score
                   232
                   2.0e-19
E value
                   58
Match length
% identity
                   83
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
                   401790
Seq. No.
                   LIB3431-046-P1-N1-D6
Seq. ID
Method
                   BLASTN
                   g2072554
NCBI GI
BLAST score
                   390
E value
                   0.0e + 00
Match length
                   390
% identity
                   100
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
Seq. No.
                   401791
                   LIB3431-046-P1-N1-D7
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI 94490317
BLAST score 302
E value 2.0e-27
Match length 113
% identity 51

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 401792



```
LIB3431-046-P1-N1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q729478
BLAST score
                  344
E value
                  2.0e-32
Match length
                  72
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                  >gi 442481 dbj BAA04616 (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa] >gi 6069649 dbj_BAA85425.1
                  (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                  a region of the predicted gene.; similar to
                  ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
Seq. No.
                  401793
Seq. ID
                  LIB3431-046-P1-N1-E12
Method
                  BLASTX
NCBI GI
                  q226263
BLAST score
                  247
                  5.0e-21
E value
Match length
                  46
% identity
                  100
                 chlorophyll a/b binding protein [Glycine max]
NCBI Description
                  401794
Seq. No.
                  LIB3431-046-P1-N1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  310
E value
                  2.0e-28
Match length
                  90
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  401795
Seq. No.
                  LIB3431-046-P1-N1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q6063542
BLAST score
                  512
                  4.0e-52
E value
Match length
                  96
% identity
                  99
                  (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
                  401796
Seq. No.
                  LIB3431-046-P1-N1-E5
```

Seq. ID

Method BLASTX g11998 NCBI GI BLAST score 292 4.0e-35 E value Match length 76 % identity 93



(X15901) ORF85 [Oryza sativa] >gi_226619_prf__1603356AR ORF 85A [Oryza sativa]

Seq. No. 401797

NCBI Description

Seq. ID LIB3431-046-P1-N1-E7

Method BLASTX
NCBI GI g3786214
BLAST score 295
E value 1.0e-26
Match length 74
% identity 74

NCBI Description (AJ002604) high pI CuZn-superoxide dismutase [Pinus

sylvestris]

Seq. No. 401798

Seq. ID LIB3431-046-P1-N1-F1

Method BLASTX
NCBI GI g115772
BLAST score 309
E value 3.0e-28
Match length 59
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I

CAB-1) (LHCP) >gi 82460 pir S03705 chlorophyll a/b-binding

protein 1R precursor - rice >gi 20178 emb CAA32108

(X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)

[Oryza sativa]

Seq. No. 401799

Seq. ID LIB3431-046-P1-N1-F11

Method BLASTN
NCBI GI g3345476
BLAST score 173
E value 1.0e-92
Match length 248
% identity 92

NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. No. 401800

Seq. ID LIB3431-046-P1-N1-F3

Method BLASTX
NCBI GI g4415940
BLAST score 172
E value 3.0e-12
Match length 51
% identity 59

NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3431-046-P1-N1-F4

401801

Method BLASTX
NCBI GI g115813
BLAST score 243
E value 2.0e-20
Match length 55
% identity 85

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

401802 Seq. No.

Seq. ID LIB3431-046-P1-N1-F5

Method BLASTX q1835731 NCBI GI 371 BLAST score 2.0e-35 E value 82 Match length % identity

(U86018) photosystem II 10 kDa polypeptide [Oryza sativa] NCBI Description

401803 Seq. No.

LIB3431-046-P1-N1-F6 Seq. ID

BLASTX Method NCBI GI g421916 178 BLAST score 6.0e-13 E value 32 Match length 100 % identity

chlorophyll a/b-binding protein - English ivy (fragment) NCBI Description

>gi 12582_emb CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

401804 Seq. No.

LIB3431-046-P1-N1-F8 Seq. ID

BLASTX Method q100614 NCBI GI BLAST score 196 3.0e-15 E value Match length 50 78 % identity

ribulose-bisphosphate carboxylase activase A long form NCBI Description precursor - barley (fragment) >gi_167089 (M55446) ribulose

1,5-bisphosphate carboxylase activase [Hordeum vulgare]

401805 Seq. No.

LIB3431-046-P1-N1-G10 Seq. ID

BLASTX Method q347451 NCBI GI BLAST score 236 9.0e-20 E value Match length 47 % identity

(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza NCBI Description

satival

Seq. No. 401806

LIB3431-046-P1-N1-G11 Seq. ID

Method BLASTX NCBI GI g3914470 BLAST score 374 E value 4.0e-39 Match length 105 68 % identity

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

```
.
```

>gi_1321868_emb_CAA66373_ (X97771) 10kD PSII protein
[Hordeum vulgare]

Seq. No. 401807

Seq. ID LIB3431-046-P1-N1-G12

Method BLASTN
NCBI GI g430946
BLAST score 41
E value 1.0e-13
Match length 65

% identity 91
NCBI Description Arabidopsis thaliana PSI type III chlorophyll a/b-binding

protein (Lhca3*1) mRNA, complete cds

Seq. No. 401808

Seq. ID LIB3431-046-P1-N1-G3

Method BLASTX
NCBI GI g482311
BLAST score 364
E value 8.0e-35
Match length 73
% identity 99

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice

(strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 401809

Seq. ID LIB3431-046-P1-N1-G6

Method BLASTN
NCBI GI g6006355
BLAST score 162
E value 4.0e-86
Match length 220
% identity 93

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 401810

Seq. ID LIB3431-046-P1-N1-G8

Method BLASTX
NCBI GI g2499417
BLAST score 289
E value 6.0e-26
Match length 68
% identity 78

NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR

>gi_1085826_pir__S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria

anomala]

Seq. No. 401811

Seq. ID LIB3431-046-P1-N1-G9

Method BLASTN
NCBI GI g4680196
BLAST score 56
E value 2.0e-22
Match length 108

% identity 88





```
NCBI Description
                 Sorghum bicolor BAC clone 25.M18, complete sequence
                  401812
Seq. No.
Seq. ID
                  LIB3431-046-P1-N1-H10
Method
                  BLASTN
NCBI GI
                  q606816
BLAST score
                  184
                  3.0e-99
E value
                  208
Match length
                  97
% identity
NCBI Description
                  Oryza sativa chloroplast carbonic anhydrase mRNA, complete
                  401813
Seq. No.
                  LIB3431-046-P1-N1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1398998
BLAST score
                  165
E value
                  9.0e-88
Match length
                  272
                  97
% identity
NCBI Description
                  Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II,
                  complete cds
Seq. No.
                  401814
Seq. ID
                  LIB3431-046-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  172
E value
                  3.0e-12
Match length
                  39
% identity
                  92
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  401815
Seq. ID
                  LIB3431-046-P1-N1-H9
Method
                  BLASTN
NCBI GI
                  g2661765
BLAST score
                  46
                  1.0e-16
E value
Match length
                  82
% identity
                  89
NCBI Description
                  Zea mays mRNA for putative porphobilinogen deaminase
                  401816
Seq. No.
                  LIB3431-047-P1-K1-A11
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g482311
BLAST score 649
E value 4.0e-68
Match length 129
% identity 98



NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No. 401817

Seq. ID LIB3431-047-P1-K1-A12

Method BLASTN
NCBI GI g20262
BLAST score 252
E value 1.0e-139
Match length 252
% identity 100

NCBI Description O.sativa light-induced mRNA

Seq. No. 401818

Seq. ID LIB3431-047-P1-K1-A3

Method BLASTX
NCBI GI g5912299
BLAST score 547
E value 3.0e-56
Match length 105
% identity 100

NCBI Description (AJ133787) gigantea homologue [Oryza sativa]

Seq. No. 401819

Seq. ID LIB3431-047-P1-K1-A4

Method BLASTX
NCBI GI g132105
BLAST score 533
E value 2.0e-54
Match length 118
% identity 86

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >qi_226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401820

Seq. ID LIB3431-047-P1-K1-A5

Method BLASTX
NCBI GI g22240
BLAST score 450
E value 7.0e-45
Match length 116
% identity 79

NCBI Description (X07157) GADPH (383 AA) [Zea mays]

Seq. No. 401821

Seq. ID LIB3431-047-P1-K1-A7

Method BLASTX NCBI GI g6016875 BLAST score 275



```
E value
                  2.0e-24
Match length
                  68
                  78
% identity
                  (AP000570) EST AU078302(C63241) corresponds to a region of
NCBI Description
                  the predicted gene.; hypothetical protein [Oryza sativa]
Seq. No.
                  401822
                  LIB3431-047-P1-K1-A8
Seq. ID
                  BLASTN
Method
                  g2072554
NCBI GI
BLAST score
                  47
                  2.0e-17
E value
Match length
                  147
% identity
                  83
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  401823
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-A9
                  BLASTN
Method
NCBI GI
                  g20369
BLAST score
                  42
                  9.0e-15
E value
Match length
                  54
                  94
% identity
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
Seq. No.
                  401824
                  LIB3431-047-P1-K1-B1
Seq. ID
Method
                  BLASTX
                  q2072555
NCBI GI
                  237
BLAST score
                  1.0e-19
E value
Match length
                   44
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   401825
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q1709846
BLAST score
                   195
                   7.0e-15
E value
```

Match length 125 % identity 48

PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) NCBI Description

22 kDa component of photosystem II [Lycopersicon

esculentum]

Seq. No. 401826

LIB3431-047-P1-K1-B12 Seq. ID

Method BLASTX



g132105 NCBI GI 444 BLAST score 4.0e-44E value 104 Match length 84 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 401827 Seq. No. Seq. ID LIB3431-047-P1-K1-B2 BLASTN Method NCBI GI g1732362 BLAST score 35 4.0e-10 E value 43 Match length 95 % identity NCBI Description Malus domestica pAFD103 mRNA, partial cds 401828 Seq. No. LIB3431-047-P1-K1-B3 Seq. ID BLASTX Method NCBI GI g4808833 BLAST score 311 7.0e-29 E value 63 Match length 84 % identity (AF117125) endoplasmic reticulum-type calcium-transporting NCBI Description ATPase 4 [Arabidopsis thaliana] 401829 Seq. No. Seq. ID LIB3431-047-P1-K1-B4 BLASTN Method g5670155 NCBI GI 42 BLAST score 2.0e-14 E value 87 Match length % identity NCBI Description Oryza sativa subsp. japonica BAC clone 34K24, complete sequence 401830 Seq. No. Seq. ID LIB3431-047-P1-K1-B5 Method BLASTX

Method BLASTX
NCBI GI g2407281
BLAST score 641
E value 4.0e-67
Match length 121
% identity 98

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

% identity

66

```
Seq. No.
                   401831
Seq. ID
                   LIB3431-047-P1-K1-B7
                   BLASTX
Method
NCBI GI
                   g671740
BLAST score
                   354
                   1.0e-33
E value
Match length
                   65
% identity
                   100
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No. Seq. ID
                   401832
                   LIB3431-047-P1-K1-B8
                   BLASTX
Method
                   g5921799
NCBI GI
BLAST score
                   314
                   4.0e-29
E value
Match length
                   87
% identity
                   71
                   PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT,
NCBI Description
                   MITOCHONDRIAL PRECURSOR (ENDOPEPTIDASE CLP)
                   >gi_3559935_emb_CAA06443_ (AJ005253) ClpP protease [Mus
musculus] >gi_4454289_emb_CAA09966_ (AJ012249) ClpP
                   protease [Mus musculus]
                    401833
Seq. No.
Seq. ID
                   LIB3431-047-P1-K1-B9
                   BLASTN
Method
NCBI GI
                   g3885887
BLAST score
                    41
                    3.0e-14
E value
Match length
                    45
                    98
% identity
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                    complete cds
                    401834
Seq. No.
Seq. ID
                   LIB3431-047-P1-K1-C10
                   BLASTN
Method
NCBI GI
                    g5714761
BLAST score
                    54
E value
                    2.0e-21
Match length
                    78
% identity
                    92
                   Oryza sativa subsp. indica serine/threonine protein
NCBI Description
                    phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete
                    cds
                    401835
Seq. No.
                    LIB3431-047-P1-K1-C11
Seq. ID
                    BLASTX
Method
NCBI GI
                    g3478700
BLAST score
                    152
E value
                    4.0e-10
Match length
                    41
```



```
(AF034387) AFT protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    401836
                    LIB3431-047-P1-K1-C12
Seq. ID
Method
                    BLASTX
                    g2370312
NCBI GI
BLAST score
                    302
E value
                    1.0e-27
Match length
                    97
% identity
                    62
                    (AJ000995) DnaJ-like protein [Medicago sativa]
NCBI Description
                    >gi 3202020 gb AAC19391.1 (AF069507) DnaJ-like protein
                    MsJ1 [Medicago sativa]
Seq. No.
                    401837
                    LIB3431-047-P1-K1-C3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g462195
BLAST score
                    211
                    5.0e-17
E value
Match length
                    48
                    83
% identity
                    PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                    >gi_100682_pir__S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                    satīva]
                    401838
Seq. No.
                    LIB3431-047-P1-K1-C4
Seq. ID
                    BLASTX
Method
NCBI GI
                    g3345477
BLAST score
                    351
                    3.0e - 33
E value
Match length
                    117
                    62
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                    401839
Seq. No.
Seq. ID
                    LIB3431-047-P1-K1-C5
                    {\tt BLASTX}
Method
NCBI GI
                    g1350986
BLAST score
                    458
E value
                    1.0e-45
Match length
                    97
% identity
                    93
                    40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
                    >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]
Seq. No.
                    401840
Seq. ID
                    LIB3431-047-P1-K1-C6
                    BLASTX
Method
                    q131283
NCBI GI
BLAST score
                    394
```

51568

1.0e-39

95

88

E value

Match length % identity



PHOTOSYSTEM II 44 KD REACTION CENTER PROTEIN (P6 PROTEIN) NCBI Description (CP43) >gi_72710_pir__F2RZ44 photosystem II chlorophyll

a-binding protein psbC - rice chloroplast

>gi 11965_emb_CAA34014_ (X15901) PSII 43kDa protein [Oryza

sativa]

Seq. No. 401841

Seq. ID LIB3431-047-P1-K1-C7

BLASTN Method NCBI GI g6103440 BLAST score 141 2.0e-73 E value 190 Match length 94 % identity

Oryza sativa metallothionein-like protein (ML2) mRNA, NCBI Description

complete cds

Seq. No. 401842

Seq. ID LIB3431-047-P1-K1-C8

Method BLASTN NCBI GI g3377792 BLAST score 106 7.0e-53 E value Match length 106 % identity 100

Oryza sativa ribulose-1,5-bisphosphate NCBI Description

carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 401843

Seq. ID LIB3431-047-P1-K1-D10

BLASTX Method NCBI GI g534982 BLAST score 156 E value 2.0e-19 73 Match length 59 % identity

NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No.

401844

LIB3431-047-P1-K1-D12 Seq. ID

Method BLASTX NCBI GI q320618 BLAST score 465 1.0e-46 E value Match length 110 % identity

chlorophyll a/b-binding protein I precursor - rice NCBI Description

>qi 218172 dbj BAA00536 (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 401845

Seq. ID LIB3431-047-P1-K1-D2

Method BLASTN NCBI GI g20181 BLAST score 338

Match length

% identity

84

```
0.0e + 00
E value
Match length
                  369
                  98
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  401846
Seq. No.
                  LIB3431-047-P1-K1-D3
Seq. ID
Method
                  BLASTX
                  q132105
NCBI GI
BLAST score
                  532
E value
                  2.0e-54
                  122
Match length
                  83
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401847
Seq. No.
                  LIB3431-047-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  a534982
NCBI GI
                   264
BLAST score
E value
                   5.0e-37
Match length
                   126
% identity
                  (X75898) phosphoglucomutase [Spinacia oleracea]
NCBI Description
                   401848
Seq. No.
                   LIB3431-047-P1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729478
BLAST score
                   476
                   7.0e-48
E value
Match length
                   102
                   85
% identity
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
                   reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
                   (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                   a region of the predicted gene.; similar to
                   ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
                   401849
Seq. No.
                   LIB3431-047-P1-K1-E1
 Seq. ID
                   BLASTX
Method
                   g115787
NCBI GI
                   349
 BLAST score
                   4.0e-33
 E value
                   86
```



CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 401850 Seq. No. LIB3431-047-P1-K1-E10 Seq. ID BLASTX Method q3913018 NCBI GI 876 BLAST score 1.0e-94 E value 171 Match length 98 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi 218155_dbj BAA02730 (D13513) chloroplastic aldolase [Oryza sativa] Seq. No. 401851 LIB3431-047-P1-K1-E11 Seq. ID BLASTX Method NCBI GI g6063542 768 BLAST score 5.0e-82 E value 151 Match length % identity (AP000615) EST C74302(E30840) corresponds to a region of NCBI Description the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa] 401852 Seq. No. LIB3431-047-P1-K1-E12 Seq. ID BLASTX Method g1617197 NCBI GI 304 BLAST score 1.0e-27 E value 76 Match length % identity (Z72488) CP12 [Nicotiana tabacum] NCBI Description 401853 Seq. No. Seq. ID LIB3431-047-P1-K1-E2 BLASTN Method NCBI GI q6103440 268 BLAST score 1.0e-149 E value 278 Match length 99 % identity

Oryza sativa metallothionein-like protein (ML2) mRNA, NCBI Description

complete cds

401854 Seq. No.

LIB3431-047-P1-K1-E3 Seq. ID

Method BLASTN g6015437 NCBI GI BLAST score 36 6.0e-11 E value

```
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  401855
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-E4
                  BLASTX
Method
NCBI GI
                  g2894534
                  625
BLAST score
                  2.0e-65
E value
                  121
Match length
                  98
% identity
NCBI Description (AJ224327) aquaporin [Oryza sativa]
                  401856
Seq. No.
                  LIB3431-047-P1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3288821
                  509
BLAST score
                  1.0e-51
E value
                  135
Match length
% identity
                  74
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
                  401857
Seq. No.
                  LIB3431-047-P1-K1-E7
Seq. ID
                  BLASTX
Method
                  g4887131
NCBI GI
                  432
BLAST score
                  7.0e-43
E value
Match length
                  101
                  77
% identity
                  (AF134732) 60S ribosomal protein L1 [Prunus armeniaca]
NCBI Description
                  401858
Seq. No.
                  LIB3431-047-P1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1653089
BLAST score
                  306
                  7.0e-28
E value
Match length
                  127
% identity
                   50
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]
                   401859
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-F1
Method
                  BLASTX
                   q5541681
NCBI GI
                   225
BLAST score
```

51572

NCBI Description (AL096859) putative protein [Arabidopsis thaliana]

1.0e-18

91

E value Match length

% identity



Seq. No. 401860

Seq. ID LIB3431-047-P1-K1-F2

Method BLASTX
NCBI GI g3915131
BLAST score 242
E value 9.0e-21
Match length 48
% identity 100

NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)

>gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza
sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin
h [Oryza sativa] >gi 1930072 (U92541) thioredoxin h [Oryza

sativa]

Seq. No. 401861

Seq. ID LIB3431-047-P1-K1-F4

Method BLASTN
NCBI GI g1103627
BLAST score 57

E value 3.0e-23 Match length 85 % identity 92

NCBI Description Z.mays Fer1 gene

Seq. No. 401862

Seq. ID LIB3431-047-P1-K1-F5

Method BLASTX
NCBI GI g3309269
BLAST score 448
E value 2.0e-44
Match length 107
% identity 80

NCBI Description (AF074940) ferric leghemoglobin reductase-2 precursor

[Glycine max]

Seq. No. 401863

Seq. ID LIB3431-047-P1-K1-F6

Method BLASTX
NCBI GI g4587615
BLAST score 453
E value 1.0e-49
Match length 135
% identity 71

NCBI Description (AC006951) putative acyl-CoA synthetase [Arabidopsis

thaliana] >gi 4689469 gb AAD27905.1_AC007213_3 (AC007213)

putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No. 401864

Seq. ID LIB3431-047-P1-K1-F8

Method BLASTX
NCBI GI g3789954
BLAST score 199
E value 6.0e-16
Match length 46
% identity 83

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]



Seq. No. 401865 Seq. ID LIB343

LIB3431-047-P1-K1-F9

Method BLASTX
NCBI GI g115787
BLAST score 504
E value 4.0e-51
Match length 118
% identity 86

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__ S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 401866

Seq. ID LIB3431-047-P1-K1-G11

Method BLASTX
NCBI GI g132105
BLAST score 470
E value 3.0e-47
Match length 107
% identity 85

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone posss1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401867

Seq. ID LIB3431-047-P1-K1-G12

Method BLASTX
NCBI GI g3345477
BLAST score 315
E value 5.0e-29
Match length 109
% identity 59

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 401868

Seq. ID LIB3431-047-P1-K1-G2

Method BLASTX
NCBI GI g115771
BLAST score 864
E value 3.0e-93
Match length 170
% identity 95

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I

CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA I - 262) [Zea mays]

Seq. No. 401869

BLAST score

Match length

% identity

E value

406

82

99

1.0e-39

```
Seq. ID
                  LIB3431-047-P1-K1-G4
                  BLASTX
Method
NCBI GI
                  g4204276
BLAST score
                   421
                  1.0e-41
E value
                  107
Match length
                   75
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401870
                  LIB3431-047-P1-K1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2570511
BLAST score
                   506
                   2.0e-51
E value
Match length
                   105
% identity
                   99
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   401871
Seq. ID
                   LIB3431-047-P1-K1-G6
Method
                  BLASTN
NCBI GI
                   g6015437
BLAST score
                   35
E value
                   2.0e-10
Match length
                   35
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   401872
                   LIB3431-047-P1-K1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3126854
BLAST score
                   478
E value
                   3.0e-48
Match length
                   90
                   99
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   401873
Seq. ID
                   LIB3431-047-P1-K1-G8
                   BLASTX
Method
NCBI GI
                   g3126854
BLAST score
                   306
                   7.0e-48
E value
Match length
                   119
                   85
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   401874
Seq. ID
                   LIB3431-047-P1-K1-G9
                   BLASTX
Method
NCBI GI
                   g224293
```

E value

Match length

2.0e-09 71



```
NCBI Description histone H4 [Triticum aestivum]
                   401875
Seq. No.
                  LIB3431-047-P1-K1-H1
Seq. ID
                  BLASTX
Method
                   g2739375
NCBI GI
                   161
BLAST score
E value
                   5.0e-11
Match length
                   93
                   42
% identity
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
                   401876
Seq. No.
                   LIB3431-047-P1-K1-H11
Seq. ID
Method
                   BLASTN
                   q536895
NCBI GI
                   139
BLAST score
                   4.0e-72
E value
                   195
Match length
                   93
% identity
                  Wheat mRNA for protein H2A, complete cds, clone wcH2A-10
NCBI Description
                   401877
Seq. No.
                   LIB3431-047-P1-K1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   443
                   4.0e-45
E value
                   123
Match length
                   75
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   satival >qi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
 Seq. No.
                   401878
                   LIB3431-047-P1-K1-H2
 Seq. ID
                   BLASTX
Method
                   q5679336
 NCBI GI
                   193
 BLAST score
E value
                   1.0e-14
Match length
                   78
 % identity
                   45
                   (AF171223) putative zinc finger protein [Oryza sativa]
NCBI Description
                   401879
 Seq. No.
                   LIB3431-047-P1-K1-H3
 Seq. ID
                   BLASTX
 Method
                   q4884370
 NCBI GI
 BLAST score
                   147
```

```
% identity
                  (AL050157) hypothetical protein [Homo sapiens]
NCBI Description
                  401880
Seq. No.
                  LIB3431-047-P1-K1-H4
Seq. ID
                  BLASTX
Method
                  q4079798
NCBI GI
                  398
BLAST score
                  9.0e-39
E value
                  108
Match length
                  73
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  401881
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-H5
                  BLASTX
Method
                  g3292829
NCBI GI
                  185
BLAST score
                  5.0e-14
E value
                  86
Match length
                  44
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                   401882
Seq. No.
                  LIB3431-047-P1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1419090
                   484
BLAST score
                   7.0e-49
E value
Match length
                   118
                   79
% identity
NCBI Description (X94968) 37kDa chloroplast inner envelope membrane
                   polypeptide precursor [Nicotiana tabacum]
                   401883
Seq. No.
Seq. ID
                   LIB3431-047-P1-K1-H7
                   BLASTX
Method
                   g3953471
NCBI GI
                   276
BLAST score
                   1.0e-24
E value
Match length
                   75
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                   401884
Seq. No.
                   LIB3431-047-P1-K1-H8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q629858
BLAST score
                   587
                   7.0e-61
E value
```

Match length 124 % identity 90

NCBI Description protein kinase C inhibitor - maize

401885 Seq. No.

LIB3431-047-P1-K1-H9 Seq. ID



```
BLASTN
Method
                  g2062705
NCBI GI
BLAST score
                  37
                  4.0e-11
E value
                  37
Match length
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  401886
Seq. No.
                  LIB3431-047-P1-N1-A3
Seq. ID
                  BLASTN
Method
NCBI GI
                  q5912298
BLAST score
                  156
E value
                  4.0e-82
                  170
Match length
                  98
% identity
NCBI Description Oryza sativa mRNA for gigantea homologue, partial
Seq. No.
                  401887
Seq. ID
                  LIB3431-047-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  354
                  2.0e-33
E value
Match length
                  65
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401888
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-A5
                  BLASTX
Method
NCBI GI
                  g120661
BLAST score
                  268
                  2.0e-23
E value
                  52
Match length
                  94
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                  PRECURSOR >gi 170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
                  401889
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  g2072555
```

Method BLASTX
NCBI GI g2072555
BLAST score 226
E value 2.0e-18
Match length 44
% identity 98

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]



>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
protein [Oryza sativa]

Seq. No. 401890

Seq. ID LIB3431-047-P1-N1-A9

Method BLASTN
NCBI GI g20369
BLAST score 291
E value 1.0e-163
Match length 326
% identity 98

NCBI Description Oryza sativa shoot GS2 mRNA for chloroplastic glutamine

synthetase (EC 6.3.1.2) (clone lambda-GS31)

>gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of

chloroplast localising glutamine synthetase

Seq. No. 401891

Seq. ID LIB3431-047-P1-N1-B1

Method BLASTN
NCBI GI g2072554
BLAST score 386
E value 0.0e+00
Match length 408
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 401892

Seq. ID LIB3431-047-P1-N1-B10

Method BLASTX
NCBI GI g6103011
BLAST score 451
E value 7.0e-45
Match length 97
% identity 51

NCBI Description (X84225) precursor of photosystem II subunit (22KDa)

[Nicotiana tabacum]

Seq. No. 401893

Seq. ID LIB3431-047-P1-N1-B12

Method BLASTN
NCBI GI g218207
BLAST score 181
E value 3.0e-97
Match length 217
% identity 96

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS1139

Seq. No. 401894

Seq. ID LIB3431-047-P1-N1-B3

Method BLASTN
NCBI GI g2160711
BLAST score 320
E value 1.0e-180
Match length 356

E value

Match length % identity

8.0e-24 82



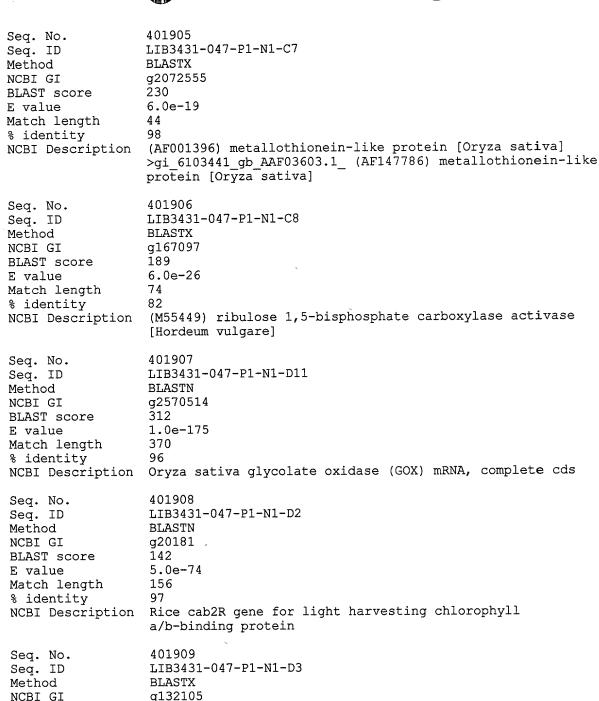
```
% identity
                  Oryza sativa Ca2+-ATPase gene, complete cds
NCBI Description
                  401895
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-B5
                  BLASTX
Method
NCBI GI
                  g671740
                  243
BLAST score
                  2.0e-20
E value
                  47
Match length
                  100
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  401896
Seq. No.
                  LIB3431-047-P1-N1-B7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g218209
                  59
BLAST score
                  2.0e-24
E value
                  75
Match length
                   95
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS2106
                   401897
Seq. No.
                  LIB3431-047-P1-N1-B9
Seq. ID
                   BLASTN
Method
                   g3885887
NCBI GI
BLAST score
                   298
                   1.0e-167
E value
Match length
                   349
% identity
                   96
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   401898
                   LIB3431-047-P1-N1-C10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g5714761
BLAST score
                   54
                   2.0e-21
E value
Match length
                   78
                   92
% identity
                   Oryza sativa subsp. indica serine/threonine protein
NCBI Description
                   phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete
                   cds
                   401899
Seq. No.
Seq. ID
                   LIB3431-047-P1-N1-C11
                   BLASTN
Method
                   g3819352
NCBI GI
BLAST score
                   58
```



```
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0813.rev
                  401900
Seq. No.
                  LIB3431-047-P1-N1-C2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20369
BLAST score
                  122
E value
                  5.0e-62
                  270
Match length
                  86
% identity
NCBI Description Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >qi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
                  401901
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  g3334346
BLAST score
                  232
E value
                  3.0e-19
Match length
                  47
                  91
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG
NCBI Description
                  >qi 2852445 dbj BAA24697 (AB003378) SUI1 homolog [Salix
                  bakko]
                  401902
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-C4
                  BLASTN
Method
                  g3345476
NCBI GI
BLAST score
                  250
                  1.0e-138
E value
Match length
                  304
                  95
% identity
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                  401903
Seq. No.
                  LIB3431-047-P1-N1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350986
BLAST score
                  412
E value
                  2.0e-40
Match length
                  83
% identity
                  100
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi 483431 dbj BAA05059 (D26060) cyc07 [Oryza sativa]
Seq. No.
                  401904
Seq. ID
                  LIB3431-047-P1-N1-C6
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  107
```

NCBI GI g11957
BLAST score 107
E value 4.0e-53
Match length 301
% identity 83

NCBI Description Rice complete chloroplast genome



NCBI GI g132105 360 BLAST score 4.0e-34 E value 67 Match length 99 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9 ribulose-bisphosphate carboxy \overline{l} ase ($\overline{E}C$ 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_



(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

 Seq. No.
 401910

 Seq. ID
 LIB3431-047-P1-N1-D4

 Method
 BLASTX

 NCBI GI
 g534982

 BLAST score
 214

 E value
 2.0e-32

Match length 106 % identity 58

NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No. 401911

Seq. ID LIB3431-047-P1-N1-D6

Method BLASTX
NCBI GI g114622
BLAST score 249
E value 4.0e-21
Match length 53
% identity 92

NCBI Description ATP SYNTHASE B CHAIN (SUBUNIT I) >gi_67929_pir__LWRZ1

H+-transporting ATP synthase (EC 3.6.1.34) chain I - rice chloroplast >gi_669080 emb_CAA33992_ (X15901) ATPase I subunit [Oryza sativa] >gi_226695_prf__1603356W ATPase I

[Oryza sativa]

Seq. No. 401912

Seq. ID LIB3431-047-P1-N1-D7

Method BLASTX
NCBI GI g729478
BLAST score 398
E value 1.0e-38
Match length 81
% identity 90

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)

>gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_

(AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to

a region of the predicted gene.; similar to

ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 401913

Seq. ID LIB3431-047-P1-N1-D8

Method BLASTX
NCBI GI g5911312
BLAST score 466
E value 1.0e-46
Match length 105
% identity 80

NCBI Description (AF026167) ankyrin repeat protein EMB506 [Arabidopsis

thaliana]

Seq. No. 401914

```
LIB3431-047-P1-N1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218154
BLAST score
                  58
E value
                  8.0e-24
Match length
                  114
                  99
% identity
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
NCBI Description
                  clone:Aldp
Seq. No.
                  401915
Seq. ID
                  LIB3431-047-P1-N1-E11
Method
                  BLASTN
NCBI GI
                  q6063530
BLAST score
                  337
E value
                  0.0e+00
Match length
                  381
% identity
                  97
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                  401916
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-E12
                  BLASTX
Method
                  q1617197
NCBI GI
                  224
BLAST score
                  3.0e-18
E value
Match length
                  47
% identity
                  87
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                   401917
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-E2
Method
                  BLASTN
NCBI GI
                   q2072554
BLAST score
                   270
E value
                   1.0e-150
Match length
                   294
% identity
                   99
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                   401918
Seq. No.
Seq. ID
                   LIB3431-047-P1-N1-E3
Method
                   BLASTN
                   g3126853
NCBI GI
BLAST score
                   168
                   2.0e-89
E value
Match length
                   222
```

% identity 98

Oryza sativa chlorophyll a/b binding protein (RCABP89) NCBI Description

mRNA, nuclear gene encoding chloroplast protein, complete

cds

401919 Seq. No.

LIB3431-047-P1-N1-E4 Seq. ID

Method BLASTX NCBI GI g2696804

```
BLAST score
                  6.0e-28
E value
                  57
Match length
                  98
% identity
NCBI Description (AB009665) water channel protein [Oryza sativa]
Seq. No.
                  401920
                  LIB3431-047-P1-N1-E6
Seq. ID
                  BLASTX
Method
                  g2754849
NCBI GI
                  250
BLAST score
E value
                  3.0e-21
                  57
Match length
                  84
% identity
                  (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                  [Fritillaria agrestis]
Seq. No.
                  401921
Seq. ID
                  LIB3431-047-P1-N1-F1
                  BLASTX
Method
NCBI GI
                  g5541681
                  213
BLAST score
                  5.0e-17
E value
                  93
Match length
% identity
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]
                  401922
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-F11
                  BLASTX
Method
NCBI GI
                  g693920
BLAST score
                  347
                   1.0e-32
E value
Match length
                  66
                   100
% identity
                  (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                   tuberosum]
                   401923
Seq. No.
                  LIB3431-047-P1-N1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g517500
BLAST score
                   389
E value
                   1.0e-37
Match length
                   93
                   82
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein [Zea mays] >gi 444338_prf__1906386A photosystem II
                   OE17 protein [Pisum sativum]
                   401924
Seq. No.
```

Seq. ID LIB3431-047-P1-N1-F2

Method BLASTN
NCBI GI g454881
BLAST score 213
E value 1.0e-116
Match length 251



% identity

NCBI Description Rice gene for thioredoxin h, complete cds

Seq. No.

401925

Seq. ID

LIB3431-047-P1-N1-F4

Method NCBI GI BLASTN q455510

BLAST score E value

132 7.0e-68

Match length % identity

136 99

NCBI Description Rice mRNA for ferritin, partial sequence

Seq. No. Seq. ID

LIB3431-047-P1-N1-F6

Method NCBI GI BLAST score BLASTX g4587615 282 5.0e-25

401926

E value Match length % identity

80 66

NCBI Description

(AC006951) putative acyl-CoA synthetase [Arabidopsis

thaliana] >gi_4689469_gb_AAD27905.1 AC007213 3 (AC007213)

putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.

Seq. ID

401927 LIB3431-047-P1-N1-F8

Method NCBI GI BLAST score

g3789954 332

BLASTX

E value 6.0e-31 Match length 63 % identity

NCBI Description

(AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No.

401928

Seq. ID

LIB3431-047-P1-N1-G11

BLASTX Method g132105 NCBI GI BLAST score 393 E value 5.0e-38 Match length 73

% identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No.

401929

Seq. ID

LIB3431-047-P1-N1-G12

Method

BLASTN

```
NCBI GI
                  q3345476
BLAST score
                  244
                  1.0e-135
E value
                  307
Match length
% identity
                  95
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                  401930
Seq. No.
                  LIB3431-047-P1-N1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q20181
BLAST score
                  56
E value
                  7.0e-23
Match length
                  67
                  96
% identity
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
Seq. No.
                  401931
Seq. ID
                  LIB3431-047-P1-N1-G4
Method
                  BLASTX
NCBI GI
                  g4204276
BLAST score
                  226
E value
                  2.0e-18
Match length
                  73
% identity
                  58
NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  401932
Seq. ID
                  LIB3431-047-P1-N1-G5
                  BLASTX
Method
NCBI GI
                  q4689380
BLAST score
                  260
E value
                  9.0e-23
Match length
                  55
% identity
                  91
                  (AF139465) LHCII type III chlorophyll a/b binding protein
NCBI Description
                  [Vigna radiata]
Seq. No.
                  401933
Seq. ID
                  LIB3431-047-P1-N1-G7
Method
                  BLASTX
NCBI GI
                  g115802
BLAST score
                  187
E value
                  3.0e-14
Match length
                  36
```

% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I

CAB-36) (LHCP) >gi 100311 pir S21827 chlorophyll

a/b-binding protein (cab-36) - common tobacco

>gi 19827 emb CAA41188 (X58230) chlorophyll a/b binding

protein [Nicotiana tabacum]

Seq. No. 401934

LIB3431-047-P1-N1-G9 Seq. ID

Method BLASTX NCBI GI q122106



BLAST score 375 E value 5.0e-36 Match length 77 % identity 97

NCBI Description HISTONE H4 >gi_70771_pir_ HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana

>gi_2119028_pir__S60475 histone H4 - garden pea

>gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 (M4C13) [783 M17133]

thaliana] >gi 168499 (M36659) histone H4 (H4C13) [Zea mays]

>gi_168501 (M13370) histone H4 [Zea mays] >gi_168503
(M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone

H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata]

>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
>gi_4580385 gb_AAD24364.1_AC007184_4 (AC007184) histone H4

[Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1

(AB018245) histone H4-like protein [Solanum melongena] >gi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 401935

Seq. ID LIB3431-047-P1-N1-H12

Method BLASTX
NCBI GI g1419090
BLAST score 320
E value 2.0e-29
Match length 85
% identity 72

NCBI Description (X94968) 37kDa chloroplast inner envelope membrane

polypeptide precursor [Nicotiana tabacum]

Seq. No. 401936

Seq. ID LIB3431-047-P1-N1-H4

Method BLASTN
NCBI GI g4079797
BLAST score 51
E value 1.0e-19
Match length 106
% identity 87

NCBI Description Oryza sativa 23 kDa polypeptide of photosystem II mRNA,

complete cds

Seq. No. 401937

Seq. ID LIB3431-048-P1-K1-A10

Method BLASTX
NCBI GI g132105
BLAST score 149
E value 4.0e-10
Match length 36
% identity 83

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone posss1139) - rice >gi 218208 dbj BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

 Seq. No.
 401938

 Seq. ID
 LIB3431-048-P1-K1-B1

 Method
 BLASTX

 NCBI GI
 g3252813

 BLAST score
 219

 E value
 9.0e-18

Match length 92 % identity 43

NCBI Description (AC004705) vacuolar sorting receptor-like protein [Arabidopsis thaliana] >gi_3810586 (AC005398) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No. 401939

Seq. ID LIB3431-048-P1-K1-B11

Method BLASTX
NCBI GI g4324967
BLAST score 195
E value 2.0e-15
Match length 38
% identity 89

NCBI Description (AF114796) ADP-ribosylation factor [Glycine max]

Seq. No. 401940

Seq. ID LIB3431-048-P1-K1-B12

Method BLASTX
NCBI GI g4689390
BLAST score 260
E value 4.0e-23
Match length 55
% identity 87

NCBI Description (AF139470) chlorophyll a/b-binding protein CP24 precursor

[Vigna radiata]

Seq. No. 401941

Seq. ID LIB3431-048-P1-K1-B2

Method BLASTN
NCBI GI g4959460
BLAST score 35
E value 4.0e-10
Match length 35
% identity 100

NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 401942

Seq. ID LIB3431-048-P1-K1-B3

Method BLASTN
NCBI GI g18957
BLAST score 39
E value 9.0e-13
Match length 55
% identity 93

NCBI Description Hordeum vulgare gene for CP29 precursor for core

chlorophyll a/b binding (CAB) protein of photosystem II

Method

NCBI GI

E value

BLAST score

Match length

BLASTX

314 2.0e-29

62

g2894534



```
401943
 Seq. No.
Seq. ID
                   LIB3431-048-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g130274
                   277
BLAST score
                   5.0e-25
E value
                   56
Match length
                   95
 % identity
                  PLASTOCYANIN >gi_82500 pir__S06105 plastocyanin - rice
NCBI Description
                   401944
 Seq. No.
                   LIB3431-048-P1-K1-B5
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g20369
 BLAST score
                   143
                   7.0e-75
E value
Match length
                   158
                   97
 % identity
                   Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
 NCBI Description
                   synthetase (EC 6.3.1.2) (clone lambda-GS31)
                   >gi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                   chloroplast localising glutamine synthetase
                   401945
 Seq. No.
 Seq. ID
                   LIB3431-048-P1-K1-B7
 Method
                   BLASTX
 NCBI GI
                   g3789954
 BLAST score
                   518
 E value
                   7.0e-53
                   97
 Match length
 % identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
 NCBI Description
                   sativa]
                   401946
 Seq. No.
 Seq. ID
                   LIB3431-048-P1-K1-B8
 Method
                   BLASTX
 NCBI GI
                   g115772
 BLAST score
                   174
 E value
                   5.0e-13
 Match length
                   40
 % identity
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
 NCBI Description
                   CAB-1) (LHCP) >qi 82460 pir S03705 chlorophyll a/b-binding
                   protein 1R precursor - rice >qi 20178 emb CAA32108
                    (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
 Seq. No.
                   401947
                   LIB3431-048-P1-K1-B9
 Seq. ID
```

Seq. No.

401953



```
% identity
NCBI Description
                  (AJ224327) aquaporin [Oryza sativa]
                  401948
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-C12
Method
                  BLASTX
                  q1917019
NCBI GI
                  252
BLAST score
                  4.0e-22
E value
Match length
                  51
                  92
% identity
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                  401949
Seq. No.
                  LIB3431-048-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2583133
BLAST score
                  230
E value
                  5.0e-19
Match length
                  127
% identity
                  38
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]
                  401950
Seq. No.
                  LIB3431-048-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678261
BLAST score
                  330
E value
                  3.0e - 31
Match length
                  66
% identity
                  91
                  (AL049657) putative proteasome regulatory subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  401951
Seq. ID
                  LIB3431-048-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g1245938
BLAST score
                  35
E value
                  7.0e-11
Match length
                  35
% identity
                  100
NCBI Description
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
                  heart atrium, mRNA, 2998 nt]
Seq. No.
                  401952
Seq. ID
                  LIB3431-048-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g20340
BLAST score
                  42
E value
                  9.0e-15
Match length
                  94
% identity
                  86
NCBI Description
                  Rice rbcS gene for ribulose 1,5-bisphosphate
                  carboxylase/oxygenase small subunit (EC 4.1.1.39)
```

Method

NCBI GI

BLASTX

q1729971



```
LIB3431-048-P1-K1-D10
Seq. ID
                  BLASTX
Method
                  g1181331
NCBI GI
                  213
BLAST score
                  1.0e-17
E value
Match length
                  57
                  77
% identity
NCBI Description (X77569) calnexin [Zea mays]
                  401954
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g6014904
BLAST score
                  145
                  3.0e-09
E value
                  54
Match length
% identity
                  52
NCBI Description DAG PROTEIN, CHLOROPLAST PRECURSOR
                  >gi_1200205_emb_CAA65064_ (X95753) DAG [Antirrhinum majus]
                  401955
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q3869067
BLAST score
                  35
                  2.0e-10
E value
                  47
Match length
% identity
                  94
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCK7, complete sequence
                  401956
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-D5
                  BLASTN
Method
                  q5257255
NCBI GI
BLAST score
                  157
E value
                  4.0e-83
Match length
                  178
                  98
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone: P0026F07
Seq. No.
                  401957
Seq. ID
                  LIB3431-048-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q5734713
BLAST score
                  152
E value
                  2.0e-10
Match length
                  37
% identity
                  86
                  (AC008075) Is a member of PF 01169 Uncharacterized
NCBI Description
                   (transmembrane domain) protein family. [Arabidopsis
                  thaliana]
Seq. No.
                  401958
                  LIB3431-048-P1-K1-D8
Seq. ID
```



```
BLAST score 258
E value 7.0e-23
Match length 54
% identity 94
```

NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)

(AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza

sativa]

Seq. No. 401959

Seq. ID LIB3431-048-P1-K1-E1

Method BLASTX
NCBI GI g5630087
BLAST score 200
E value 1.0e-15
Match length 111
% identity 41

NCBI Description (AC004876) similar to predicted proteins AAB54240

(PID:g2088822) and S67138 (PID:g2132925) [Homo sapiens]

Seq. No. 401960

Seq. ID LIB3431-048-P1-K1-E11

Method BLASTN
NCBI GI g304219
BLAST score 80
E value 4.0e-37
Match length 199
% identity 85

NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit

mRNA, complete cds

Seq. No. 401961

Seq. ID LIB3431-048-P1-K1-E2

Method BLASTN
NCBI GI g4959460
BLAST score 38
E value 3.0e-12
Match length 38
% identity 100

NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 401962

Seq. ID LIB3431-048-P1-K1-E4

Method BLASTX
NCBI GI g132105
BLAST score 222
E value 1.0e-18
Match length 63
% identity 73

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

Seq. ID



carboxylase S [Oryza sativa]

```
401963
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-E5
                  BLASTX
Method
NCBI GI
                  g4105131
BLAST score
                  139
                  6.0e-09
E value
                  31
Match length
                  94
% identity
NCBI Description (AF043539) ClpC protease [Spinacia oleracea]
Seq. No.
                  401964
Seq. ID
                  LIB3431-048-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g5733874
                  351
BLAST score
E value
                  2.0e-33
                  112
Match length
                  56
% identity
NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]
                  401965
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  315
                  1.0e-29
E value
Match length
                  68
                  87
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  401966
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-F4
                  BLASTN
Method
NCBI GI
                  g2306980
BLAST score
                  99
E value
                  1.0e-48
Match length
                  112
% identity
                  97
NCBI Description Oryza sativa photosystem I antenna protein (Lhca) mRNA,
                  complete cds
                  401967
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-F6
                  BLASTN
Method
NCBI GI
                  q21843
BLAST score
                  39
E value
                  1.0e-12
Match length
                  76
                  88
% identity
NCBI Description
                  Wheat PsbO mRNA for 33kDa oxygen evolving protein of
                  photosystem II
Seq. No.
                  401968
```

LIB3431-048-P1-K1-F7

```
BLASTX
Method
                  g3126854
NCBI GI
                  151
BLAST score
                  4.0e-10
E value
                  33
Match length
                  91
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  401969
Seq. No.
                  LIB3431-048-P1-K1-G10
Seq. ID
                  BLASTX
Method
                   g733454
NCBI GI
                   266
BLAST score
                   2.0e-23
E value
                   74
Match length
                   73
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   401970
Seq. No.
                   LIB3431-048-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2501189
BLAST score
                   444
E value
                   2.0e-44
                   90
Match length
                   94
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
                   401971
Seq. No.
                   LIB3431-048-P1-K1-G4
Seq. ID
                   BLASTX
Method
                   g671740
NCBI GI
                   416
BLAST score
                   6.0e-41
E value
                   75
Match length
                   100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   401972
Seq. No.
Seq. ID
                   LIB3431-048-P1-K1-G9
                   BLASTN
Method
                   q218207
NCBI GI
BLAST score
                   104
                   9.0e-52
E value
Match length
                   112
```

98 % identity

Oryza sativa mRNA for the small subunit of NCBI Description

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

p0SSS1139

401973 Seq. No.

LIB3431-048-P1-K1-H1 Seq. ID



```
BLASTX
Method
NCBI GI
                  g320618
BLAST score
                  275
E value
                  8.0e-25
Match length
                  51
% identity
                  96
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >qi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  401974
Seq. ID
                  LIB3431-048-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3891918
BLAST score
                  339
E value
                  2.0e-32
                  67
Match length
                  93
% identity
                  Ferredoxin:nadp+ Oxidoreductase (Ferredoxin Reductase)
NCBI Description
                  Mutant E3121
Seq. No.
                  401975
Seq. ID
                  LIB3431-048-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q606817
BLAST score
                  143
E value
                  2.0e-09
Match length
                  36
                  78
% identity
NCBI Description
                  (U08404) carbonic anhydrase [Oryza sativa]
                  >qi 5917783 qb AAD56038.1 AF182806 1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
                  401976
Seq. No.
                  LIB3431-048-P1-K1-H3
Seq. ID
Method
                  BLASTN
                  g1235663
NCBI GI
BLAST score
                  103
E value
                  4.0e-51
Match length
                  115
% identity
                  97
                  Oryza sativa clone pFDRSC61 novel calmodulin-like protein
NCBI Description
                  mRNA, complete cds
Seq. No.
                  401977
Seq. ID
                  LIB3431-048-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g3063710
BLAST score
                  188
```

E value 1.0e-14 Match length 54 % identity 57

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 401978



Seq. ID LIB3431-048-P1-K1-H8

Method BLASTX
NCBI GI g2244786
BLAST score 158
E value 4.0e-11
Match length 39
% identity 69

NCBI Description (Z97335) ribonucleoprotein like protein [Arabidopsis

thaliana]

Seq. No. 401979

Seq. ID LIB3431-048-P1-N1-A10

Method BLASTX
NCBI GI g132105
BLAST score 385
E value 4.0e-37
Match length 72
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401980

Seq. ID LIB3431-048-P1-N1-A12

Method BLASTX
NCBI GI g115813
BLAST score 257
E value 4.0e-22
Match length 61
% identity 82

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi 19182 emb CAA33330 (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 401981

Seq. ID LIB3431-048-P1-N1-A2

Method BLASTX
NCBI GI g2499417
BLAST score 370
E value 2.0e-35
Match length 91
% identity 77

NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR

>gi_1085826_pir__S49248 H-protein - Flaveria anomala >gi_547558_emb_CAA85761 (Z37524) H-protein [Flaveria

anomala]

Seq. No. 401982

Seq. ID LIB3431-048-P1-N1-A3

Method BLASTX NCBI GI q115813

```
BLAST score
                  3.0e-22
E value
Match length
                  61
                  82
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  401983
Seq. No.
                  LIB3431-048-P1-N1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1663724
BLAST score
                  357
E value
                  9.0e-34
Match length
                  105
                  66
% identity
NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
Seq. No.
                  401984
Seq. ID
                  LIB3431-048-P1-N1-A6
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  63
                  1.0e-26
E value
                  174
Match length
                  85
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  401985
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-A8
```

Method BLASTN
NCBI GI g3789953
BLAST score 184
E value 4.0e-99
Match length 255
% identity 93

NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor

(Cab26) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 401986

Seq. ID LIB3431-048-P1-N1-B11

Method BLASTX
NCBI GI g2293566
BLAST score 166
E value 2.0e-11
Match length 30
% identity 100

NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 401987

Seq. ID LIB3431-048-P1-N1-B4

Method BLASTX
NCBI GI g481190
BLAST score 301
E value 2.0e-27

```
Match length
                  95
% identity
                  plastocyanin precursor - barley >gi_22705 emb CAA68696
NCBI Description
                  (Y00704) plastocyanin precursor [Hordeum vulgare]
                  >gi 431920 emb_CAA82201 (Z28347) plastocyanin [Hordeum
                  vulgare]
                  401988
Seq. No.
                  LIB3431-048-P1-N1-B5
Seq. ID
                  BLASTN
Method
                  g20369
NCBI GI
BLAST score
                  321
E value
                  0.0e+00
                  355
Match length
                  98
% identity
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
                 chloroplast localising glutamine synthetase
                  401989
Seq. No.
                  LIB3431-048-P1-N1-B7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3789954
                  299
BLAST score
                  5.0e-27
E value
                  57
Match length
                  98
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                   401990
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-B8
                  BLASTX
Method
                  q3036946
NCBI GI
BLAST score
                   301
                   2.0e-27
E value
                   61
Match length
% identity
                  (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   401991
Seq. No.
Seq. ID
                   LIB3431-048-P1-N1-B9
Method
                   BLASTX
                   g2696804
NCBI GI
BLAST score
                   406
                   1.0e-39
E value
Match length
                   79
% identity
NCBI Description (AB009665) water channel protein [Oryza sativa]
```

Seq. No. 401992

Seq. ID LIB3431-048-P1-N1-C12

Method BLASTX
NCBI GI g1917019
BLAST score 195

```
5.0e-15
E value
Match length
                  67
                  69
% identity
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                  401993
Seq. No.
                  LIB3431-048-P1-N1-C3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4138289
BLAST score
                  243
                  1.0e-134
E value
Match length
                  343
                  93
% identity
NCBI Description Oryza sativa mRNA for thioredoxin {\tt M}
                  401994
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-C4
                  BLASTX
Method
NCBI GI
                   g4678261
BLAST score
                   388
                   2.0e-37
E value
                  85
Match length
% identity
                   92
                   (AL049657) putative proteasome regulatory subunit
NCBI Description
                   [Arabidopsis thaliana]
                   401995
Seq. No.
                   LIB3431-048-P1-N1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4585875
                   395
BLAST score
                   3.0e-38
E value
Match length
                   89
                   75
% identity
NCBI Description (AC005850) Unknown protein [Arabidopsis thaliana]
                   401996
Seq. No.
                   LIB3431-048-P1-N1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g671740
BLAST score
                   155
                   2.0e-10
E value
Match length
                   33
% identity
                   91
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   401997
                   LIB3431-048-P1-N1-C9
Seq. ID
                   BLASTN
Method
                   g3345476
NCBI GI
BLAST score
                   235
E value
                   1.0e-129
                   305
Match length
                   95
% identity
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
```



```
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-D3
Method
                  BLASTX
NCBI GI
                  q3256035
BLAST score
                  222
E value
                  5.0e-18
Match length
                  81
% identity
                  52
                  (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                  bicolor]
                  401999
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-D5
Method
                  BLASTX
NCBI GI
                  g5257277
BLAST score
                  331
E value
                  7.0e-31
Match length
                  68
% identity
                  99
NCBI Description
                  (AP000364) ESTs C98431(E0144), C71728(E0144) correspond to a
                  region of the predicted gene.; Similar to Medicago sativa
                  S-adenosyl-L-methionine. (U20736) [Oryza sativa]
                  402000
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-D8
                  BLASTN
Method
NCBI GI
                  g435648
BLAST score
                  69
E value
                  2.0e-30
Match length
                  105
% identity
                  91
NCBI Description Rice mRNA for gamma-Tip, complete cds
                  402001
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-D9
Method
                  BLASTX
NCBI GI
                  q1651922
BLAST score
                  175
E value
                  2.0e-12
Match length
                  60
% identity
NCBI Description
                 (D90901) hypothetical protein [Synechocystis sp.]
Seq. No.
                  402002
                  LIB3431-048-P1-N1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q19565
BLAST score
                  35
                  4.0e-10
E value
Match length
                  47
% identity
                  94
```

NCBI Description M.liliiflora GADPH mRNA for glycolytic

glyceraldehyde-3-phosphate dehydrogenase

Seq. No. 402003

Seq. ID LIB3431-048-P1-N1-E11

Method BLASTX



NCBI GI g548605 BLAST score 162 E value 2.0e-11 Match length 37 % identity 89

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor
- barley >gi 304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 402004

Seq. ID LIB3431-048-P1-N1-E2

Method BLASTX
NCBI GI g131176
BLAST score 260
E value 1.0e-22
Match length 62
% identity 85

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR

(PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)

>gi_72683_pir__F1BH4 photosystem I chain IV precursor barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
-46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A

10.8kD photosystem I protein [Hordeum vulgare var.

distichum]

Seq. No. 402005

Seq. ID LIB3431-048-P1-N1-E4

Method BLASTX
NCBI GI g347451
BLAST score 359
E value 5.0e-34
Match length 72
% identity 92

NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza

sativa]

Seq. No. 402006

Seq. ID LIB3431-048-P1-N1-E5

Method BLASTX
NCBI GI g461753
BLAST score 321
E value 1.0e-29
Match length 87
% identity 69

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi_169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 402007

Seq. ID LIB3431-048-P1-N1-E6

Method BLASTN
NCBI GI g2196541
BLAST score 161



E value 2.0e-85 Match length 221 % identity 93

NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds

Seq. No.

402008

Seq. ID

LIB3431-048-P1-N1-E7

Method BLASTX NCBI GI q5733874 243 BLAST score E value 1.0e-20 75 Match length 56 % identity

NCBI Description (AC007932) F11A17.8 [Arabidopsis thaliana]

Seq. No.

402009

Seq. ID

LIB3431-048-P1-N1-F1

Method BLASTX NCBI GI g131176 BLAST score 288 8.0e-26 E value Match length 60 % identity 93

PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR NCBI Description

(PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)

>gi 72683 pir F1BH4 photosystem I chain IV precursor barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A

10.8kD photosystem I protein [Hordeum vulgare var.

distichum]

Seq. No.

402010 Seq. ID

LIB3431-048-P1-N1-F10

Method BLASTN NCBI GI g218207 BLAST score 164 E value 3.0e-87 Match length 249 % identity 92

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

p0SSS1139

Seq. No.

402011

Seq. ID

LIB3431-048-P1-N1-F12

Method BLASTX NCBI GI g115807 BLAST score 234 E value 1.0e-19 Match length 61 % identity 75

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN E PRECURSOR (LHCII TYPE I

> CAB-E) (LHCP) >gi 72736 pir CDNTEC chlorophyll a/b-binding protein type I precursor (cab-E) - curled-leaved tobacco >gi 170212 (M21398) chlorophyll a/b-binding protein-E

[Nicotiana plumbaginifolia]



95

[Zea mays]

% identity

NCBI Description

```
402012
Seq. No.
                   LIB3431-048-P1-N1-F4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2306980
BLAST score
                   74
                   1.0e-33
E value
Match length
                   88
% identity
                   97
                  Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                   complete cds
                   402013
Seq. No.
                   LIB3431-048-P1-N1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g482311
BLAST score
                   298
E value
                   6.0e-27
Match length
                   69
                   90
% identity
                   photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292 prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
Seq. No.
                   402014
                   LIB3431-048-P1-N1-F7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3126853
BLAST score
                   122
E value
                   4.0e-62
Match length
                   188
% identity
                   96
                   Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                   mRNA, nuclear gene encoding chloroplast protein, complete
                   cds
                   402015
Seq. No.
                   LIB3431-048-P1-N1-F8
Seq. ID
                   BLASTN
Method
                   g430946
NCBI GI
BLAST score
                   37
                   3.0e-11
E value
Match length
                   65
% identity
                   89
                   Arabidopsis thaliana PSI type III chlorophyll a/b-binding
NCBI Description
                   protein (Lhca3*1) mRNA, complete cds
                   402016
Seq. No.
                   LIB3431-048-P1-N1-G1
Seq. ID
Method
                   BLASTX
                   g733454
NCBI GI
BLAST score
                   402
E value
                   4.0e-39
Match length
                   81
```

(U23188) chlorophyll a/b-binding apoprotein CP26 precursor

```
402017
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-G2
Method
                  BLASTX
NCBI GI
                  g4105794
BLAST score
                  175
E value
                  2.0e-12
                  47
Match length
                  60
% identity
                  (AF049928) PGP224 [Petunia x hybrida]
NCBI Description
                  402018
Seq. No.
                  LIB3431-048-P1-N1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3063523
BLAST score
                  39
E value
                  1.0e-12
Match length
                  59
% identity
                  92
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                  402019
Seq. ID
                  LIB3431-048-P1-N1-G8
Method
                  BLASTX
NCBI GI
                  g4757718
BLAST score
                  190
E value
                  4.0e-14
Match length
                  53
% identity
                  66
                  actin-like 6 >gi_4001803 (AF041474) BAF53a [Homo sapiens]
NCBI Description
                  >gi 4218064 dbj BAA74577 (AB015907) actin-related protein
                   [Homo sapiens]
Seq. No.
                  402020
                  LIB3431-048-P1-N1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  34
E value
                  1.0e-09
Match length
                  98
% identity
                  84
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  402021
Seq. No.
                  LIB3431-048-P1-N1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729478
```

NCBI GI g729478
BLAST score 171
E value 2.0e-12
Match length 39
% identity 79

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)

>gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1

(AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to





a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

402022 Seq. No. Seq. ID LIB3431-048-P1-N1-H12 Method BLASTX NCBI GI g1170937 BLAST score 189 3.0e-14 E value Match length 33 % identity 100

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

 $>gi_450549$ _emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 402023

Seq. ID LIB3431-048-P1-N1-H2

Method BLASTX
NCBI GI g3345477
BLAST score 346
E value 2.0e-32
Match length 66
% identity 98

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 402024

Seq. ID LIB3431-048-P1-N1-H3

Method BLASTX
NCBI GI g1235664
BLAST score 314
E value 7.0e-29
Match length 88
% identity 75

NCBI Description (U37936) novel calmodulin-like protein [Oryza sativa]

>gi 3171148 (AF064456) calmodulin-like protein [Oryza

satīva subsp. indica]

Seq. No. 402025

Seq. ID LIB3431-048-P1-N1-H5

Method BLASTX
NCBI GI g3063710
BLAST score 175
E value 2.0e-12
Match length 35
% identity 80

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3431-049-P1-K1-A10

402026

Method BLASTN
NCBI GI g20181
BLAST score 71
E value 4.0e-32
Match length 113
% identity 93

NCBI Description Rice cab2R gene for light harvesting chlorophyll



a/b-binding protein

```
Seq. No.
                  402027
Seq. ID
                  LIB3431-049-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q4510363
BLAST score
                  242
E value
                  5.0e-21
Match length
                  50
% identity
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
```

Seq. No. 402028

Seq. ID LIB3431-049-P1-K1-B11 Method BLASTX NCBI GI g445116 BLAST score 226

E value 2.0e-28 Match length 71 % identity 92

NCBI Description light-harvesting complex IIa protein; [Hordeum vulgare]

402029 Seq. No.

Seq. ID LIB3431-049-P1-K1-B12

Method BLASTX NCBI GI q606817 BLAST score 295 E value 2.0e-32 Match length 87 % identity 86

NCBI Description (U08404) carbonic anhydrase [Oryza sativa]

>gi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic

anhydrase 3 [Oryza sativa]

402030 Seq. No.

Seq. ID LIB3431-049-P1-K1-B2

Method BLASTN NCBI GI g20181 BLAST score 74 E value 7.0e-34Match length 81 % identity 99

NCBI Description Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein

Seq. No. 402031

Seq. ID LIB3431-049-P1-K1-B3

Method BLASTN NCBI GI g20181 BLAST score 48 E value 2.0e-18 Match length 72 92 % identity

NCBI Description Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein



97

complete cds

% identity

```
Seq. No.
                  402032
                  LIB3431-049-P1-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4079797
BLAST score
                  144
E value
                  2.0e-75
Match length
                  155
% identity
                  99
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                  complete cds
                  402033
Seq. No.
                  LIB3431-049-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q549063
BLAST score
                  276
                  5.0e-37
E value
Match length
                  82
                  99
% identity
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                  21kd polypeptide [Oryza sativa]
Seq. No.
                  402034
Seq. ID
                  LIB3431-049-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g606817
BLAST score
                  661
E value
                  4.0e-81
Match length
                  155
% identity
                  99
                  (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                  >gi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
Seq. No.
                  402035
                  LIB3431-049-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  q1805617
NCBI GI
BLAST score
                  163
E value
                  5.0e-20
Match length
                  56
% identity
                  96
                  (D49704) OSH44 transcript; homeobox gene [Oryza sativa]
NCBI Description
Seq. No.
                  402036
                  LIB3431-049-P1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885885
BLAST score
                  191
E value
                  1.0e-103
Match length
                  226
```

NCBI Description Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,



```
Seq. No.
                  402037
                  LIB3431-049-P1-K1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218171
BLAST score
                  83
E value
                  4.0e-39
Match length
                  138
                  91
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
                  cds
Seq. No.
                  402038
Seq. ID
                  LIB3431-049-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2739360
BLAST score
                  152
E value
                  6.0e-18
Match length
                  102
% identity
                  51
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3075385 (AC004484) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                  402039
Seq. ID
                  LIB3431-049-P1-K1-D1
Method
                  BLASTN
                  g4218534
NCBI GI
BLAST score
                  45
E value
                  2.0e-16
Match length
                  45
% identity
                  100
NCBI Description Triticum sp. mRNA for GRAB1 protein
Seq. No.
                  402040
                  LIB3431-049-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score
                  367
E value
                  4.0e-45
Match length
                  100
% identity
                  95
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  satival
                  402041
Seq. No.
                  LIB3431-049-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g3676294
NCBI GI
BLAST score
                  151
```

E value

5.0e-21

Match length 66 % identity

77 NCBI Description

(U96496) mitochondrial ATPase beta subunit [Nicotiana

sylvestris]

Seq. No.



```
LIB3431-049-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3126854
BLAST score
                   345
E value
                   6.0e - 35
Match length
                   78
                   97
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   402043
Seq. No.
Seq. ID
                  LIB3431-049-P1-K1-E10
                   BLASTN
Method
                   g3126853
NCBI GI
                   150
BLAST score
                   6.0e-79
E value
Match length
                   222
% identity
                   93
NCBI Description
                   Oryza sativa chlorophyll a/b binding protein (RCABP89)
                   mRNA, nuclear gene encoding chloroplast protein, complete
                   402044
Seq. No.
                   LIB3431-049-P1-K1-E11
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4138289
BLAST score
                   68
                   4.0e-30
E value
Match length
                   72
                   99
% identity
NCBI Description Oryza sativa mRNA for thioredoxin M
                   402045
Seq. No.
Seq. ID
                   LIB3431-049-P1-K1-E9
                   BLASTN
Method
NCBI GI
                   q3885891
BLAST score
                   80
E value
                   7.0e-37
Match length
                   95
                   97
% identity
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                   mRNA, complete cds
Seq. No.
                   402046
Seq. ID
                   LIB3431-049-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q3885894
BLAST score
                   266
E value
                   9.0e-34
Match length
                   91
% identity
                   86
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
Seq. No.
                   402047
                   LIB3431-049-P1-K1-F2
Seq. ID
```

51610

BLASTX

219

g2130089

Method

NCBI GI BLAST score



```
4.0e-18
E value
Match length
                   49
% identity
                   90
                   2-oxoglutarate/malate translocator (clone OMT103),
NCBI Description
                   mitochondrial membrane - proso millet
>gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                   translocator [Panicum miliaceum]
Seq. No.
                   402048
Seq. ID
                   LIB3431-049-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   332
E value
                   1.0e-33
Match length
                   95
% identity
                   75
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   402049
Seq. ID
                   LIB3431-049-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   g409581
BLAST score
                   38
E value
                   1.0e-12
Match length
                   62
% identity
                   90
NCBI Description Rice mRNA for serine carboxypeptidase-like protein
Seq. No.
                   402050
                   LIB3431-049-P1-K1-F8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218207
BLAST score
                   107
                   2.0e-53
E value
                   142
Match length
% identity
                   94
NCBI Description
                   Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   p0SSS1139
Seq. No.
                   402051
                   LIB3431-049-P1-K1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218132
BLAST score
                   137
```

3.0e-71E value Match length 162 % identity 96

NCBI Description Rice mRNA for Heat shock protein

402052 Seq. No.

LIB3431-049-P1-K1-G7 Seq. ID

Method BLASTX

% identity



```
NCBI GI
                  g4741940
BLAST score
                  255
E value
                  1.0e-30
Match length
                  75
% identity
NCBI Description
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
                  402053
Seq. No.
Seq. ID
                  LIB3431-049-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  35
E value
                  2.0e-10
Match length
                  35
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  402054
                  LIB3431-049-P1-K1-H5
Seq. ID
Method
                  BLASTX
                  q4262142
NCBI GI
BLAST score
                  157
                  1.0e-10
E value
Match length
                  61
% identity
                  54
NCBI Description
                  (AC005275) putative alcohol dehydrogenase [Arabidopsis
                  thaliana]
                  402055
Seq. No.
Seq. ID
                  LIB3431-049-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  g21840
BLAST score
                  34
E value
                  1.0e-09
Match length
                  50
% identity
                  92
NCBI Description Triticum aestivum RNA for phosphoribulokinase
                  402056
Seq. No.
                  LIB3431-049-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510363
BLAST score
                  175
E value
                  2.0e-12
Match length
                  36
% identity
                  89
                  (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  402057
Seq. No.
                  LIB3431-049-P1-N1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3158476
BLAST score
                  317
                  5.0e-29
E value
Match length
                  76
```





```
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  402058
Seq. ID
                  LIB3431-049-P1-N1-A7
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  248
E value
                  4.0e-21
Match length
                  56
% identity
                  86
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  402059
Seq. No.
Seq. ID
                  LIB3431-049-P1-N1-A8
                  BLASTX
Method
NCBI GI
                  q563235
BLAST score
                  513
E value
                  4.0e-52
Match length
                  117
% identity
                  (U15964) xyloglucan endo-transglycosylase homolog; similar
NCBI Description
                  to Triticum aestivum endo-xyloglucan transferase, PIR
                  Accession Number E49539 [Zea mays] >gi_563927 (U15781)
                  xyloglucan endo-transglycosylase homolog [Zea mays]
                  >qi 1097378 prf 2113418A xyloglucan endotransglycosylase
                  homolog [Zea mays]
                  402060
Seq. No.
                  LIB3431-049-P1-N1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2326947
BLAST score
                  153
                  6.0e-10
E value
Match length
                  34
% identity
                  91
                  (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  402061
                  LIB3431-049-P1-N1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3036949
BLAST score
                  309
                  3.0e-28
E value
Match length
                  59
                  100
% identity
                  (AB012638) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
```

Seq. No. 402062

Seq. ID LIB3431-049-P1-N1-B5

Method BLASTX
NCBI GI g4079798
BLAST score 385
E value 4.0e-37

```
Match length
                  76
                  97
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  402063
Seq. No.
                  LIB3431-049-P1-N1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q549063
BLAST score
                  283
E value
                  3.0e-25
Match length
                  53
                  98
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                  21kd polypeptide [Oryza sativa]
                  402064
Seq. No.
                  LIB3431-049-P1-N1-B8
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2624325
BLAST score
                  150
                  5.0e-79
E value
                  201
Match length
% identity
                  94
                  Oryza sativa mRNA for glycine-rich RNA-binding protein
NCBI Description
                   (OsGRP1)
Seq. No.
                  402065
Seq. ID
                  LIB3431-049-P1-N1-C10
Method
                  BLASTX
NCBI GI
                  q400879
BLAST score
                  257
E value
                  2.0e-22
Match length
                   53
% identity
                   83
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_479690_pir__S35159 photosystem I chain psaN -
                  barley >gi 19095 emb CAA47056 (X66428) photosystem I
                   subunit N [Hordeum vulgare]
Seq. No.
                   402066
                  LIB3431-049-P1-N1-C2
Seq. ID
Method
                   BLASTX
                   g2130069
NCBI GI
                   200
BLAST score
                   2.0e-15
E value
Match length
                   39
% identity
                   97
```

catalase (EC 1.11.1.6) catA - rice NCBI Description

>gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]

Seq. No. 402067

LIB3431-049-P1-N1-C4 Seq. ID

BLASTN Method NCBI GI q1805615

51614

```
BLAST score
                   0.0e + 00
E value
Match length
                   432
% identity
                   94
                  Rice OSH45 gene for OSH42, OSH44 and OSH45 transcripts,
NCBI Description
                   exon 2, 3, 4, 5, 6 and 7, complete cds
Seq. No.
                   402068
Seq. ID
                   LIB3431-049-P1-N1-C5
Method
                  BLASTN
NCBI GI
                   q3885885
BLAST score
                   195
E value
                   1.0e-105
Match length
                   202
                   100
% identity
NCBI Description
                  Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
                  complete cds
Seq. No.
                   402069
Seq. ID
                   LIB3431-049-P1-N1-C7
Method
                   BLASTX
NCBI GI
                   q289920
BLAST score
                   284
E value
                   3.0e-25
Match length
                   56
                   96
% identity
NCBI Description
                   (L07119) chlorophyll A/B binding protein [Gossypium
                   hirsutum]
Seq. No.
                   402070
Seq. ID
                   LIB3431-049-P1-N1-C8
Method
                   BLASTX
NCBI GI
                   q2739360
BLAST score
                   261
```

E value 1.0e-22 Match length 111 % identity 52

(AC002505) unknown protein [Arabidopsis thaliana] NCBI Description >gi 3075385 (AC004484) unknown protein [Arabidopsis

thaliana]

402071 Seq. No.

LIB3431-049-P1-N1-C9 Seq. ID

Method BLASTN g2970050 NCBI GI BLAST score 38 E value 7.0e-12 Match length 102 % identity 84

NCBI Description Vigna radiata mRNA for ARG10, complete cds

Seq. No. 402072

LIB3431-049-P1-N1-D1 Seq. ID

Method BLASTN g398603 NCBI GI BLAST score 39 E value 2.0e-12



```
Match length
% identity
                  90
NCBI Description A.thaliana ATAF1 mRNA
Seq. No.
                  402073
Seq. ID
                  LIB3431-049-P1-N1-D10
Method
                  BLASTX
                  q3789954
NCBI GI
                  184
BLAST score
                  1.0e-13
E value
Match length
                  47
% identity
                  79
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  402074
Seq. No.
                  LIB3431-049-P1-N1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  389
                  1.0e-37
E value
Match length
                  82
% identity
                  90
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  402075
Seq. No.
Seq. ID
                  LIB3431-049-P1-N1-D6
Method
                  BLASTX
NCBI GI
                  g5478797
BLAST score
                  415
E value
                  9.0e-41
Match length
                  91
% identity
                  87
NCBI Description (AB021310) chlorophyll b synthase [Oryza sativa]
                  402076
Seq. No.
                  LIB3431-049-P1-N1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  177
                  7.0e-13
E value
Match length
                  36
% identity
                  89
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  402077
Seq. No.
```

LIB3431-049-P1-N1-E10 Seq. ID

Method BLASTN NCBI GI g3126853 BLAST score 63 E value 5.0e-27

· Match length 98 % identity

NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete



```
402078
Seq. No.
                  LIB3431-049-P1-N1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4138289
BLAST score
                  163
E value
                  2.0e-86
                  324
Match length
% identity
                  87
NCBI Description Oryza sativa mRNA for thioredoxin M
                  402079
Seq. No.
                  LIB3431-049-P1-N1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q128690
BLAST score
                  529
E value
                  8.0e-54
Match length
                  116
% identity
                  90
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
NCBI Description
                  >qi 66161 pir DERZN3 NADH dehydrogenase (ubiquinone) (EC
                  1.6.5.3) chain 3 - rice chloroplast >gi 11989 emb CAA34001
                  (X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]
                  >gi_226610 prf__1603356AG NADH dehydrogenase ND3 [Oryza
                  sativa]
Seq. No.
                  402080
                  LIB3431-049-P1-N1-E9
Seq. ID
Method
                  BLASTX
                  g3885892
NCBI GI
BLAST score
                  200
E value
                  1.0e-15
Match length
                  49
% identity
                  82
NCBI Description
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                  402081
                  LIB3431-049-P1-N1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885894
                  178
BLAST score
E value
                  5.0e-13
Match length
                  59
% identity
                  68
NCBI Description
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
                  402082
Seq. No.
                  LIB3431-049-P1-N1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130089
BLAST score
                  439
E value
                  2.0e-43
```

Match length 88 % identity 90

NCBI Description 2-oxoglutarate/malate translocator (clone OMT103),

mitochondrial membrane - proso millet

>gi 1100743 dbj BAA08105 (D45075) 2-oxoglutarate/malate

translocator [Panicum miliaceum]



```
Seq. No.
                  402083
                  LIB3431-049-P1-N1-F4
Seq. ID
Method
                  BLASTX
                  q320618
NCBI GI
BLAST score
                  241
                  2.0e-20
E value
                  54
Match length
                  87
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  402084
Seq. No.
                  LIB3431-049-P1-N1-F6
Seq. ID
                  BLASTN
Method
                  q409581
NCBI GI
BLAST score
                  416
E value.
                  0.0e + 00
Match length
                  452
% identity
                  98
NCBI Description Rice mRNA for serine carboxypeptidase-like protein
Seq. No.
                  402085
                  LIB3431-049-P1-N1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
                  252
BLAST score
E value
                  1.0e-21
Match length
                  57
% identity
                  82
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  402086
Seq. No.
                  LIB3431-049-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q829283
                   273
BLAST score
E value
                  5.0e-24
Match length
                   68
                   82
% identity
NCBI Description (Z15018) heat shock protein hsp82 [Oryza sativa]
                   402087
Seq. No.
                  LIB3431-049-P1-N1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3885892
BLAST score
                   389
                   1.0e-37
E value
                   75
Match length
                  100
% identity
```

Seq. No. 402088

NCBI Description

(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. ID

Method



```
LIB3431-049-P1-N1-G3
Seq. ID
                  BLASTN
Method
                  g3885891
NCBI GI
BLAST score
                  34
                  5.0e-10
E value
Match length
                  58
% identity
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
Seq. No.
                  402089
Seq. ID
                  LIB3431-049-P1-N1-G6
                  BLASTX
Method
                  g6006283
NCBI GI
BLAST score
                  162
                  3.0e-11
E value
Match length
                  41
                  71
% identity
                  (AB015861) photosystem I subunit PSI-L [Arabidopsis
NCBI Description
                  thaliana]
                  402090
Seq. No.
                  LIB3431-049-P1-N1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g551047
BLAST score
                  243
                  2.0e-20
E value
Match length
                  55
% identity
NCBI Description (X79277) type II LHCI [Lolium temulentum]
                  402091
Seq. No.
Seq. ID
                  LIB3431-049-P1-N1-G8
                  BLASTN
Method
NCBI GI
                  g218207
BLAST score
                  180
E value
                   1.0e-96
Match length
                  279
                   90
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  posss1139
Seq. No.
                   402092
Seq. ID
                  LIB3431-049-P1-N1-H5
Method
                  BLASTX
NCBI GI
                   q4262142
BLAST score
                   145
                   5.0e-09
E value
Match length
                   69
% identity
                   49
                  (AC005275) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   402093
Seq. No.
```

51619

LIB3431-049-P1-N1-H6

BLASTX

```
q671740
NCBI GI
BLAST score
                  380
E value
                  2.0e-36
Match length
                  69
% identity
                  100
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  402094
Seq. No.
                  LIB3431-049-P1-N1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21839
BLAST score
                  336
E value
                  2.0e-31
Match length
                  75
% identity
                  87
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
Seq. No.
                  402095
                  LIB3431-050-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  35
                  5.0e-10
E value
Match length
                  35
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  402096
                  LIB3431-050-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131192
BLAST score
                  449
                  1.0e-44
E value
Match length
                  97
% identity
                  87
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606 pir S20937
                  photosystem I chain V precursor - barley
                  >gi 19091 emb CAA42727 (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
                  402097
Seq. No.
                  LIB3431-050-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
                  339
BLAST score
                  4.0e-32
E value
Match length
                  79
% identity
                  86
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
```

precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza



sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

 Seq. No.
 402098

 Seq. ID
 LIB3431-050-P1-K1-A5

 Method
 BLASTX

 NCBI GI
 g671740

 BLAST score
 449

 E value
 1.0e-44

 Match length
 83

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 402099

% identity

Seq. ID LIB3431-050-P1-K1-A6

99

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 6.0e-20
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402100

Seq. ID LIB3431-050-P1-K1-A7

Method BLASTX
NCBI GI g1170507
BLAST score 627
E value 2.0e-65
Match length 130
% identity 92

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)

>gi_100276_pir__S22579 translation initiation factor eIF-4A
- curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)
nicotiana eukaryotic translation initiation factor 4A

[Nicotiana plumbaginifolia]

Seq. No. 402101

Seq. ID LIB3431-050-P1-K1-A8

Method BLASTX
NCBI GI g3080391
BLAST score 526
E value 1.0e-53
Match length 125
% identity 76

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3431-050-P1-K1-B1

402102

Method BLASTN
NCBI GI g218207
BLAST score 101
E value 2.0e-49
Match length 116



```
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
                  402103
Seq. No.
                  LIB3431-050-P1-K1-B10
Seq. ID
                  BLASTN
Method
                  g20262
NCBI GI
BLAST score
                  268
                  1.0e-149
E value
                  308
Match length
% identity
                  97
NCBI Description O.sativa light-induced mRNA
Seq. No.
                  402104
                  LIB3431-050-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  290
E value
                  3.0e-26
Match length
                  70
% identity
                  79
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  402105
Seq. No.
                  LIB3431-050-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3367596
BLAST score
                  311
                  6.0e-32
E value
Match length
                  98
% identity >
                  70
                  (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                  402106
Seq. No.
Seq. ID
                  LIB3431-050-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2924785
BLAST score
                  165
                  2.0e-11
E value
Match length
                  79
% identity
                  47
                  (AC002334) similar to disease resistance protein
NCBI Description
```

NCBI Description (ACU02334) similar to disease resistance [Arabidopsis thaliana]

Seq. No. 402107

Seq. ID LIB3431-050-P1-K1-C1

Method BLASTX
NCBI GI g3236242
BLAST score 435
E value 4.0e-43
Match length 106



% identity 80

NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis

thaliana]

Seq. No. 402108

Seq. ID LIB3431-050-P1-K1-C12

Method BLASTX
NCBI GI g82080
BLAST score 364
E value 8.0e-35
Match length 103
% identity 70

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 402109

Seq. ID LIB3431-050-P1-K1-C2

Method BLASTX
NCBI GI g3036953
BLAST score 273
E value 5.0e-24
Match length 51
% identity 100

NCBI Description (AB012640) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No. 402110

Seq. ID LIB3431-050-P1-K1-C7

Method BLASTX
NCBI GI g3808101
BLAST score 335
E value 2.0e-33
Match length 99
% identity 70

NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]

Seq. No. 402111

Seq. ID LIB3431-050-P1-K1-C9

Method BLASTX
NCBI GI g132105
BLAST score 480
E value 2.0e-48
Match length 112
% identity 82

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402112

Seq. ID LIB3431-050-P1-K1-D1



```
BLASTX
Method
NCBI GI
                  g3929924
                  210
BLAST score
                  4.0e-17
E value
Match length
                  41
                  100
% identity
                  (AB020502) catalase [Oryza sativa]
NCBI Description
                  402113
Seq. No.
                  LIB3431-050-P1-K1-D10
Seq. ID
Method
                  BLASTX
                  g462195
NCBI GI
BLAST score
                  281
                  5.0e-25
E value
Match length
                  69
% identity
                  81
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir S21636 GOS2 protein - rice
                  >qi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >qi 3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
Seq. No.
                  402114
                  LIB3431-050-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  7.0e-20
E value
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  402115
Seq. No.
                  LIB3431-050-P1-K1-D2
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
BLAST score
                  36
E value
                  8.0e-11
Match length
                  36
% identity
                  100
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                  402116
Seq. No.
                  LIB3431-050-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1370188
BLAST score
                  304
E value
                  5.0e-28
```

Match length 71 % identity 79

(Z73943) RAB7D [Lotus japonicus] NCBI Description

402117 Seq. No.

Seq. ID LIB3431-050-P1-K1-D6

Method BLASTX

```
q733454
NCBI GI
BLAST score
                  317
E value
                  4.0e-29
Match length
                  66
% identity
                  94
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  402118
                  LIB3431-050-P1-K1-D7
Seq. ID
Method
                  BLASTX
                  g5541681
NCBI GI
BLAST score
                  225
                  3.0e-18
E value
Match length
                  165
% identity
                  39
NCBI Description (AL096859) putative protein [Arabidopsis thaliana]
Seq. No.
                  402119
                  LIB3431-050-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6015065
BLAST score
                  308
E value
                  9.0e-29
Match length
                   64
                  92
% identity
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 2369714_emb_CAB09900_
                   (Z97178) elongation factor 2 [Beta vulgaris]
                   402120
Seq. No.
                  LIB3431-050-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  g1835731
NCBI GI
                   357
BLAST score
                   5.0e-34
E value
                   81
Match length
% identity
                   89
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   402121
Seq. No.
                   LIB3431-050-P1-K1-E10
Seq. ID
Method
                   BLASTN
                   g6015437
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
                   47
Match length
% identity
                   65
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   402122
Seq. No.
                   LIB3431-050-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2346966
BLAST score
                   144
```

8.0e-09

57

53

E value Match length

% identity





NCBI Description (AB004871) CPC [Arabidopsis thaliana] >gi 4559383 gb AAD23043.1 AC006526 8 (AC006526) putative DNA binding protein CPC [Arabidopsis thaliana] 402123 Seq. No. LIB3431-050-P1-K1-E4 Seq. ID Method BLASTX g3915186 NCBI GI BLAST score 231 E value 4.0e-19 Match length 86 55 % identity UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >qi 3128447 (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta] Seq. No. 402124 LIB3431-050-P1-K1-E7 Seq. ID Method BLASTN g6015437 NCBI GI BLAST score 36 9.0e-11 E value Match length 36 100 % identity NCBI Description Homo sapiens PEX1 mRNA, complete cds Seq. No. 402125 LIB3431-050-P1-K1-E9 Seq. ID Method BLASTX NCBI GI q3036946 BLAST score 281 E value 3.0e-25 Match length 56 % identity 95 NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris] Seq. No. 402126 LIB3431-050-P1-K1-F1 Seq. ID Method BLASTX NCBI GI q125580 BLAST score 155 E value 8.0e-11 Match length 48 % identity 73 PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) NCBI Description

(PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19 - wheat $> gi_5924030$ emb_CAB56544.1_ (X51608)

phosphoribulokinase [Triticum aestivum]

Seq. No. 402127

Seq. ID LIB3431-050-P1-K1-F11

Method BLASTX NCBI GI q4572679 BLAST score 161 2.0e-11 E value



Match length 65 % identity 52

NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No. 402128

Seq. ID LIB3431-050-P1-K1-F3

Method BLASTX
NCBI GI g1172558
BLAST score 201
E value 7.0e-16
Match length 79

% identity 47

NCBI Description OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT

ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)

>gi 480122 pir S36454 porin por1 - garden pea

>gi 396819 emb CAA80988 (Z25540) Porin [Pisum sativum]

Seq. No. 402129

Seq. ID LIB3431-050-P1-K1-F4

Method BLASTX
NCBI GI g115787
BLAST score 344
E value 1.0e-32
Match length 80
% identity 91

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 402130

Seq. ID LIB3431-050-P1-K1-F6

Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 4.0e-11
Match length 36
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402131

Seq. ID LIB3431-050-P1-K1-F8

Method BLASTX
NCBI GI g3688182
BLAST score 367
E value 2.0e-37
Match length 92
% identity 89

NCBI Description (AL031804) P-Protein - like protein [Arabidopsis thaliana]

Seq. No. 402132

Seq. ID LIB3431-050-P1-K1-F9

Method BLASTX
NCBI GI g3789952
BLAST score 497



```
E value
                   2.0e-50
Match length
                   102
% identity
                   96
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
Seq. No.
                   402133
Seq. ID
                  LIB3431-050-P1-K1-G1
Method
                  BLASTN
NCBI GI
                   q6006355
BLAST score
                   125
E value
                   8.0e-64
```

% identity 100 NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No. 402134

Match length

Seq. ID LIB3431-050-P1-K1-G10

260

Method BLASTX
NCBI GI g4680501
BLAST score 216
E value 2.0e-17
Match length 91
% identity 52

NCBI Description (AF119222) hypothetical protein [Oryza sativa]

Seq. No. 402135

Seq. ID LIB3431-050-P1-K1-G11

Method BLASTX
NCBI GI g21693
BLAST score 450
E value 5.0e-45
Match length 83
% identity 92

NCBI Description (X66012) cathepsin B [Triticum aestivum]

Seq. No. 402136

Seq. ID LIB3431-050-P1-K1-G4

Method BLASTN
NCBI GI g4959460
BLAST score 38
E value 9.0e-12
Match length 38
% identity 100

NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No. 402137

Seq. ID LIB3431-050-P1-K1-G5

Method BLASTX
NCBI GI g3687440
BLAST score 310
E value 1.0e-28
Match length 107
% identity 54

NCBI Description (AL022577) dJ353H6.2.1 (SW1/SNF related, matrix associated,

actin dependent regulator of chromatin, subfamily a, member

1 (SNF2L1)) [Homo sapiens]

Match length

% identity

104



```
Seq. No.
                    402138
 Seq. ID
                    LIB3431-050-P1-K1-G7
 Method
                    BLASTX
 NCBI GI
                    g417260
 BLAST score
                    349
 E value
                    5.0e-33
Match length
                    110
 % identity
 NCBI Description
                    LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                    lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                    light-regulated gene [Oryza sativa]
 Seq. No.
                    402139
 Seq. ID
                    LIB3431-050-P1-K1-G8
 Method
                    BLASTX
 NCBI GI
                    q1944407
 BLAST score
                    265
                    3.0e-23
 E value
 Match length
                    65
                    72
 % identity
 NCBI Description (D86988) KIAA0221 [Homo sapiens]
                    402140
 Seq. No.
 Seq. ID
                    LIB3431-050-P1-K1-H11
 Method
                    BLASTX
 NCBI GI
                    q2072555
 BLAST score
                    233
 E value
                    2.0e-19
 Match length
                    44
  % identity
                    98
 NCBI Description
                    (AF001396) metallothionein-like protein [Oryza sativa]
                    >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                    protein [Oryza sativa]
  Seq. No.
                    402141
  Seq. ID
                    LIB3431-050-P1-K1-H2
 Method
                    BLASTX
 NCBI GI
                    g320618
 BLAST score
                    406
 E value
                    9.0e-40
 Match length
                    96
  % identity
                    80
                    chlorophyll a/b-binding protein I precursor - rice
 NCBI Description
                    >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                    chlorophyll a/b-binding protein [Oryza sativa]
                    >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
  Seq. No.
                    402142
                    LIB3431-050-P1-K1-H3
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g430947
                    390
 BLAST score
                    6.0e-38
 E value
```





NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 402143

Seq. ID LIB3431-050-P1-K1-H4

Method BLASTX
NCBI GI g132105
BLAST score 251
E value 8.0e-22
Match length 67
% identity 76

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >qi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402144

Seq. ID LIB3431-050-P1-K1-H5

Method BLASTX
NCBI GI g2570515
BLAST score 488
E value 3.0e-49
Match length 110
% identity 86

NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 402145

Seq. ID LIB3431-050-P1-K1-H9

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 7.0e-20
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402146

Seq. ID LIB3431-050-P1-N1-A11

Method BLASTX
NCBI GI g131192
BLAST score 359
E value 3.0e-34
Match length 74
% identity 89

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR

(PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 100606 pir S20937

photosystem I chain V precursor - barley

>gi 19091_emb_CAA42727_ (X60158) photosystem I polypeptide

PSI-G precursor [Hordeum vulgare]

% identity

NCBI Description

45

800



```
Seq. No.
                   402147
                  LIB3431-050-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  291
                   4.0e-26
E value
Match length
                  57
% identity
                   98
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   402148
Seq. No.
                  LIB3431-050-P1-N1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  279
E value
                  1.0e-24
Match length
                  54
% identity
                   93
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   402149
Seq. No.
Seq. ID
                  LIB3431-050-P1-N1-A9
Method
                  BLASTX
NCBI GI
                  g2499417
BLAST score
                  277
E value
                  1.0e-24
Match length
                   62
% identity
                  82
NCBI Description
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
                  >gi 1085826 pir S49248 H-protein - Flaveria anomala
                  >gi 547558 emb CAA85761 (Z37524) H-protein [Flaveria
                  anomala]
                  402150
Seq. No.
                  LIB3431-050-P1-N1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  146
E value
                  2.0e-76
Match length
                  274
% identity
                  89
NCBI Description O.sativa light-induced mRNA
Seq. No.
                  402151
Seq. ID
                  LIB3431-050-P1-N1-B11
Method
                  BLASTX
                  g4587570
NCBI GI
BLAST score
                  144
E value
                  8.0e-09
Match length
                  66
```

(AC006550) Strong similarity to gi_2244833 centromere protein homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from



this gene

```
Seq. No.
                    402152
                    LIB3431-050-P1-N1-B2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q115787
 BLAST score
                    480
                    3.0e-48
 E value
 Match length
                    92
 % identity
                    99
 NCBI Description
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                    protein 2R precursor - rice >gi 20182 emb CAA32109
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
 Seq. No.
                    402153
 Seq. ID
                    LIB3431-050-P1-N1-B5
 Method
                    BLASTX
 NCBI GI
                    g1429226
 BLAST score
                    228
                    1.0e-18
 E value
 Match length
                    47
 % identity
                    85
 NCBI Description (X98861) TFIIA [Arabidopsis thaliana]
 Seq. No.
                    402154
                    LIB3431-050-P1-N1-B8
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q5729802
 BLAST score
                    452
 E value
                    6.0e-45
 Match length
                    91
 % identity
                    89
 NCBI Description
                   similar to S. pombe dim1+ >gi 2565275 (AF023611) Dim1p
                    homolog [Homo sapiens]
Seq. No.
                    402155
                    LIB3431-050-P1-N1-C1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3236242
 BLAST score
                    334
 E value
                    4.0e-31
 Match length
                    98
 % identity
 NCBI Description
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
                    thaliana]
 Seq. No.
                    402156
 Seq. ID
                    LIB3431-050-P1-N1-C11
 Method
                    BLASTX
 NCBI GI
                    q131176
 BLAST score
                    203
 E value
                    6.0e-16
 Match length
                    47
 % identity
                    87
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
```



distichum]

(PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
>gi_72683_pir__F1BH4 photosystem I chain IV precursor barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
-46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A
10.8kD photosystem I protein [Hordeum vulgare var.

Seq. No. 402157 LIB3431-050-P1-N1-C12 Seq. ID Method BLASTX NCBI GI g115813 201 BLAST score E value 1.0e-15 Match length 46 % identity 80

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi 19182 emb_CAA33330_ (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

 Seq. No.
 402158

 Seq. ID
 LIB3431-050-P1-N1-C2

 Method
 BLASTX

 NCBI GI
 g289920

 BLAST score
 267

 E value
 3.0e-23

Match length 51 % identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 402159

Seq. ID LIB3431-050-P1-N1-C4

Method BLASTX
NCBI GI g2492487
BLAST score 330
E value 1.0e-30
Match length 76
% identity 87

NCBI Description 14-3-3-LIKE PROTEIN B (14-3-3B) >gi_1070354_emb_CAA63658_

(X93170) Hv14-3-3b [Hordeum vulgare]

Seq. No. 402160

Seq. ID LIB3431-050-P1-N1-C9

Method BLASTN
NCBI GI g218207
BLAST score 124
E value 2.0e-63
Match length 231
% identity 88

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS1139

Seq. No. 402161

Seq. ID LIB3431-050-P1-N1-D1

Method BLASTN NCBI GI g3868755

```
BLAST score
                  8.0e-79
E value
                  250
Match length
% identity
                  91
                  Oryza sativa CatC gene for catalase, complete cds
NCBI Description
                  402162
Seq. No.
                  LIB3431-050-P1-N1-D10
Seq. ID
                  BLASTN
Method
                  g3789949
NCBI GI
                  186
BLAST score
                  1.0e-100
E value
                  298
Match length
% identity
                  91
                  Oryza sativa translation initiation factor (GOS2) mRNA,
NCBI Description
                  complete cds
                  402163
Seq. No.
                  LIB3431-050-P1-N1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2072555
BLAST score
                  333
E value
                  5.0e-31
Match length
                  62
% identity
                  97
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  402164
                  LIB3431-050-P1-N1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4680212
BLAST score
                  187
                  7.0e-14
E value
Match length
                  53
% identity
                  66
                  (AF114171) hypothetical protein [Sorghum bicolor]
NCBI Description
                  402165
Seq. No.
                  LIB3431-050-P1-N1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5541681
                  212
BLAST score
                  7.0e-17
E value
Match length
                  92
                  55
% identity
                  (AL096859) putative protein [Arabidopsis thaliana]
NCBI Description
                  402166
Seq. No.
```

Seq. ID LIB3431-050-P1-N1-E1

Method BLASTX NCBI GI q1835731 187 BLAST score 1.0e-28 E value Match length 88 80 % identity



```
(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  402167
Seq. No.
Seq. ID
                  LIB3431-050-P1-N1-E5
Method
                  BLASTN
NCBI GI
                  q11957
BLAST score
                  323
                  0.0e + 00
E value
                  431
Match length
                  99
% identity
NCBI Description Rice complete chloroplast genome
                  402168
Seq. No.
Seq. ID
                  LIB3431-050-P1-N1-E9
                  BLASTN
Method
NCBI GI
                  g20181
BLAST score
                  43
                  6.Qe-15
E value
Match length
                  146
                  82
% identity
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
                  402169
Seq. No.
                  LIB3431-050-P1-N1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q21839
BLAST score
                  340
                  8.0e-32
E value
Match length
                  73
                  93
% identity
NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]
Seq. No.
                  402170
                  LIB3431-050-P1-N1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3273244
BLAST score
                  46
                  1.0e-16
E value
Match length
                  62
% identity
                  94
NCBI Description Oryza sativa DNA for NLS receptor, complete cds
                  402171
Seq. No.
                  LIB3431-050-P1-N1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172555
BLAST score
                  184
                  2.0e-13
E value
Match length
                  61
% identity
                  57
NCBI Description
                  34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
                   (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   (POM 34) >gi_629720_pir__S46936 34K porin - potato
```

51635

porin [Solanum tuberosum]

>gi_1076682_pir_ A55364_porin (clone pPOM-34) - potato
mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDA

Seq. ID

NCBI GI

Method



```
Seq. No.
                  402172
                  LIB3431-050-P1-N1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g710308
BLAST score
                  174
                  2.0e-12
E value
Match length
                  49
% identity
                  67
NCBI Description (U11693) victorin binding protein [Avena sativa]
                  402173
Seq. No.
                  LIB3431-050-P1-N1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6006355
BLAST score
                  265
E value
                  1.0e-147
Match length
                  360
% identity
                  93
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  402174
Seq. No.
                  LIB3431-050-P1-N1-G10
Seq. ID
Method
                  BLASTX
                  g4680338
NCBI GI
BLAST score
                  194
E value
                  8.0e-15
Match length
                  51
% identity
                  73
NCBI Description
                  (AF128457) hypothetical protein [Oryza sativa subsp.
                  indica]
Seq. No.
                  402175
                  LIB3431-050-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362615
BLAST score
                  256
E value
                  6.0e-22
Match length
                  99
                  54
% identity
NCBI Description iswi protein - fruit fly (Drosophila melanogaster)
                  >gi 439197 (L27127) ISWI protein [Drosophila melanogaster]
Seq. No.
                  402176
Seq. ID
                  LIB3431-050-P1-N1-G7
Method
                  BLASTN
                  g20262
NCBI GI
BLAST score
                  78
E value
                  3.0e-36
Match length
                  121
% identity
                  92
NCBI Description O.sativa light-induced mRNA
                  402177
Seq. No.
```

51636

LIB3431-050-P1-N1-H11

BLASTN

g2570514



```
BLAST score
E value
                  5.0e-12
Match length
                  42
% identity
                  98
NCBI Description
                  Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
Seq. No.
                  402178
                  LIB3431-050-P1-N1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421916
```

BLAST score 168 E value 1.0e-11 Match length 31

% identity 100

NCBI Description chlorophyll a/b-binding protein - English ivy (fragment)

>gi 12582 emb CAA48410 (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix]

Seq. No. 402179

Seq. ID LIB3431-050-P1-N1-H4

Method BLASTN NCBI GI q218207 BLAST score 72 E value 3.0e-32 Match length 174 % identity 85

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

p0SSS1139

Seq. No. 402180

LIB3431-050-P1-N1-H5 Seq. ID

Method BLASTN NCBI GI g2570514 BLAST score 240 E value 1.0e-132 Match length 335. 93 % identity

NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No. 402181

LIB3431-050-P1-N1-H9 Seq. ID

Method BLASTN NCBI GI g2072554 BLAST score 135 E value 6.0e-70 Match length 183 % identity 93

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

Seq. No. 402182

Seq. ID LIB3431-051-P1-K1-A11

Method BLASTX NCBI GI q2072555 BLAST score 313 E value 8.0e-29



Match length 62 % identity 90

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402183

Seq. ID LIB3431-051-P1-K1-A3

Method BLASTN
NCBI GI g20177
BLAST score 102
E value 2.0e-50
Match length 123
% identity 98

NCBI Description Rice cablR gene for light harvesting chlorophyll

a/b-binding protein

Seq. No. 402184

Seq. ID LIB3431-051-P1-K1-A5

Method BLASTX
NCBI GI g5103807
BLAST score 349
E value 5.0e-33
Match length 93
% identity 69

NCBI Description (AC007591) Contains similarity to gb_AF014403 type-2

phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo sapiens. ESTs gb T88254 and gb AA394650 come from this

gene. [Arabidopsis thaliana]

Seq. No. 402185

Seq. ID LIB3431-051-P1-K1-A6

Method BLASTN
NCBI GI g5456937
BLAST score 54
E value 1.0e-21
Match length 54
% identity 100

NCBI Description Oryza sativa rps9 mRNA for ribosomal protein S9, complete

cds

Seq. No. 402186

Seq. ID LIB3431-051-P1-K1-A9

Method BLASTX
NCBI GI g3885886
BLAST score 642
E value 2.0e-67
Match length 125
% identity 100

NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 402187

Seq. ID LIB3431-051-P1-K1-B1

Method BLASTX
NCBI GI g3913018
BLAST score 494
E value 5.0e-50



```
Match length
% identity
                  99
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  (ALDP) >qi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  402188
Seq. ID
                  LIB3431-051-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  450
E value
                  8.0e-45
Match length
                  108
                  80
% identity
NCBI Description
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
Seq. No.
                  402189
Seq. ID
                  LIB3431-051-P1-K1-B2
                  BLASTX
Method
NCBI GI
                  q2407281
BLAST score
                  517
                  1.0e-52
E value
                  107
Match length
                  93
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  402190
Seq. No.
Seq. ID
                  LIB3431-051-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  534
E value
                  8.0e-55
Match length
                  102
% identity
                  96
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  402191
Seq. No.
                  LIB3431-051-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g606817
NCBI GI
BLAST score
                  489
                  2.0e-49
E value
Match length
                  93
                  99
% identity
                  (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                  >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
                  402192
Seq. No.
```

Seq. ID LIB3431-051-P1-K1-B7

Method BLASTN
NCBI GI g2624327
BLAST score 141
E value 2.0e-73
Match length 201

51639

% identity Oryza sativa mRNA for glycine rich RNA-binding protein 2 NCBI Description (OsGRP2) Seq. No. 402193 LIB3431-051-P1-K1-B8 Seq. ID BLASTX Method q2499932 NCBI GI BLAST score 479 E value 2.0e-48 105 Match length % identity 87 ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305 NCBI Description (U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]

Seq. No. 402194

Seq. ID LIB3431-051-P1-K1-C1

Method BLASTX
NCBI GI g2982453
BLAST score 474
E value 9.0e-48
Match length 109
% identity 83

NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein

[Arabidopsis thaliana]

Seq. No. 402195

Seq. ID LIB3431-051-P1-K1-C10

Method BLASTX
NCBI GI g124224
BLAST score 511
E value 9.0e-55
Match length 121
% identity 90

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi_100345_pir__S21060 translation initiation factor eIF-5A

- common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 402196

Seq. ID LIB3431-051-P1-K1-C11

Method BLASTX
NCBI GI g2492514
BLAST score 525
E value 1.0e-53
Match length 110
% identity 94

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR

>gi 1483215_emb_CAA68141_ (X99808) chloroplast FtsH

protease [Arabidopsis thaliana]

Seq. No. 402197

Seq. ID LIB3431-051-P1-K1-C12

Method BLASTX NCBI GI g115825 BLAST score 272



```
7.0e-24
E value
Match length
                  56
                  96
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 3C PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-3C) (LHCP) >gi 72734 pir CDTO3C chlorophyll
                  a/b-binding protein 3C precursor - tomato
                  >gi 224932 prf 1204205G protein 3C,chlorophyll binding
                  [Lycopersicon esculentum]
Seq. No.
                  402198
                  LIB3431-051-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                  513
E value
                  3.0e-52
Match length
                  115
% identity
                  85
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >qi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  402199
                  LIB3431-051-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  468
E value
                  4.0e-47
Match length
                  87
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                  402200
Seq. No.
                  LIB3431-051-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  g3075488
NCBI GI
BLAST score
                  718
E value
                  4.0e-76
Match length
                  143
                  97
% identity
NCBI Description
                 (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  402201
Seq. No.
                  LIB3431-051-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  464
E value
                  2.0e-46
Match length
                  112
% identity
                  79
```

NCBI Description

(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

402202 Seq. No.

Seq. ID LIB3431-051-P1-K1-D11

Method BLASTN

51641



```
NCBI GI
                   g304219
BLAST score
                   80
                   4.0e-37
E value
Match length
                   179
% identity
                   86
NCBI Description
                   Hordeum vulgare chloroplast photosystem I PSK-I subunit
                   mRNA, complete cds
Seq. No.
                   402203
Seq. ID
                   LIB3431-051-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   g5106774
BLAST score
                   63
E value
                   7.0e-27
Match length
                   188
% identity
                   84
                  Hordeum vulgare ribosomal protein S12 (rps12) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   402204
Seq. ID
                   LIB3431-051-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q4585882
BLAST score
                   532
E value
                   2.0e-54
Match length
                   119
% identity
NCBI Description
                  (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   402205
Seq. ID
                   LIB3431-051-P1-K1-D3
Method
                   BLASTN
NCBI GI
                   g3789951
BLAST score
                   111
E value
                   2.0e-55
Match length
                   252
% identity
                   92
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein presursor
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   402206
Seq. ID
                  LIB3431-051-P1-K1-D4
Method
                  BLASTN
NCBI GI
                   g20181
BLAST score
                   123
E value
                   1.0e-62
Match length
                  130
% identity
                   98
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
```

Seq. No. 402207

Seq. ID LIB3431-051-P1-K1-D5

Method BLASTX NCBI GI g132166



BLAST score 160 E value 6.0e-11 Match length 31 % identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,

CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)

>gi_81660_pir__S04048 ribulose-bisphosphate carboxylase

activase precursor - Arabidopsis thaliana

>gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 -

473) [Arabidopsis thaliana]

Seq. No. 402208

Seq. ID LIB3431-051-P1-K1-D6

Method BLASTX
NCBI GI g2072555
BLAST score 150
E value 3.0e-10
Match length 30
% identity 90

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402209

Seq. ID LIB3431-051-P1-K1-D7

Method BLASTN
NCBI GI g3377792
BLAST score 106
E value 2.0e-52
Match length 309
% identity 84

NCBI Description Oryza sativa ribulose-1,5-bisphosphate

carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 402210

Seq. ID LIB3431-051-P1-K1-D8

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 47
% identity 66

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 402211

Seq. ID LIB3431-051-P1-K1-D9

Method BLASTX
NCBI GI g131388
BLAST score 264
E value 5.0e-23
Match length 108
% identity 60

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)





33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 402212

Seq. ID LIB3431-051-P1-K1-E1

Method BLASTX
NCBI GI g320618
BLAST score 205
E value 2.0e-16
Match length 68
% identity 66

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 402213

Seq. ID LIB3431-051-P1-K1-E10

Method BLASTX
NCBI GI g3345477
BLAST score 576
E value 1.0e-59
Match length 111
% identity 98

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 402214

Seq. ID LIB3431-051-P1-K1-E11

Method BLASTX
NCBI GI g115772
BLAST score 523
E value 2.0e-53
Match length 99
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I

CAB-1) (LHCP) >gi 82460 pir S03705 chlorophyll a/b-binding

protein 1R precursor - rice >gi 20178 emb CAA32108

(X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)

[Oryza sativa]

Seq. No. 402215

Seq. ID LIB3431-051-P1-K1-E12

Method BLASTX
NCBI GI g671740
BLAST score 420
E value 4.0e-41
Match length 78
% identity 97

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 402216

Seq. ID LIB3431-051-P1-K1-E2

Method BLASTX
NCBI GI g2961176
BLAST score 356

```
6.0e-34
  E value
  Match length
                    104
                    73
  % identity
                    (AF050674) ribosomal protein L27 precursor [Oryza sativa]
  NCBI Description
                    402217
  Seq. No.
                    LIB3431-051-P1-K1-E5
  Seq. ID
                    BLASTX
  Method
NCBI GI
                    g4512707
  BLAST score
                    419
                    5.0e-41
  E value
                    151
  Match length
  % identity
                    54
                    (AC006569) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                    402218
                    LIB3431-051-P1-K1-E6
  Seq. ID
                    BLASTN
  Method
                    q505134
  NCBI GI
  BLAST score
                    63
```

5.0e-27 E value 163 Match length

85

% identity NCBI Description Rice mRNA for ferredoxin, complete cds

Seq. No. 402219 LIB3431-051-P1-K1-E8 Seq. ID Method BLASTX g320618 NCBI GI BLAST score 303 E value 4.0e-28

Match length 61 % identity 92

chlorophyll a/b-binding protein I precursor - rice NCBI Description

>gi 218172 dbj BAA00536 (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

402220 Seq. No.

LIB3431-051-P1-K1-E9 Seq. ID

BLASTX Method g1617197 NCBI GI BLAST score 292 2.0e-26 E value Match length 76 % identity 74

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

402221 Seq. No.

Seq. ID LIB3431-051-P1-K1-F1

Method BLASTX q115808 NCBI GI 472 BLAST score 1.0e-47 E value Match length 92 % identity 97



NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 91R PRECURSOR (LHCII TYPE I

CAB-91R) (LHCP) >gi 72732 pir CDPJ91 chlorophyll

a/b-binding protein 91R precursor - petunia

>gi 20487 emb CAA26209 (X02356) cab 91R precursor

polypeptide (aa -34 to 233) [Petunia sp.]

Seq. No. 402222

Seq. ID LIB3431-051-P1-K1-F10

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 1.0e-19
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402223

Seq. ID LIB3431-051-P1-K1-F11

Method BLASTX
NCBI GI g320618
BLAST score 542
E value 2.0e-56
Match length 133
% identity 86

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 402224

Seq. ID LIB3431-051-P1-K1-F3

Method BLASTN
NCBI GI g3789951
BLAST score 254
E value 1.0e-141
Match length 297
% identity 97

NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 402225

Seq. ID LIB3431-051-P1-K1-F4

Method BLASTX
NCBI GI g3913018
BLAST score 565
E value 2.0e-58
Match length 116
% identity 94

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi 218155 dbj BAA02730_ (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No. 402226

```
Seq. ID
                  LIB3431-051-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g4582787
BLAST score
                  373
                  5.0e-36
E value
Match length
                  96
                  79
% identity
NCBI Description (AJ012281) adenosine kinase [Zea mays]
Seq. No.
                  402227
                  LIB3431-051-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  304
E value
                  1.0e-27
Match length
                  93
% identity
                  69
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  402228
Seq. ID
                  LIB3431-051-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g2306981
BLAST score
                  170
E value
                  3.0e-12
Match length
                  78
% identity
                  45
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.
                  402229
                  LIB3431-051-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  348
E value
                  5.0e-33
Match length
                  69
% identity
                  97
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  402230
Seq. ID
                  LIB3431-051-P1-K1-G10
Method
                  BLASTX
                  q4091129
                  198
```

NCBI GI BLAST score E value 4.0e-15 Match length 154 % identity 31

NCBI Description (AF050165) protein phosphatase 2A regulatory subunit PR59;

PP2A regulatory subunit PR59 [Mus musculus]

402231 Seq. No.

Seq. ID LIB3431-051-P1-K1-G11

Method BLASTX NCBI GI g3126854 BLAST score 541



E value 2.0e-55 Match length 112 % identity 92

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402232

Seq. ID LIB3431-051-P1-K1-G12

Method BLASTX
NCBI GI g132105
BLAST score 268
E value 9.0e-43
Match length 109
% identity 82

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >qi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402233

Seq. ID LIB3431-051-P1-K1-G3

Method BLASTX
NCBI GI g5523862
BLAST score 367
E value 3.0e-35
Match length 99

% identity 69

NCBI Description (AF085169) LRk-type protein [Triticum aestivum]

Seq. No. 402234

Seq. ID LIB3431-051-P1-K1-G4

Method BLASTX
NCBI GI g3789954
BLAST score 458
E value 1.0e-45
Match length 109
% identity 83

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 402235

Seq. ID LIB3431-051-P1-K1-G5

Method BLASTX
NCBI GI g82080
BLAST score 230
E value 3.0e-19
Match length 76
% identity 63

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi_226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 402236



```
Seq. ID
                   LIB3431-051-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  35
E value
                  3.0e-10
Match length
                  35
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  402237
                  LIB3431-051-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133936
BLAST score
                  674
E value
                  5.0e-71
Match length
                  134
% identity
                  100
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70867 pir R3RZ3
NCBI Description
                  ribosomal protein S3 - rice chloroplast
                  >gi 12025 emb CAA33934 (X15901) ribosomal protein S3
                   [Oryza sativa] >gi 226646 prf 1603356BW ribosomal protein
                  S3 [Oryza sativa]
Seq. No.
                  402238
Seq. ID
                  LIB3431-051-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  241
E value
                  1.0e-20
Match length
                  63
% identity
                  76
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  402239
Seq. ID
                  LIB3431-051-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1519251
BLAST score
                  490
E value
                  9.0e-50
Match length
                  101
% identity
                  99
NCBI Description
                  (U65957) GF14-c protein [Oryza sativa]
Seq. No.
                  402240
Seq. ID
                  LIB3431-051-P1-K1-H3
                  BLASTX
                  g417260
                  248
                  3.0e-21
```

Method NCBI GI BLAST score E value Match length 105 % identity 50

NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >qi 422003 pir S33632 lir1 protein - rice >gi 20263 emb CAA48706 (X68807)



light-regulated gene [Oryza sativa]

Seq. No. 402241 Seq. ID LIB3431-051-P1-K1-H4 Method BLASTN NCBI GI q3345476 BLAST score 260 E value 1.0e-144 Match length 282 % identity 99

402242

NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Seq. ID LIB3431-051-P1-K1-H7
Method BLASTX
NCBI GI g4678947
BLAST score 353
E value 2.0e-33
Match length 101
% identity 65

Seq. No.

NCBI Description (AL049711) putative protein [Arabidopsis thaliana]

Seq. No. 402243
Seq. ID LIB3433

Seq. ID LIB3431-051-P1-N1-A1

Method BLASTX
NCBI GI g1170606
BLAST score 159
E value 1.0e-10
Match length 49
% identity 65

NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)

>gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3),
chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A,

Adenylate Kinase From Maize In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)

>gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize

In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No. 402244

Seq. ID LIB3431-051-P1-N1-A10

Method BLASTN
NCBI GI g2072554
BLAST score 164
E value 4.0e-87
Match length 296
% identity 89

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 402245

Seq. ID LIB3431-051-P1-N1-A12

Method BLASTX
NCBI GI g2864617
BLAST score 179
E value 4.0e-13
Match length 60

E value

Match length

```
% identity
                  (AL021811) H+-transporting ATP synthase chain9 - like
NCBI Description
                  protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1_
                  (AJ245574) ATP synthase beta chain precursor (subunit II)
                  [Arabidopsis thaliana]
                  402246
Seq. No.
                  LIB3431-051-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g693920
BLAST score
                  356
                  8.0e-34
E value
Match length
                  68
                  100
% identity
NCBI Description
                  (U21113) chlorophyll a/b binding protein [Solanum
                  tuberosum]
                  402247
Seq. No.
                  LIB3431-051-P1-N1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5456937
BLAST score
                  329
E value
                  0.0e + 00
Match length
                  329
                  100
% identity
NCBI Description Oryza sativa rps9 mRNA for ribosomal protein S9, complete
                  cds
                  402248
Seq. No.
                  LIB3431-051-P1-N1-A6
Seq. ID
Method
                  BLASTX
                  g4508079
NCBI GI
BLAST score
                  350
E value
                  4.0e-33
Match length
                  95
% identity
                  66
NCBI Description (AC005882) 66284 [Arabidopsis thaliana]
                  402249
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-A9
Method
                  BLASTN
NCBI GI
                  g18266
BLAST score
                  35
E value
                  3.0e-10
Match length
                  47
% identity
                  94
NCBI Description C.stellata mRNA for ribosomal protein L27
Seq. No.
                  402250
                  LIB3431-051-P1-N1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  537
```

% identity 99 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

5.0e-55

99



402251



(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. LIB3431-051-P1-N1-B10 Seq. ID Method BLASTX NCBI GI g3036951 BLAST score 323 E value 5.0e-30

Match length 63 % identity 98

(AB012639) light harvesting chlorophyll a/b-binding protein NCBI Description

[Nicotiana sylvestris]

Seq. No. 402252

Seq. ID LIB3431-051-P1-N1-B11

Method BLASTX NCBI GI g4538963 BLAST score 169 E value 5.0e-12 Match length 48 % identity 71

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No. 402253

Seq. ID LIB3431-051-P1-N1-B12

Method BLASTX NCBI GI g733456 BLAST score 335 E value 2.0e-31 Match length 73 % identity 92

NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 402254

Seq. ID LIB3431-051-P1-N1-B4

Method BLASTN NCBI GI g2072554 BLAST score 134 E value 4.0e-69 Match length 354 % identity 85

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

Seq. No. 402255

Seq. ID LIB3431-051-P1-N1-B5

Method BLASTX

```
NCBI GI
                   q3345477
BLAST score
                  172
E value
                  3.0e-12
Match length
                  32
% identity
                  97
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                  402256
Seq. No.
                  LIB3431-051-P1-N1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2624327
BLAST score
                  240
E value
                  1.0e-132
Match length
                  284
% identity
                  96
NCBI Description Oryza sativa mRNA for glycine rich RNA-binding protein 2
                  (OsGRP2)
                  402257
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-B8
Method
                  BLASTX
NCBI GI
                  q2440046
BLAST score
                  163
E value
                  3.0e-11
Match length
                  40
% identity
                  70
NCBI Description (AJ001294) major intrinsic protein PIPC [Craterostigma
                  plantagineum]
Seq. No.
                  402258
Seq. ID
                  LIB3431-051-P1-N1-C1
Method
                  BLASTN
NCBI GI
                  g20191
BLAST score
                  215
E value
                  1.0e-117
Match length
                  279
% identity
                  94
NCBI Description O.sativa mRNA for catalase
                  402259
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-C10
Method
                  BLASTX
NCBI GI
                  g5734790
                  373
BLAST score
E value
                  9.0e-36
Match length
                  80
% identity
                  90
NCBI Description
                  (AC007980) ATP-dependent metalloprotease [Arabidopsis
                  thaliana]
```

Seq. No. 402260
Seq. ID LIB343

Seq. ID LIB3431-051-P1-N1-C11 Method BLASTN

Method BLASTN
NCBI GI g20177
BLAST score 44
E value 7.0e-16
Match length 88



% identity NCBI Description Rice cab1R gene for light harvesting chlorophyll a/b-binding protein 402261 Seq. No. LIB3431-051-P1-N1-C12 Seq. ID Method BLASTX NCBI GI q3036951 BLAST score 323 E value 5.0e-30 Match length 63 % identity 98

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 402262

LIB3431-051-P1-N1-C6 Seq. ID

Method BLASTN NCBI GI q3377792 BLAST score 94 E value 1.0e-45 Match length 149 % identity 92

NCBI Description Oryza sativa ribulose-1,5-bisphosphate

carboxylase/oxygenase activase (rca) mRNA, complete cds

Seq. No. 402263

Seq. ID LIB3431-051-P1-N1-C7

Method BLASTN NCBI GI q3075487 BLAST score 244 E value 1.0e-135 Match length 260 % identity 98

NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69)

mRNA, complete cds

Seq. No. 402264

LIB3431-051-P1-N1-D1 Seq. ID

Method BLASTX g430947 NCBI GI BLAST score 198 E value 4.0e-15 Match length 63 57 % identity

NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 402265

Seq. ID LIB3431-051-P1-N1-D10

Method BLASTX g733454 NCBI GI BLAST score 363 E value 1.0e-34 Match length 77 % identity 92

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor



```
[Zea mays]
                  402266
Seq. No.
                  LIB3431-051-P1-N1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5106775
BLAST score
                  363
E value
                  1.0e-34
Match length
                  71
% identity
                  96
                  (AF067732) ribosomal protein S12 [Hordeum vulgare]
NCBI Description
                  402267
Seq. No.
                  LIB3431-051-P1-N1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5106775
BLAST score
                  259
E value
                  2.0e-22
Match length
                  52
% identity
                  92
NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]
Seq. No.
                  402268
                  LIB3431-051-P1-N1-D4
Seq. ID
```

Method BLASTX
NCBI GI g132166
BLAST score 160
E value 5.0e-11
Match length 31
% identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,

CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)

>gi 81660 pir S04048 ribulose-bisphosphate carboxylase

activase precursor - Arabidopsis thaliana

>gi_16471_emb_CAA32429 (X14212) rubisco activase (AA 1 -

473) [Arabidopsis thaliana]

Seq. No. 402269

Seq. ID LIB3431-051-P1-N1-D5

Method BLASTX
NCBI GI g167097
BLAST score 142
E value 7.0e-09
Match length 30
% identity 83

NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase

[Hordeum vulgare]

Seq. No. 402270

Seq. ID LIB3431-051-P1-N1-D6

Method BLASTN
NCBI GI g3377792
BLAST score 97
E value 4.0e-47
Match length 267
% identity 84

NCBI Description Oryza sativa ribulose-1,5-bisphosphate



carboxylase/oxygenase activase (rca) mRNA, complete cds

```
402271
Seq. No.
                  LIB3431-051-P1-N1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q416266
BLAST score
                  211
                  1.0e-115
E value
Match length
                  269
% identity
                  94
NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence
                  402272
Seq. No.
                  LIB3431-051-P1-N1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  158
                  8.0e-11
E value
Match length
                  45
% identity
                  69
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  402273
Seq. No.
                  LIB3431-051-P1-N1-E1
Seq. ID
Method
                  BLASTX
                  g2961176
NCBI GI
BLAST score
                  322
E value
                  7.0e-30
Match length
                  81
% identity
                  80
                  (AF050674) ribosomal protein L27 precursor [Oryza sativa]
NCBI Description
                  402274
Seq. No.
                  LIB3431-051-P1-N1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928140
BLAST score
                  166
                  1.0e-11
E value
Match length
                  34
% identity
                  88
                  (AJ131044) chlorophyll a/b binding protein [Cicer
NCBI Description
                  arietinum]
                  402275
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-E5
Method
                  BLASTX
NCBI GI
                  g1070408
BLAST score
                  166
E value
                  1.0e-11
Match length
                  47
% identity
                  74
NCBI Description ferredoxin [2Fe-2S] I - rice
                  402276
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-E7
Method
                  BLASTX
```

51656

NCBI GI g115786
BLAST score 202
E value 8.0e-16
Match length 52
% identity 75

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 82680 pir A29119 chlorophyll a/b-binding protein - maize >gi 22357 emb CAA68451 (Y00379) LHCP [Zea

mays]

Seq. No. 402277

Seq. ID LIB3431-051-P1-N1-E9

Method BLASTN
NCBI GI g5917782
BLAST score 139
E value 2.0e-72
Match length 228
% identity 89

NCBI Description Oryza sativa carbonic anhydrase 3 mRNA, complete cds

Seq. No. 402278

Seq. ID LIB3431-051-P1-N1-F10

Method BLASTX
NCBI GI g3036949
BLAST score 262
E value 7.0e-23
Match length 53
% identity 94

NCBI Description (AB012638) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No. 402279

Seq. ID LIB3431-051-P1-N1-F2

Method BLASTN
NCBI GI g3789951
BLAST score 136
E value 2.0e-70
Match length 311
% identity 99

NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 402280

Seq. ID LIB3431-051-P1-N1-F8

Method BLASTX
NCBI GI g551047
BLAST score 241
E value 2.0e-20
Match length 50
% identity 90

NCBI Description (X79277) type II LHCI [Lolium temulentum]

Seq. No. 402281

Seq. ID LIB3431-051-P1-N1-F9

Method BLASTN NCBI GI g2306980

```
BLAST score
                  9.0e-97
E value
Match length
                  240
% identity
                  94
```

Oryza sativa photosystem I antenna protein (Lhca) mRNA, NCBI Description

complete cds

402282 Seq. No.

LIB3431-051-P1-N1-G10 Seq. ID

Method BLASTX g3126854 NCBI GI BLAST score 270 1.0e-23 E value Match length 52 % identity 98

(AF061577) chlorophyll a/b binding protein [Oryza sativa] NCBI Description

Seq. No.

402283

LIB3431-051-P1-N1-G11 Seq. ID

BLASTX Method NCBI GI q671740 BLAST score 170 5.0e-12 E value Match length 41 % identity 83

(X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description

construct]

Seq. No. 402284

LIB3431-051-P1-N1-G12 Seq. ID

Method BLASTX q132105 NCBI GI BLAST score 167 E value 1.0e-11 Match length 33 % identity 97

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402285

LIB3431-051-P1-N1-G2 Seq. ID

Method BLASTX NCBI GI g5679314 BLAST score 317 E value 3.0e-29 100 Match length 66 % identity

NCBI Description (AF164021) receptor kinase [Oryza sativa]

Seq. No. 402286



```
Seq. ID
                  LIB3431-051-P1-N1-G3
Method
                  BLASTN
NCBI GI
                  q3789953
BLAST score
                  39
                  1.0e-12
E value
Match length
                  43
                  98
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein precursor
                  (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  402287
Seq. No.
                  LIB3431-051-P1-N1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1617197
BLAST score
                  225
                  2.0e-18
E value
Match length
                  47
                  87
% identity
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                  402288
                  LIB3431-051-P1-N1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20369
BLAST score
                  292
E value
                  1.0e-163
Match length
                  308
% identity
                  99
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
Seq. No.
                  402289
                  LIB3431-051-P1-N1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1519250
BLAST score
                  385
E value
                  0.0e + 00
Match length
                  421
% identity
                  98
NCBI Description Oryza sativa GF14-c protein mRNA, complete cds
Seq. No.
                  402290
                  LIB3431-051-P1-N1-H10
Seq. ID
Method
                  BLASTX
                  g133936
NCBI GI
BLAST score
                  610
E value
                  1.0e-63
Match length
                  125
% identity
                  97
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70867 pir R3RZ3
```

ribosomal protein S3 - rice chloroplast

>gi 12025 emb CAA33934 (X15901) ribosomal protein S3 [Oryza sativa] >gi 226646 prf 1603356BW ribosomal protein

S3 [Oryza sativa]

Match length

NCBI Description

% identity

45

69

```
Seq. No.
                   402291
Seq. ID
                  LIB3431-051-P1-N1-H11
Method
                  BLASTN
NCBI GI
                   g218171
BLAST score
                  128
E value
                   1.0e-65
Match length
                  184
% identity
                   92
NCBI Description
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
                  a/b binding protein of photosystem II (LHCPII), complete
Seq. No.
                  402292
Seq. ID
                  LIB3431-051-P1-N1-H12
Method
                  BLASTX
                  q2804572
NCBI GI
BLAST score
                  186
E value
                  7.0e-14
Match length
                  36
% identity
                  (AB006081) chlorophyll a/b-binding protein [Fagus crenata]
NCBI Description
Seq. No.
                  402293
Seq. ID
                  LIB3431-051-P1-N1-H2
Method
                  BLASTN
NCBI GI
                  g5091597
BLAST score
                  152
E value
                  8.0e-80
Match length
                  252
% identity
                  27
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
Seq. No.
                  402294
Seq. ID
                  LIB3431-051-P1-N1-H5
Method
                  BLASTX
NCBI GI
                  g1174778
BLAST score
                  215
E value
                  2.0e-17
Match length
                  41
% identity
                  98
NCBI Description
                  TRYPTOPHAN SYNTHASE BETA CHAIN 1 (ORANGE PERICARP 1)
                  >gi_320136 pir PQ0449 tryptophan synthase (EC 4.2.1.20)
                  beta-1 chain - maize (fragment) >gi_168572 (M76684)
                  tryptophan synthase beta-subunit [Zea mays]
Seq. No.
                  402295
Seq. ID
                  LIB3431-052-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g710626
BLAST score
                  188
E value
                  3.0e-14
```

51660

(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis



```
thaliana]
                  402296
Seq. No.
                  LIB3431-052-P1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  41
                  6.0e-14
E value
                  52
Match length
                  68
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  402297
Seq. No.
Seq. ID
                  LIB3431-052-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g131225
                  308
BLAST score
                  2.0e-28
E value
                  70
Match length
% identity
                  87
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  402298
Seq. No.
                  LIB3431-052-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g168643
BLAST score
                  260
                  7.0e-23
E value
                  83
Match length
% identity
                  65
NCBI Description (L02540) NADPH HC-toxin reductase [Zea mays]
                  402299
Seq. No.
                  LIB3431-052-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
E value
                  9.0e-11
                  36
Match length
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  402300
                  LIB3431-052-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3158476
                  230
BLAST score
```

E value 2.0e-19 Match length 62 % identity 71

(AF067185) aquaporin 2 [Samanea saman] NCBI Description

Seq. No. 402301

Seq. ID LIB3431-052-P1-K1-B4

51661

```
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  300
                  8.0e-28
E value
                  67
Match length
                  88
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  402302
Seq. No.
                  LIB3431-052-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4835588
BLAST score
                  400
                  6.0e-39
E value
Match length
                  77
                  100
% identity
                  (AB027054) nitrilase-like protein [Oryza sativa]
NCBI Description
                  402303
Seq. No.
                  LIB3431-052-P1-K1-B8
Seq. ID
Method
                  BLASTX
                  g4678311
NCBI GI
BLAST score
                  212
                  4.0e-17
E value
Match length
                  63
% identity
                  67
NCBI Description
                  (AL049655) aquaporin/MIP-like protein [Arabidopsis
                  thaliana]
                  402304
Seq. No.
                  LIB3431-052-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570494
BLAST score
                  109
E value
                  1.0e-54
Match length
                  140
% identity
                  96
                 Oryza sativa glyceralehyde-3-phosphate dehydrogenase
NCBI Description
                  subunit (GAPDH) mRNA, partial cds
                  402305
Seq. No.
                  LIB3431-052-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g416869
NCBI GI
BLAST score
                  301
                  2.0e-27
E value
```

Match length 93 % identity 61

NCBI Description CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE

SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_303902_dbj_BAA03542_ (D14722) cysteine synthase

[Spinacia oleracea]

402306 Seq. No.

```
LIB3431-052-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2501189
BLAST score
                  152
                  2.0e-10
E value
Match length
                  51
                  59
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
                  402307
Seq. No.
Seq. ID
                  LIB3431-052-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q6041792
BLAST score
                  311
E value
                  1.0e-28
Match length
                  127
% identity
                  52
NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]
                  402308
Seq. No.
                  LIB3431-052-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q11957
BLAST score
                  212
E value
                  1.0e-116
Match length
                  316
% identity
                  90
NCBI Description Rice complete chloroplast genome
                  402309
Seq. No.
                  LIB3431-052-P1-K1-D12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20262
BLAST score
                  254
                  1.0e-141
E value
Match length
                  254
% identity
                  100
NCBI Description O.sativa light-induced mRNA
                  402310
Seq. No.
                  LIB3431-052-P1-K1-D3
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2765817
BLAST score 163
E value 3.0e-11
Match length 63
% identity 54

NCBI Description (Z95352) AtMlo-hl [Arabidopsis thaliana]

>gi 3892049 gb AAC78258.1 AAC78258 (AC002330) AtMlo-h1

[Arabidopsis thaliana]

Seq. No. 402311

Seq. ID LIB3431-052-P1-K1-D4

Method BLASTX



```
q132105
NCBI GI
BLAST score
                  629
                  1.0e-65
E value
Match length
                  142
% identity
                  85
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir_ RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  402312
                  LIB3431-052-P1-K1-D6
Seq. ID
Method
                  BLASTN
                  g20340
NCBI GI
BLAST score
                  90
E value
                  2.0e-43
Match length
                  105
% identity
                  96
                  Rice rbcS gene for ribulose 1,5-bisphosphate
NCBI Description
                  carboxylase/oxygenase small subunit (EC 4.1.1.39)
Seq. No.
                  402313
                  LIB3431-052-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  q4566614
NCBI GI
BLAST score
                  375
                  3.0e-36
E value
Match length
                  81
% identity
                  85
                  (AF112887) actin depolymerizing factor [Populus alba x
NCBI Description
                  Populus tremula]
                  402314
Seq. No.
                  LIB3431-052-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244781
                  170
BLAST score
                  5.0e-12
E value
                  97
Match length
                  39
% identity
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
                  402315
Seq. No.
                  LIB3431-052-P1-K1-E11
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g5230785
BLAST score 185
E value 7.0e-14
Match length 51
% identity 67

NCBI Description (AF107024) histone H1 WH1B.1 [Triticum aestivum]



```
Seq. No.
                  402316
                  LIB3431-052-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2947060
BLAST score
                  469
                  4.0e-47
E value
                  118
Match length
% identity
                  75
                  (AC002521) putative membrane protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402317
                  LIB3431-052-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  405
E value
                  1.0e-39
Match length
                  77
% identity
                  96
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  402318
                  LIB3431-052-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  487
E value
                  2.0e-53
Match length
                  107
% identity
                  94
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  402319
                  LIB3431-052-P1-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI '
                  g1519252
BLAST score
                  54
                  6.0e-22
E value
Match length
                  102
% identity
                  88
NCBI Description Oryza sativa GF14-d protein mRNA, complete cds
                  402320
Seq. No.
                  LIB3431-052-P1-K1-E7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132105
BLAST score
                  293
E value
                  1.0e-26
```

Match length 76 79 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_





(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

 Seq. No.
 402321

 Seq. ID
 LIB3431-052-P1-K1-E9

 Method
 BLASTX

 NCBI GI
 g1173347

 BLAST score
 401

 E value
 3.0e-39

E value 3.0e
Match length 80
% identity 94

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >qi 100803 pir S23452 sedoheptulose-bisphosphatase (EC

3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_(X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 402322

Seq. ID LIB3431-052-P1-K1-F1

Method BLASTX
NCBI GI g733454
BLAST score 382
E value 6.0e-37
Match length 95
% identity 79

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 402323

Seq. ID LIB3431-052-P1-K1-F10

Method BLASTN
NCBI GI g3789951
BLAST score 70
E value 1.0e-31
Match length 81
% identity 98

NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 402324

Seq. ID LIB3431-052-P1-K1-F11

Method BLASTX
NCBI GI g21839
BLAST score 368
E value 2.0e-35
Match length 84
% identity 88

NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402325

Seq. ID LIB3431-052-P1-K1-F12

Method BLASTX

Match length

% identity

71



```
NCBI GI
                  g3789952
BLAST score
                  341
                  5.0e-32
E value
Match length
                  66
% identity
                  98
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
                  402326
Seq. No.
                  LIB3431-052-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  303
                  9.0e-28
E value
Match length
                  82
% identity
                  72
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  402327
                  LIB3431-052-P1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4959460
BLAST score
                  33
E value
                  3.0e-09
Match length
                  33
% identity
                  100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
                  402328
                  LIB3431-052-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3360289
BLAST score
                  230
                  4.0e-19
E value
Match length
                  59
                  76
% identity
NCBI Description
                  (AF023164) leucine-rich repeat transmembrane protein kinase
                  1 [Zea mays]
Seq. No.
                  402329
                  LIB3431-052-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5302772
BLAST score
                  148
                  1.0e-09
E value
Match length
                  83
% identity
                  40
NCBI Description
                  (Z97336) SNF1 like protein kinase [Arabidopsis thaliana]
Seq. No.
                  402330
Seq. ID
                  LIB3431-052-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2129622
BLAST score
                  296
E value
                  5.0e-27
```

```
NCBI Description
                  immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406
                  (U52046) immunophilin [Arabidopsis thaliana]
Seq. No.
                  402331
                  LIB3431-052-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  203
                  2.0e-16
E value
Match length
                  47
% identity
                  85
NCBI Description
                 (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  402332
Seq. ID
                  LIB3431-052-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  590
E value
                  3.0e-61
Match length
                  111
                  99
% identity
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  402333
Seq. ID
                  LIB3431-052-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  164
E value
                  1.0e-11
Match length
                  61
% identity
                  64
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  402334
Seq. ID
                  LIB3431-052-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  261
E value
                  6.0e-23
Match length
                  78
% identity
                  72
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  402335
Seq. ID
                  LIB3431-052-P1-K1-G4
Method
                  BLASTN
```

NCBI GI g2062705 BLAST score 34 E value 4.0e-10 Match length 34 % identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds



```
402336
Seq. No.
Seq. ID
                  LIB3431-052-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  q3885893
BLAST score
                  99
                  2.0e-48
E value
Match length
                  127
% identity
                  94
NCBI Description
                 Oryza sativa photosystem-1 H subunit GOS5 (PSI-H) mRNA,
                  complete cds
                  402337
Seq. No.
Seq. ID
                  LIB3431-052-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q125580
BLAST score
                  173
E value
                  1.0e-12
Match length
                  37
% identity
                  95
NCBI Description
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
                  (PRK) >gi 100839 pir S15743 phosphoribulokinase (EC
                  2.7.1.19) - wheat >gi 5924030 emb CAB56544.1 (X51608)
                  phosphoribulokinase [Triticum aestivum]
Seq. No.
                  402338
Seq. ID
                  LIB3431-052-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  279
E value
                  7.0e-25
Match length
                  77
% identity
                  77
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  402339
Seq. ID
                  LIB3431-052-P1-K1-H1
Method
                  BLASTX
                  g320618
NCBI GI
BLAST score
                  259
                  2.0e-22
                  67
                  76
% identity
                  chlorophyll a/b-binding protein I precursor - rice
```

E value Match length

NCBI Description

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 402340

Seq. ID LIB3431-052-P1-K1-H10

Method BLASTX NCBI GI g82080



BLAST score 161 E value 3.0e-11 Match length 83 % identity 47

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 402341

Seq. ID LIB3431-052-P1-K1-H11

Method BLASTX
NCBI GI g2494261
BLAST score 299
E value 3.0e-27
Match length 98
% identity 62

NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)

>gi_99903_pir__S21567 translation elongation factor Tu
precursor - soybean chloroplast >gi_18776_emb_CAA46864_
(X66062) EF-Tu [Glycine max] >gi_448921 prf 1918220A

elongation factor Tu [Glycine max]

Seq. No. 402342

Seq. ID LIB3431-052-P1-K1-H2

Method BLASTX
NCBI GI g115787
BLAST score 418
E value 4.0e-41
Match length 112
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 402343

Seq. ID LIB3431-052-P1-K1-H6

Method BLASTX
NCBI GI g1652848
BLAST score 143
E value 2.0e-09
Match length 36
% identity 64

NCBI Description (D90909) DNA photolyase [Synechocystis sp.]

Seq. No. 402344

Seq. ID LIB3431-052-P1-K1-H7

Method BLASTX
NCBI GI g131176
BLAST score 293
E value 1.0e-26
Match length 55
% identity 100

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR

(PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)

>gi_72683_pir__F1BH4 photosystem I chain IV precursor -





barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No. 402345

Seq. ID LIB3431-052-P1-K1-H9

Method BLASTX
NCBI GI g3183079
BLAST score 413
E value 4.0e-44
Match length 107
% identity 84

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi 1375075 dbj BAA12870.1 (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

Seq. No. 402346

Seq. ID LIB3431-052-P1-N1-A7

Method BLASTX
NCBI GI g2289010
BLAST score 389
E value 2.0e-37
Match length 86
% identity 86

NCBI Description (AC002335) FKBP type peptidyl-prolyl cis-trans isomerase

isolog [Arabidopsis thaliana]

Seq. No. 402347

Seq. ID LIB3431-052-P1-N1-B1

Method BLASTN
NCBI GI g6069643
BLAST score 120
E value 6.0e-61
Match length 207
% identity 10

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0514G12

Seq. No. 402348

Seq. ID LIB3431-052-P1-N1-B4

Method BLASTX
NCBI GI g131225
BLAST score 514
E value 4.0e-52
Match length 127
% identity 80

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_100605_pir A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 402349

Seq. ID LIB3431-052-P1-N1-B5

Method BLASTX
NCBI GI g126896
BLAST score 392
E value 6.0e-38



Match length 91 % identity 87

NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR

>gi 319831 pir DEPUMW malate dehydrogenase (EC 1.1.1.37)

precursor, mitochondrial - watermelon

>gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27

to 320) [Citrullus lanatus]

Seq. No. 402350

Seq. ID LIB3431-052-P1-N1-B6

Method BLASTX
NCBI GI g115813
BLAST score 163
E value 2.0e-11
Match length 41
% identity 76

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi 19182 emb CAA33330 (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402351

Seq. ID LIB3431-052-P1-N1-B7

Method BLASTN
NCBI GI g4835587
BLAST score 93
E value 1.0e-44
Match length 93
% identity 100

NCBI Description Oryza sativa ONIT4 mRNA for nitrilase-like protein,

complete cds

Seq. No. 402352

 Seq. ID
 LIB3431-052-P1-N1-B8

 Method
 BLASTN

 NCBI GI
 g3885891

 BLAST score
 58

 E value
 7.0e-24

Match length 110 % identity 88

NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)

mRNA, complete cds

Seq. No. 402353

Seq. ID LIB3431-052-P1-N1-B9

Method BLASTX
NCBI GI g120661
BLAST score 264
E value 3.0e-23
Match length 56
% identity 89

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST

PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum]

Seq. No. 402354

Seq. ID LIB3431-052-P1-N1-C11

Method BLASTX

```
q6056418
NCBI GI
BLAST score
                   287
E value
                   1.0e-25
Match length
                   94
% identity
                   (AC009525) Similar to beta-glucosidases [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   402355
Seq. ID
                   LIB3431-052-P1-N1-C12
Method
                   BLASTX
NCBI GI
                   q3328221
                   443
```

BLAST score 7.0e-44 E value 96 Match length % identity 89

NCBI Description (AF076920) thioredoxin peroxidase [Secale cereale]

402356 Seq. No. Seq. ID LIB3431-052-P1-N1-C2 Method BLASTX NCBI GI q2982456 312

BLAST score E value 2.0e-28 Match length 90 % identity

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 402357 Seq. ID LIB3431-052-P1-N1-C3 Method BLASTX NCBI GI g2754849

BLAST score 280 E value 9.0e-25 Match length 65 % identity 85

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No. 402358

LIB3431-052-P1-N1-C4 Seq. ID

Method BLASTX NCBI GI q399333 BLAST score 205 E value 5.0e-16 Match length 44 % identity 89

CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE NCBI Description

SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8) precursor - pepper >gi_17944_emb_CAA46086_ (X64874)

O-acetylserine (thiol)-lyase [Capsicum annuum]

Séq. No. 402359

LIB3431-052-P1-N1-C5 Seq. ID

Method BLASTX NCBI GI g4566614



```
BLAST score
                  2.0e-13
E value
Match length
                  42
% identity
                  81
NCBI Description
                  (AF112887) actin depolymerizing factor [Populus alba x
                  Populus tremula]
                  402360
Seq. No.
                  LIB3431-052-P1-N1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2501190
BLAST score
                  282
E value
                  6.0e-25
Match length
                  76
% identity
                  78
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                  >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  402361
Seq. ID
                  LIB3431-052-P1-N1-C8
Method
                  BLASTX
NCBI GI
                  q5921663
BLAST score
                  206
E value
                  3.0e-16
Match length
                  41
% identity
                  93
                  (AF162279) 10-formyltetrahydrofolate synthetase
NCBI Description
                  [Arabidopsis thaliana]
                  402362
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-C9
Method
                  BLASTN
NCBI GI
                  g2739216
BLAST score
                  76
E value
                  1.0e-34
Match length
                  84
% identity
                  98
NCBI Description Hordeum vulgare L41 ribosomal protein
Seq. No.
                  402363
Seq. ID
                  LIB3431-052-P1-N1-D4
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  213
                  6.0e-17
E value
Match length
                  68
% identity
                  68
```

(L22155) ribulose 1,5-bisphosphate carboxylase [Oryza NCBI Description

sativa]

Seq. No. 402364

LIB3431-052-P1-N1-D5 Seq. ID

BLASTX Method NCBI GI g517500 BLAST score 217

```
E value
                  8.0e-18
Match length
                  55
% identity
NCBI Description
                  (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  402365
Seq. No.
                  LIB3431-052-P1-N1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  426
                  7.0e-42
E value
                  77
Match length
                  100
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  402366
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-D7
Method
                  BLASTX
NCBI GI
                  q4335763
BLAST score
                  167
                  1.0e-11
E value
                  75
Match length
% identity
                  45
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                  402367
Seq. No.
```

Seq. ID LIB3431-052-P1-N1-D9
Method BLASTX
NCBI GI g4566614
BLAST score 306
E value 9.0e-28
Match length 69
% identity 84

NCBI Description (AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

 Seq. No.
 402368

 Seq. ID
 LIB3431-052-P1-N1-E1

 Method
 BLASTN

 NCBI GI
 g218207

 BLAST score
 295

 E value
 1.0e-165

Match length 295 % identity 100 NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

posss1139

Seq. No. 402369

Seq. ID LIB3431-052-P1-N1-E12

Method BLASTX
NCBI GI g3510256
BLAST score 298
E value 6.0e-27

```
Match length
                  52
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402370
                  LIB3431-052-P1-N1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2947060
BLAST score
                  165
E value
                  3.0e-11
Match length
                  40
                  78
% identity
                  (AC002521) putative membrane protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   402371
                  LIB3431-052-P1-N1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g347451
BLAST score
                   186
E value
                   9.0e-14
Match length
                   37
% identity
                   95
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
Seq. No.
                   402372
                   LIB3431-052-P1-N1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   396
                   2.0e-38
E value
Match length
                   77
                   97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   402373
                   LIB3431-052-P1-N1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1519253
BLAST score
                   277
                   2.0e-24
E value
                   58
Match length
% identity
                   93
                  (U65958) GF14-d protein [Oryza sativa]
NCBI Description
                   402374
Seq. No.
                   LIB3431-052-P1-N1-E6
Seq. ID
Method
                   BLASTX
                   g3126854
NCBI GI
                   494
BLAST score
                   8.0e-50
E value
Match length
                   110
% identity
```

```
(AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  402375
Seq. ID
                  LIB3431-052-P1-N1-E7
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  346
                  9.0e-33
E value
Match length
                  76
                  84
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  402376
Seq. No.
                  LIB3431-052-P1-N1-E9
Seq. ID
Method
                  BLASTX
                  q1173347
NCBI GI
BLAST score
                  331
                  1.0e-30
E value
                  82
Match length
                  83
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                   402377
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-F10
Method
                  BLASTN
NCBI GI
                   q3789951
BLAST score
                  77
                   3.0e-35
E value
                   245
Match length
                   82
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   402378
                   LIB3431-052-P1-N1-F11
Seq. ID
Method
                   BLASTX
                   q21839
NCBI GI
                   343
BLAST score
                   4.0e-32
E value
Match length
                   72
% identity
                   94
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
```

Seq. No. 402379

Seq. ID LIB3431-052-P1-N1-F12

Method BLASTN
NCBI GI g21838
BLAST score 36
E value 1.0e-10
Match length 139

```
% identity 88
NCBI Description T.aestivum PRK gene for ribulose-5-phosphate kinase
Seq. No. 402380
Seq. ID LIB3431-052-P1-N1-F8
```

Method BLASTX
NCBI GI g2129623
BLAST score 199
E value 1.0e-31
Match length 83

% identity 84
NCBI Description immunophilin FKBP15-2 - Arabidopsis thaliana >gi_1272408
(U52047) immunophilin [Arabidopsis thaliana]

Seq. No. 402381

Seq. ID LIB3431-052-P1-N1-F9

Method BLASTX
NCBI GI g115802
BLAST score 251
E value 2.0e-21
Match length 47
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I

CAB-36) (LHCP) >gi_100311_pir__\$21827 chlorophyll

a/b-binding protein (cab-36) - common tobacco

>gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding

protein [Nicotiana tabacum]

Seq. No. 402382

Seq. ID LIB3431-052-P1-N1-G1

Method BLASTX
NCBI GI g3126854
BLAST score 620
E value 1.0e-64
Match length 121
% identity 97

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402383

Seq. ID LIB3431-052-P1-N1-G10

Method BLASTX
NCBI GI g3914466
BLAST score 242
E value 1.0e-20
Match length 45
% identity 93

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN

subunit precursor [Zea mays]

Seq. No. 402384

Seq. ID LIB3431-052-P1-N1-G11

Method BLASTX
NCBI GI g82080
BLAST score 297
E value 9.0e-27
Match length 75

```
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  402385
                  LIB3431-052-P1-N1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501190
BLAST score
                  470
E value
                  5.0e-47
Match length
                  117
                  83
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                  >gi 2130147 pir S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >qi 596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
                  402386
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-G8
                  BLASTN
Method
NCBI GI
                  q21838
BLAST score
                  70
                  5.0e-31
E value
                  207
Match length
                  85
% identity
NCBI Description T.aestivum PRK gene for ribulose-5-phosphate kinase
                  402387
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-G9
Method
                  BLASTX
NCBI GI
                  g693920
BLAST score
                  403
                  4.0e-39
E value
Match length
                  77
% identity
                  99
                  (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                  tuberosum]
                   402388
Seq. No.
                  LIB3431-052-P1-N1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q115787
BLAST score
                   495
                   6.0e-50
E value
                   98
Match length
                   97
% identity
```

CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

402389 Seq. No.

Seq. ID LIB3431-052-P1-N1-H10

BLASTX Method NCBI GI g82080

```
BLAST score
                  4.0e-26
E value
Match length
                  71
% identity
                  82
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >qi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  402390
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-H11
Method
                  BLASTX
NCBI GI
                  g119194
BLAST score
                  270
                  9.0e-24
E value
                  62
Match length
% identity
                  85
                  ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
NCBI Description
                  >gi_81607_pir__S09152 translation elongation factor Tu
                  precursor, chloroplast - Arabidopsis thaliana
                  >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu
                  precursor [Arabidopsis thaliana]
                  >gi_5738381_emb_CAB45802.2_ (AL080253) translation
                  elongation factor EF-Tu precursor, chloroplast [Arabidopsis
                  thaliana] >gi_226817_prf__1607332A elongation factor Tu
                   [Arabidopsis thaliana]
Seq. No.
                  402391
                  LIB3431-052-P1-N1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g226263
BLAST score
                  158
E value
                  1.0e-10
Match length
                  29
                   97
% identity
                  chlorophyll a/b binding protein [Glycine max]
NCBI Description
Seq. No.
                   402392
                  LIB3431-052-P1-N1-H3
Seq. ID
Method
                   BLASTX
                   q3789954
NCBI GI
BLAST score
                   237
E value
                   7.0e-20
Match length
                   44
                   95
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   402393
Seq. No.
                   LIB3431-052-P1-N1-H5
Seq. ID
                   BLASTN
Method
```

g14264 NCBI GI 60 BLAST score 5.0e-25 E value 100 Match length 90 % identity

T.aestivum gene for sedoheptulose-1,7-bisphoshatase NCBI Description

NCBI GI

E value Match length

BLAST score

% identity

g131225

322 3.0e-30

71

87

```
402394
 Seq. No.
                    LIB3431-052-P1-N1-H7
 Seq. ID
                    BLASTX
Method
 NCBI GI
                     g131176
                     251
 BLAST score
                     1.0e-21
 E value
                     48
 Match length
                     98
 % identity
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
 NCBI Description
                     (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                     >gi_72683_pir__F1BH4 photosystem I chain IV precursor -
                     barley >gi 19087_emb CAA68782 (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi 226163_prf 1413233A
                     10.8kD photosystem I protein [Hordeum vulgare var.
                     distichum]
                     402395
  Seq. No.
                     LIB3431-052-P1-N1-H9
  Seq. ID
 Method
                     BLASTX
                     g3183079
 NCBI GI
                     209
 BLAST score
                     1.0e-16
 E value
 Match length
                     54
  % identity
                     76
                    MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
  NCBI Description
                     >qi 1375075 dbj BAA12870.1 (D85763) glyoxysomal malate
                     dehydrogenase [Oryza sativa]
  Seq. No.
                     402396
                     LIB3431-053-P1-K1-A1
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     q871931
  BLAST score
                     387
                     2.0e-37
  E value
                     78
  Match length
                     99
  % identity
  NCBI Description (D30763) ferredoxin [Oryza sativa]
  Seq. No.
                     402397
                     LIB3431-053-P1-K1-A10
  Seq. ID
                     BLASTX
  Method
                     g729479
  NCBI GI
  BLAST score
                     667
                     1.0e-72
. E value
 Match length
                     147
                     82
  % identity
  NCBI Description FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi 551131
                     (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
                     402398
  Seq. No.
                     LIB3431-053-P1-K1-A11
  Seq. ID
  Method
                     BLASTX
```



NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

402399 Seq. No.

LIB3431-053-P1-K1-A12 Seq. ID

BLASTX Method - g4585882 NCBI GI BLAST score 638 8.0e-67 E value 143 Match length 79 % identity

(AC005850) PSI type III chlorophyll a/b-binding protein NCBI Description

[Arabidopsis thaliana]

402400 Seq. No.

LIB3431-053-P1-K1-A2 Seq. ID

BLASTX Method q2894534 NCBI GI BLAST score 392 4.0e-38 E value 103 Match length 77 % identity

(AJ224327) aquaporin [Oryza sativa] NCBI Description

402401 Seq. No.

LIB3431-053-P1-K1-A3 Seq. ID

Method BLASTX q4038699 NCBI GI 198 BLAST score 3.0e-23 E value 65 Match length 82 % identity

(AB020947) ribulose-1,5-bisphosphate carboxylase/oxygenase NCBI Description

small subunit [Aegilops speltoides]

402402 Seq. No.

LIB3431-053-P1-K1-A6 Seq. ID

BLASTX Method g417154 NCBI GI 429 BLAST score 3.0e-42E value 135 Match length 63 % identity

HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock NCBI Description

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

402403 Seq. No.

LIB3431-053-P1-K1-A7 Seq. ID

BLASTX Method NCBI GI q2407281 BLAST score 399 5.0e-39 E value Match length 81

BLAST score

634

```
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  402404
Seq. No.
Seq. ID
                  LIB3431-053-P1-K1-A8
                  BLASTX
Method
                  q6006848
NCBI GI
                  570
BLAST score
                  7.0e-59
E value
                  132
Match length
                  79
% identity
                  (AC009540) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  402405
Seq. No.
                  LIB3431-053-P1-K1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115787
                  370
BLAST score
                  1.0e-35
E value
                  94
Match length
                  82
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   402406
Seq. No.
Seq. ID
                   LIB3431-053-P1-K1-B11
                   BLASTX
Method
NCBI GI
                   g2407281
                   638
BLAST score
                   8.0e-67
E value
                   124
Match length
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
                   402407
Seq. No.
                   LIB3431-053-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q82080
BLAST score
                   346
                   1.0e-32
E value
Match length
                   98
                   69
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   402408
                   LIB3431-053-P1-K1-B2
Seq. ID
                   BLASTX
Method
                   g2499819
NCBI GI
```

NCBI Description

```
3.0e-66
E value
Match length
                   121
% identity
                   99
                   ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
NCBI Description
                   >gi_2130068_pir__S66516 aspartic proteinase 1 precursor -
                   rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
                   protease [Oryza sativa]
                   402409
Seq. No.
                   LIB3431-053-P1-K1-B3
Seq. ID
Method
                   BLASTX
                   g4982478
NCBI GI
BLAST score
                   518
E value
                   9.0e-53
Match length
                   136
% identity
                   71
                   (AF069441) putative leucyl tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   402410
                   LIB3431-053-P1-K1-B4
Seq. ID
Method
                   BLASTX
                   g320618
NCBI GI
BLAST score
                   265
E value
                   3.0e-23
Match length
                   65
% identity
                   74
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
                   402411
Seq. No.
                   LIB3431-053-P1-K1-B5
Seq. ID
                   BLASTX
Method
                   g1661160
NCBI GI
BLAST score
                   246
                   2.0e-27
E value
Match length
                   91
                   78
% identity
                   (U74295) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                    402412
Seq. No.
                   LIB3431-053-P1-K1-B8
Seq. ID
Method
                    BLASTX
                    g400983
NCBI GI
                    272
BLAST score
                    7.0e-24
E value
                    61
Match length
% identity
                    82
```

L11 [Spinacia oleracea]

50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)

>gi_279648_pir__R5SP11 ribosomal protein L11 precursor spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein

```
Seq. No.
                  LIB3431-053-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  q1835731
NCBI GI
BLAST score
                  319
E value
                  1.0e-29
                  66
Match length
                  95
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   402414
Seq. No.
                  LIB3431-053-P1-K1-C1
Seq. ID
                  BLASTX
Method
                   q5734636
NCBI GI
                   297
BLAST score
                   8.0e-27
E value
Match length
                   106
                   50
% identity
                   (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
                   402415
Seq. No.
                   LIB3431-053-P1-K1-C11
Seq. ID
                   BLASTX
Method
                   g2130042
NCBI GI
                   688
BLAST score
                   1.0e-72
E value
                   149
Match length
% identity
                   Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916)
NCBI Description
                   protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                   vulgare]
                   402416
Seq. No.
                   LIB3431-053-P1-K1-C12
Seq. ID
                   BLASTX
Method
                   g115772
NCBI GI
BLAST score
                   675
                   4.0e-71
E value
Match length
                   136
                   94
 % identity
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
                   protein 1R precursor - rice >gi_20178_emb_CAA32108
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
                   402417
 Seq. No.
                   LIB3431-053-P1-K1-C2
 Seq. ID
                   BLASTX
 Method
                   g2072555
 NCBI GI
                   194
 BLAST score
                   6.0e-15
 E value
                   52
 Match length
                   73
 % identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
 NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
```



protein [Oryza sativa]

```
      Seq. No.
      402418

      Seq. ID
      LIB3431-053-P1-K1-C3

      Method
      BLASTX

      NCBI GI
      g132105

      BLAST score
      638

      E value
      1.0e-66

      Match length
      119
```

% identity 98 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

 Seq. No.
 402419

 Seq. ID
 LIB3431-053-P1-K1-C4

 Method
 BLASTN

 NCBI GI
 g6015437

 BLAST score
 36

E value 2.0e-10
Match length 36
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402420

Seq. ID LIB3431-053-P1-K1-C5

Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 2.0e-10
Match length 36
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402421

Seq. ID LIB3431-053-P1-K1-C6

Method BLASTX
NCBI GI g82734
BLAST score 812
E value 4.0e-87
Match length 164
% identity 31

NCBI Description ubiquitin precursor - maize (fragment)

>gi 226763 prf 1604470A poly-ubiquitin [Zea mays]

Seq. No. 402422

Seq. ID LIB3431-053-P1-K1-C8

Method BLASTX
NCBI GI g320618
BLAST score 455
E value 2.0e-45



Match length 102 % identity 84

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 402423

Seq. ID LIB3431-053-P1-K1-D10

Method BLASTX
NCBI GI g548605
BLAST score 488
E value 3.0e-49
Match length 113
% identity 87

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir_ A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 402424

Seq. ID LIB3431-053-P1-K1-D12

Method BLASTX
NCBI GI g3288821
BLAST score 422
E value 2.0e-41
Match length 106
% identity 75

NCBI Description (AF063901) alanine:glyoxylate aminotransferase;

transaminase [Arabidopsis thaliana]

>gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)

alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No. 402425

Seq. ID LIB3431-053-P1-K1-D2

Method BLASTN
NCBI GI g5852170
BLAST score 86
E value 2.0e-40
Match length 130
% identity 46

NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC

clone:t17804

Seq. No. 402426

Seq. ID LIB3431-053-P1-K1-D3

Method BLASTX
NCBI GI g4972052
BLAST score 372
E value 1.0e-35
Match length 134
% identity 40

NCBI Description (AL078470) putative protein [Arabidopsis thaliana]

Seq. No. 402427

```
LIB3431-053-P1-K1-D4
Seq. ID
                  BLASTN
Method
                  g19094
NCBI GI
                  33
BLAST score
                  3.0e-09
E value
                  57
Match length
% identity
                  89
NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N
                  402428
Seq. No.
Seq. ID
                  LIB3431-053-P1-K1-D5
Method
                  BLASTN
NCBI GI
                  g19094
                  44
BLAST score
                  7.0e-16
E value
                   64
Match length
% identity
                   92
NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N
                   402429
Seq. No.
Seq. ID
                  LIB3431-053-P1-K1-D6
                  BLASTX
Method
NCBI GI
                   q115787
                   616
BLAST score
                   3.0e-64
E value
                   140
Match length
                   88
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi_20182 emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   402430
Seq. No.
                   LIB3431-053-P1-K1-D8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3789952
BLAST score
                   364
                   6.0e-35
E value
                   77
Match length
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   402431
Seq. No.
                   LIB3431-053-P1-K1-D9
Seq. ID
                   BLASTX
Method
                   q5042413
NCBI GI
BLAST score
                   278
                   1.0e-24
E value
                   90
Match length
% identity
NCBI Description (AC006193) Hypothetical Protein [Arabidopsis thaliana]
                   402432
Seq. No.
                   LIB3431-053-P1-K1-E1
 Seq. ID
```

51688

BLASTN

Method

```
g3885891
NCBI GI
BLAST score
                  171
                  2.0e-91
E value
                  209
Match length
% identity
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                  mRNA, complete cds
                  402433
Seq. No.
Seq. ID
                  LIB3431-053-P1-K1-E11
Method
                  BLASTX
                  g4544390
NCBI GI
BLAST score
                  364
                  1.0e-34
E value
                  141
Match length
% identity
NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]
                  402434
Seq. No.
Seq. ID
                  LIB3431-053-P1-K1-E12
                  BLASTX
Method
NCBI GI
                  q2072555
                  237
BLAST score
                  1.0e-19
E value
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                   402435
Seq. ID
                   LIB3431-053-P1-K1-E2
Method
                  BLASTN
NCBI GI
                   q218209
BLAST score
                   66
                   2.0e-28
E value
Match length.
                   94
                   93
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
Seq. No.
                   402436
                   LIB3431-053-P1-K1-E3
Seq. ID
                   BLASTX
Method
                   g2072727
NCBI GI
                   736
BLAST score
                   3.0e-78
E value
                   143
Match length
                   99
% identity
NCBI Description (Y12595) Fd-GOGAT protein [Oryza sativa]
```

Seq. No. 402437

Seq. ID LIB3431-053-P1-K1-E4

Method BLASTN
NCBI GI g3821780
BLAST score 35

```
E value
Match length
                  35
                  100
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  402438
                  LIB3431-053-P1-K1-E5
Seq. ID
                  BLASTN
Method
```

g3821780 NCBI GI 35 BLAST score E value 8.0e-11 35 Match length % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

402439

Seq. No. Seq. ID LIB3431-053-P1-K1-E6 Method BLASTX q131388 NCBI GI 403 BLAST score 3.0e-39 E value Match length 131

67 % identity OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831_pir__S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 402440

LIB3431-053-P1-K1-E7 Seq. ID Method BLASTX

NCBI GI g4417296 BLAST score 368 E value 3.0e-35 Match length 102 % identity 68

(AC007019) unknown protein [Arabidopsis thaliana] NCBI Description

>gi_4587592_gb_AAD25820.1_AC007232_10 (AC007232) unknown

protein [Arabidopsis thaliana]

402441 Seq. No.

LIB3431-053-P1-K1-E9 Seq. ID

BLASTX Method g3885894 NCBI GI BLAST score 463 2.0e-46 E value 104 Match length % identity 88

(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa] NCBI Description

402442 Seq. No.

LIB3431-053-P1-K1-F1 Seq. ID

BLASTX Method NCBI GI g2570511

```
BLAST score 628
E value 1.0e-65
Match length 121
% identity 98
NCBI Description (AF022738)
```

I Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

 Seq. ID
 LIB3431-053-P1-K1-F10

 Method
 BLASTX

 NCBI GI
 g2501189

 BLAST score
 459

 E value
 8.0e-46

E value 8.0e
Match length 124
% identity 74

Seq. No.

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

402443

Seq. No. 402444

% identity 86 NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 402445

Seq. ID LIB3431-053-P1-K1-F2

Method BLASTX
NCBI GI g320618
BLAST score 597
E value 6.0e-62
Match length 132
% identity 86

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 402446

Seq. ID LIB3431-053-P1-K1-F6

Method BLASTX
NCBI GI g6063542
BLAST score 308
E value 8.0e-30
Match length 76
% identity 97

NCBI Description (AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate



dehydrogenase. (M64118) [Oryza sativa]

```
402447
Seq. No.
Seq. ID
                  LIB3431-053-P1-K1-F8
Method
                  BLASTN
                  q4835587
NCBI GI
BLAST score
                  67
                  1.0e-29
E value
                  67
Match length
                  100
% identity
NCBI Description Oryza sativa ONIT4 mRNA for nitrilase-like protein,
                  complete cds
                  402448
Seq. No.
                  LIB3431-053-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q733456
BLAST score
                   631
                   6.0e-66
E value
                  141
Match length
                   85
% identity
                   (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   402449
Seq. No.
Seq. ID
                   LIB3431-053-P1-K1-G1
Method
                   BLASTX
                   g3047064
NCBI GI
BLAST score
                   406
E value
                   1.0e-39
                   143
Match length
                   57
% identity
                  (AF058825) contains similarity to peptidyl-prolyl cis-trans
NCBI Description
                   isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41
                   [Arabidopsis thaliana]
Seq. No.
                   402450
                   LIB3431-053-P1-K1-G10
Seq. ID
                   BLASTX
Method
                   q671740
NCBI GI
BLAST score
                   338
E value
                   2.0e-31
Match length
                   63
                   98
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   402451
Seq. No.
                   LIB3431-053-P1-K1-G11
Seq. ID
                   BLASTX
Method
                   g132105
NCBI GI
BLAST score
                   653
                   2.0e-68
E value
Match length
                   141
                   88
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

402452 Seq. No. LIB3431-053-P1-K1-G2 Seq. ID Method BLASTN NCBI GI g20262 BLAST score 340 0.0e+00E value 340 Match length % identity 100 O.sativa light-induced mRNA NCBI Description 402453 Seq. No. Seq. ID LIB3431-053-P1-K1-G3 BLASTX Method NCBI GI q3510256 250 BLAST score 3.0e-21 E value 118 Match length 47 % identity (AC005310) unknown protein [Arabidopsis thaliana] NCBI Description 402454 Seq. No. Seq. ID LIB3431-053-P1-K1-G4 Method BLASTX NCBI GI q132105 BLAST score 525 E value 1.0e-53 Match length 117 % identity 85 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxy \overline{l} ase ($\overline{E}C$ 4. $\overline{1}$.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

 Seq. No.
 402455

 Seq. ID
 LIB3431-053-P1-K1-G5

 Method
 BLASTX

 NCBI GI
 g132105

 BLAST score
 313

 E value
 6.0e-29

 Match length
 80

% identity 80 NCBI Description RI

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

carboxylase S [Oryza sativa]

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402456

Seq. ID LIB3431-053-P1-K1-G7

Method BLASTX
NCBI GI g2735017
BLAST score 523
E value 3.0e-53
Match length 155
% identity 63

NCBI Description (U82481) KI domain interacting kinase 1 [Zea mays]

Seq. No. 402457

Seq. ID LIB3431-053-P1-K1-G9

Method BLASTX
NCBI GI g82080
BLAST score 535
E value 1.0e-54
Match length 148
% identity 69

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872_prf__1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 402458

Seq. ID LIB3431-053-P1-K1-H10

Method BLASTX
NCBI GI g132105
BLAST score 541
E value 2.0e-55
Match length 121
% identity 85

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402459

Seq. ID LIB3431-053-P1-K1-H11

Method BLASTN
NCBI GI g4680178
BLAST score 84
E value 3.0e-39

Match length 129 % identity 90

NCBI Description Oryza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete



sequences; and unknown genes

```
402460
Seq. No.
                  LIB3431-053-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g733454
NCBI GI
                  357
BLAST score
                  6.0e-34
E value
                  101
Match length
                  72
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  402461
Seq. No.
                  LIB3431-053-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  q4582459
NCBI GI
BLAST score
                  329
                  1.0e-30
E value
                  98
Match length
                   63
% identity
                   (AC007071) putative RanBP7/importin protein [Arabidopsis
NCBI Description
                  thaliana]
                   402462
Seq. No.
                  LIB3431-053-P1-K1-H6
Seq. ID
Method
                  BLASTN
                   g2570496
NCBI GI
BLAST score
                   118
                   1.0e-59
E value
                   126
Match length
% identity
                   98
                  Oryza sativa H protein subunit of glycine decarboxylase
NCBI Description
                   mRNA, complete cds
                   402463
Seq. No.
                   LIB3431-053-P1-K1-H7
Seq. ID
                   BLASTX
Method
                   g5442410
NCBI GI
                   380
BLAST score
                   2.0e-36
E value
                   133
Match length
% identity
                   58
                  (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
NCBI Description
                   402464
Seq. No.
                   LIB3431-053-P1-K1-H8
Seq. ID
                   BLASTX
Method
                   g2407281
NCBI GI
                   661
BLAST score
                   2.0e-69
E value
Match length
                   129
% identity
                   94
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
```

51695

402465

Seq. No.

```
LIB3431-053-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g3789952
NCBI GI
BLAST score
                  469
                  4.0e-47
E value
                  107
Match length
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  402466
Seq. No.
                  LIB3431-053-P1-N1-A1
Seq. ID
                  BLASTN
Method
                  g218209
NCBI GI
BLAST score
                  214
E value
                  1.0e-117
Match length
                  302
% identity
                  93
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  posss2106
Seq. No.
                   402467
                  LIB3431-053-P1-N1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q729477
BLAST score
                   498
                   3.0e-50
E value
Match length
                   110
% identity
                   84
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
NCBI Description
                   >gi 320548 pir__A44974 ferredoxin--NADP+ reductase (EC
                   1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
                   ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                   [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A
                   ferredoxin NADP reductase [Mesembryanthemum crystallinum]
                   402468
Seq. No.
                   LIB3431-053-P1-N1-A11
Seq. ID
                   BLASTX
Method
                   g131225
NCBI GI
                   179
BLAST score
                   4.0e-13
E value
                   48
Match length
                   69
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
```

Seq. No. 402469 LIB3431-053-P1-N1-A12 Seq. ID BLASTX Method g115813 NCBI GI 211

E value 8.0e-25 82 Match length

BLAST score

NCBI Description

```
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  402470
Seq. No.
                  LIB3431-053-P1-N1-A2
Seq. ID
Method
                  BLASTX
                  g2696804
NCBI GI
BLAST score
                  309
                  1.0e-44
E value
                  95
Match length
                  91
% identity
NCBI Description (AB009665) water channel protein [Oryza sativa]
                  402471
Seq. No.
                  LIB3431-053-P1-N1-A3
Seq. ID
                  BLASTX
Method
                  g132105
NCBI GI
BLAST score
                  354
                  1.0e-40
E value
Match length
                  83
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  402472
Seq. No.
                  LIB3431-053-P1-N1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q417154
                  302
BLAST score
                  7.0e-41
E value
Match length
                  109
% identity
                  85
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
Seq. No.
                  402473
Seq. ID
                  LIB3431-053-P1-N1-A7
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  202
                  9.0e-16
E value
Match length
                  38
                  100
% identity
```

(X84730) ribulose-bisphosphate carboxylase [synthetic

NCBI Description

```
402474
Seq. No.
                  LIB3431-053-P1-N1-A9
Seq. ID
Method
                  BLASTX
                  g2407281
NCBI GI
BLAST score
                  266
                  2.0e-23
E value
                  67
Match length
                  75
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  402475
Seq. No.
                  LIB3431-053-P1-N1-B10
Seq. ID
Method
                  BLASTX
                  g3036942
NCBI GI
BLAST score
                  181
                  3.0e-13
E value
Match length
                  37
                  89
% identity
                   (AB012636) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                  402476
Seq. No.
                  LIB3431-053-P1-N1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g347451
BLAST score
                  229
                  9.0e-19
E value
Match length
                   48
                  92
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
Seq. No.
                   402477
                  LIB3431-053-P1-N1-B12
Seq. ID
                  BLASTX
Method
                   g115813
NCBI GI
BLAST score
                   212
                   8.0e-17
E value
                   75
Match length
% identity
                   61
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                   402478
                   LIB3431-053-P1-N1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2499819
BLAST score
                   215
E value
                   1.0e-30
Match length
                   73
% identity
                   86
```

>gi_2130068_pir__S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic

ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR



protease [Oryza sativa]

```
402479
Seq. No.
                  LIB3431-053-P1-N1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4982478
BLAST score
                  168
                  1.0e-11
E value
Match length
                  47
% identity
                  68
                  (AF069441) putative leucyl tRNA synthetase [Arabidopsis
NCBI Description
                  thaliana]
                  402480
Seq. No.
                  LIB3431-053-P1-N1-B4
Seq. ID
Method
                  BLASTX
                  g421916
NCBI GI
                  237
BLAST score
                  5.0e-20
E value
Match length
                   49
% identity
                   90
                   chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                   >gi 12582 emb CAA48410_ (X68333) light harvesting
                   chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                   402481
                   LIB3431-053-P1-N1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g400983
BLAST score
                   250
                   3.0e-21
E value
Match length
                   70
                   69
% identity
                   50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)
NCBI Description
                   >gi_279648_pir__R5SP11 ribosomal protein L11 precursor -
                   spinach >gi 21313 emb CAA39950 (X56615) ribosomal protein
                   L11 [Spinacia oleracea]
Seq. No.
                   402482
                   LIB3431-053-P1-N1-B9
Seq. ID
Method
                   BLASTX
                   g1835731
NCBI GI
BLAST score
                   230
                   5.0e-19
E value
                   55
Match length
                   82
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   402483
Seq. No.
                   LIB3431-053-P1-N1-C10
Seq. ID
Method
                   BLASTX
                   q687677
NCBI GI
                   235
BLAST score
                   1.0e-19
E value
                   51
Match length
% identity
                   88
                  (U19925) unknown [Arabidopsis thaliana]
NCBI Description
```

```
402484
Seq. No.
                  LIB3431-053-P1-N1-C11
Seq. ID
                  BLASTX
Method
                  g2130042
NCBI GI
                  317
BLAST score
                  3.0e-32
E value
                  100
Match length
                  75
% identity
                  Mg-chelatase chain Xantha-f - barley >gi 861199 (U26916)
NCBI Description
                  protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                  vulgare]
                   402485
Seq. No.
                  LIB3431-053-P1-N1-C12
Seq. ID
                  BLASTX
Method
                  g2645999
NCBI GI
                   219
BLAST score
                   8.0e-18
E value
                   56
Match length
                   73
% identity
                   (AF034631) chlorophyll a/b binding protein of LHCII type I
NCBI Description
                   precursor [Panax ginseng]
                   402486
Seq. No.
                   LIB3431-053-P1-N1-C2
Seq. ID
Method
                   BLASTX
                   g2072555
NCBI GI
BLAST score
                   217
                   2.0e-17
E value
                   44
Match length
                   93
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   402487
Seq. No.
                   LIB3431-053-P1-N1-C3
Seq. ID
                   BLASTX
Method
                   g671740
NCBI GI
                   245
BLAST score
                   1.0e-20
E value
                   49
Match length
                   96
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   402488
 Seq. No.
                   LIB3431-053-P1-N1-C5
 Seq. ID
                   BLASTX
Method
                   g1835731
NCBI GI
 BLAST score
                   459
                   1.0e-45
 E value
                   102
 Match length
                   86
 % identity
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
 NCBI Description
```

Seq. ID

Method



```
Seq. No.
                  402489
                  LIB3431-053-P1-N1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q170354
BLAST score
                  422
                  2.0e-41
E value
Match length
                  85
                  21
% identity
                  (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
                  402490
Seq. No.
                  LIB3431-053-P1-N1-C8
Seq. ID
                  BLASTX
Method
                  g289920
NCBI GI
BLAST score
                  319
                  2.0e-29
E value
Match length
                  61
                  100
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  402491
Seq. No.
                  LIB3431-053-P1-N1-D10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g304219
BLAST score
                  52
                  2.0e-20
E value
Match length
                  80
% identity
                  91
                  Hordeum vulgare chloroplast photosystem I PSK-I subunit
NCBI Description
                  mRNA, complete cds
                   402492
Seq. No.
                  LIB3431-053-P1-N1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2754849
                  192
BLAST score
E value
                  2.0e-29
Match length
                  74
                  85
% identity
                  (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                   [Fritillaria agrestis]
                   402493
Seq. No.
                  LIB3431-053-P1-N1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3789952
BLAST score
                  196
                   7.0e-15
E value
Match length
                   39
% identity
                   95
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   402494
Seq. No.
```

51701

LIB3431-053-P1-N1-E1

BLASTX

Match length

84

```
q3885892
NCBI GI
                  302
BLAST score
                  2.0e-27
E value
Match length
                  61
% identity
                  95
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                  402495
Seq. No.
                  LIB3431-053-P1-N1-E10
Seq. ID
                  BLASTX
Method
                  g5734636
NCBI GI
BLAST score
                  187
                  6.0e-16
E value
Match length
                  87
% identity
                  49
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                  sativa]
                  402496
Seq. No.
                  LIB3431-053-P1-N1-E11
Seq. ID
Method
                  BLASTX
                  q4544390
NCBI GI
                  188
BLAST score
                  6.0e-14
E value
Match length
                  62
% identity
                  50
                 (AC007047) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402497
                  LIB3431-053-P1-N1-E2
Seq. ID
Method
                  BLASTN
                  g218209
NCBI GI
BLAST score
                  58
                  1.0e-23
E value
Match length
                  94
                  90
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  posss2106
                  402498
Seq. No.
                  LIB3431-053-P1-N1-E3
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2072726
BLAST score
                  460
E value
                  0.0e+00
                  491
Match length
                  99
% identity
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
Seq. No.
                  402499
                  LIB3431-053-P1-N1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q482311
                  420
BLAST score
E value
                  4.0e-41
```



% identity photosystem II oxygen-evolving complex protein 1 - rice NCBI Description (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa] 402500 Seq. No. LIB3431-053-P1-N1-E7 Seq. ID BLASTX Method q4417296 NCBI GI BLAST score 163 5.0e-22 E value 78 Match length 59 % identity (AC007019) unknown protein [Arabidopsis thaliana] NCBI Description >gi 4587592_gb AAD25820.1_AC007232_10 (AC007232) unknown protein [Arabidopsis thaliana] 402501 Seq. No. LIB3431-053-P1-N1-E9 Seq. ID BLASTX Method q3885894 NCBI GI BLAST score 330 2.0e-38 E value 113 Match length 77 % identity NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa] 402502 Seq. No. Seq. ID LIB3431-053-P1-N1-F1 Method BLASTX g2570511 NCBI GI BLAST score 163 E value 3.0e-22 Match length 67 78 % identity NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa] 402503 Seq. No. Seq. ID LIB3431-053-P1-N1-F10 BLASTX Method NCBI GI g2501190 BLAST score 167 E value 6.0e-19 78 Match length 71 % identity THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR NCBI Description >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays] 402504 Seq. No. LIB3431-053-P1-N1-F11 Seq. ID

BLASTX Method g115787 NCBI GI 471 BLAST score 4.0e-47 E value 106 Match length

```
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  402505
Seq. No.
                  LIB3431-053-P1-N1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036949
BLAST score
                  254
E value
                  1.0e-21
Match length
                  49
% identity
                  98
```

NCBI Description (AB012638) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

402506 Seq. No. Seq. ID LIB3431-053-P1-N1-F3 Method BLASTX NCBI GI q134034 BLAST score 250 E value 3.0e-21 Match length 87 56 % identity

NCBI Description 30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5)

(CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1)

>gi_279640_pir__R3SPS5 ribosomal protein CS-S22 precursor,
chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270)
chloroplast ribosomal protein S22 [Spinacia oleracea]
>gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein

[Spinacia oleracea]

Seq. No. 402507

Seq. ID LIB3431-053-P1-N1-F4

Method BLASTN
NCBI GI g483443
BLAST score 79
E value 3.0e-36
Match length 154
% identity 90

NCBI Description Z.mays IBP2 mRNA for initiator-binding protein

Seq. No. 402508

Seq. ID LIB3431-053-P1-N1-F5

Method BLASTX
NCBI GI g671740
BLAST score 294
E value 2.0e-26
Match length 56
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 402509

Seq. ID LIB3431-053-P1-N1-F6



88

% identity

NCBI Description

```
BLASTX
Method
NCBI GI
                  q6063542
BLAST score
                  198
                  7.0e-16
E value
                  45
Match length
                  98
% identity
                  (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
                  402510
Seq. No.
                  LIB3431-053-P1-N1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4835587
BLAST score
                  154
                  6.0e-81
E value
Match length
                  166
                  99
% identity
                  Oryza sativa ONIT4 mRNA for nitrilase-like protein,
NCBI Description
                  complete cds
                  402511
Seq. No.
                  LIB3431-053-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  240
                  2.0e-37
E value
Match length
                  90
                  92
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                  402512
Seq. No.
Seq. ID
                  LIB3431-053-P1-N1-G1
Method
                  BLASTX
NCBI GI
                  q3047064
BLAST score
                   374
                  9.0e-36
E value
                   90
Match length
% identity
                   73
                  (AF058825) contains similarity to peptidyl-prolyl cis-trans
NCBI Description
                   isomerase (Pfam: pro isomerase.hmm, score: 23.86 and 28.41
                   [Arabidopsis thaliana]
Seq. No.
                   402513
                  LIB3431-053-P1-N1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q132105
BLAST score
                   156
                  1.0e-16
E value
Match length
                   47
```

51705

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(D00643) small subunit of ribulose-1,5-bisphosphate

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_



carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

```
Seq. No.
                     402514
                     LIB3431-053-P1-N1-G11
  Seq. ID
  Method
                     BLASTX
NCBI GI
                     q671740
  BLAST score
                     443
  E value
                     7.0e-44
  Match length
                     86
   % identity
  NCBI Description
                     (X84730) ribulose-bisphosphate carboxylase [synthetic
                     construct]
  Seq. No.
                     402515
  Seq. ID
                     LIB3431-053-P1-N1-G12
  Method
                     BLASTX
  NCBI GI
                     q5107149
  BLAST score
                     309
  E value
                     4.0e-28
  Match length
                     84
                     75
   % identity
  NCBI Description
                    (AF150080) small zinc finger-like protein [Oryza sativa]
  Seq. No.
                     402516
  Seq. ID
                     LIB3431-053-P1-N1-G2
  Method
                     BLASTN
  NCBI GI
                     g20262
  BLAST score
                     147
  E value
                     9.0e-77
  Match length
                     174
   % identity
                     97
  NCBI Description O.sativa light-induced mRNA
   Seq. No.
                     402517
                     LIB3431-053-P1-N1-G3
   Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g3510256
  BLAST score
                     266
  E value
                     4.0e-23
  Match length
                     89
   % identity
                     56
                    (AC005310) unknown protein [Arabidopsis thaliana]
  NCBI Description
                     402518
   Seq. No.
                     LIB3431-053-P1-N1-G4
   Seq. ID
  Method
                     BLASTX
                     g347451
  NCBI GI
  BLAST score
                     207
  E value
                     2.0e-16
  Match length
                     48
   % identity
                     88
                     (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
  NCBI Description
```

sativa]

Match length

102

```
Seq. No.
Seq. ID
                  LIB3431-053-P1-N1-G5
Method
                  BLASTX
                  g4530591
NCBI GI
BLAST score
                  483
E value
                  2.0e-48
Match length
                  116
% identity
                  (AF132475) heme oxygenase 1 [Arabidopsis thaliana]
NCBI Description
                  >qi 4530593 qb AAD22108.1 (AF132476) heme oxygenase 1
                  [Arabidopsis thaliana] >gi 4877362 dbj BAA77758.1
                  (AB021857) plastid heme oxygenase [Arabidopsis thaliana]
                  >gi 4877397 dbj BAA77759.1_ (AB021858) plastid heme
                  oxygenase [Arabidopsis thaliana] >gi_4883666_gb_AAB95301.2_
                  (AC003105) heme oxygenase 1 (HO1) [Arabidopsis thaliana]
Seq. No.
                  402520
                  LIB3431-053-P1-N1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  257
                  2.0e-35
E value
Match length
                  95
                  83
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  402521
Seq. No.
Seq. ID
                  LIB3431-053-P1-N1-H10
                  BLASTX
Method
NCBI GI
                  g671740
BLAST score
                  486
E value
                  7.0e-49
                  88
Match length
                  100
% identity
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  402522
Seq. No.
                  LIB3431-053-P1-N1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2384956
BLAST score
                  275
                  1.0e-25
E value
Match length
                  149
% identity
                  43
NCBI Description (AF022985) No definition line found [Caenorhabditis
                  elegans]
                  402523
Seq. No.
                  LIB3431-053-P1-N1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q733454
BLAST score
                  310
                  6.0e-45
E value
```

51707

% identity (U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description [Zea mays] 402524 Seq. No. LIB3431-053-P1-N1-H5 Seq. ID Method BLASTX NCBI GI g131225 BLAST score 318 E value 3.0e - 37101 Match length % identity 81 PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT NCBI Description V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi 167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare] 402525 Seq. No. LIB3431-053-P1-N1-H6 Seq. ID Method BLASTX NCBI GI g2499417 BLAST score 327 E value 2.0e-30 Match length 78 % identity 79 GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR NCBI Description >qi 1085826 pir S49248 H-protein - Flaveria anomala >qi 547558 emb CAA85761 (Z37524) H-protein [Flaveria anomala] 402526 Seq. No. LIB3431-053-P1-N1-H7 Seq. ID BLASTX Method

NCBI GI g5442410 BLAST score 157 E value 1.0e-15 109 Match length 43 % identity

NCBI Description (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]

402527 Seq. No.

LIB3431-053-P1-N1-H8 Seq. ID

BLASTX Method NCBI GI g132081 BLAST score 170 E value 2.0e-15 53 Match length 84 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi_68093_pir__RKRZS

ribulose-bisphosphate carboxylase (EC $\overline{4}$.1.1.39) small chain precursor - rice >gi 20341_emb_CAA30393_ (X07515) ribulose

bisphosphate carboxylase [Oryza sativa]

Seq. No. 402528

LIB3431-053-P1-N1-H9 Seq. ID

BLASTN Method



```
q3789951
NCBI GI
BLAST score
                  102
                  6.0e-50
E value
                  212
Match length
                  87
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  402529
Seq. ID
                  LIB3431-054-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q3913426
BLAST score
                  784
                  8.0e-84
E value
Match length
                  164
% identity
                  87
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >gi 1532048 emb CAA69074_ (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
Seq. No.
                  402530
                  LIB3431-054-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100880
BLAST score
                  282
E value
                  2.0e-25
Match length
                  86
% identity
                  71
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
NCBI Description
                  (phosphorylating) (EC 1.2.1.13) A, chloroplast - maize
Seq. No.
                  402531
Seq. ID
                  LIB3431-054-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  591
E value
                  2.0e-61
                  115
Match length
% identity
                  93
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                  402532
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-A4
```

Method BLASTN NCBI GI g3241924 BLAST score 45 E value 5.0e-16

Match length 185 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MNC6, complete sequence



```
Seq. No.
                   402533
Seq. ID
                   LIB3431-054-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   373
                   7.0e-36
E value
Match length
                   91
% identity
                   78
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   402534
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g4972093
BLAST score
                   466
                   1.0e-46
E value
Match length
                   125
% identity
NCBI Description (AL078468) putative protein [Arabidopsis thaliana]
Seq. No.
                   402535
Seq. ID
                   LIB3431-054-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   402536
Seq. No.
                   LIB3431-054-P1-K1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   717
                   6.0e-76
E value
Match length
                   152
% identity
                   89
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
```

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208 dbj_BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402537

LIB3431-054-P1-K1-B2 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g2435519
BLAST score
                  388
E value
                  2.0e-37
                  117
Match length
                  64
% identity
NCBI Description
                  (AF024504) similar to mouse MEM3 (GB:U47024 and S.
                  cerevisiae vacuolar sorting protein 35 (SW; P34110)
                  [Arabidopsis thaliana]
                  402538
Seq. No.
                  LIB3431-054-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q461812
BLAST score
                  245
E value
                  1.0e-20
Match length
                  94
                  45
% identity
                  CYTOCHROME P450 72A1 (CYPLXXII) (PROBABLE
NCBI Description
                  GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                  Cytochrome P-450 protein [Catharanthus roseus]
                  >gi 445604 prf 1909351A cytochrome P450 [Catharanthus
                  roseus]
Seq. No.
                  402539
Seq. ID
                  LIB3431-054-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  629
E value
                  9.0e-66
                  126
Match length
                  94
% identity
                 (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  402540
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                  561
E value
                  8.0e-58
Match length
                  124
% identity
                  88
NCBI Description (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  402541
                  LIB3431-054-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3024871
BLAST score
                  216
```

E value 3.0e-17 Match length 160 % identity 34

HYPOTHETICAL 77.3 KD PROTEIN SLL0005 NCBI Description

>gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis

sp.]

Seq. No. 402542



```
LIB3431-054-P1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3913018
BLAST score
                  681
                  6.0e-72
E value
                  136
Match length
                  99
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  402543
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-B9
Method
                  BLASTX
                  g3789954
NCBI GI
BLAST score
                  336
                  2.0e-31
E value
Match length
                  63
% identity
                  98
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  402544
Seq. No.
                  LIB3431-054-P1-K1-C1
Seq. ID
Method
                  BLASTX .
                  q167097
NCBI GI
                  151
BLAST score
                  1.0e-21
E value
                  64
Match length
                  84
% identity
NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase
                   [Hordeum vulgare]
                  402545
Seq. No.
                  LIB3431-054-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1653935
BLAST score
                  182
E value
                  3.0e-13
Match length
                  64
% identity
NCBI Description (D90917) hypothetical protein [Synechocystis sp.]
Seq. No.
                   402546
                  LIB3431-054-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2651310
BLAST score
                  375
E value
                  7.0e-36
                  148
Match length
% identity
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. ID BLASTX

Seq. No.

LIB3431-054-P1-K1-C12

402547

Method

BLAST score

E value

120 5.0e-61

```
g3927827
NCBI GI
                  195
BLAST score
                  7.0e-15
E value
                  115
Match length
                  42
% identity
                  (AC005727) osmotin-like protein precursor [Arabidopsis
NCBI Description
                  thaliana]
                  402548
Seq. No.
                  LIB3431-054-P1-K1-C2
Seq. ID
                  BLASTX
Method
                  g2306981
NCBI GI
                  441
BLAST score
                  9.0e-44
E value
                  125
Match length
                   74
% identity
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
                   402549
Seq. No.
                  LIB3431-054-P1-K1-C3
Seq. ID
                  BLASTX
Method
                   g417260
NCBI GI
                   421
BLAST score
                   2.0e-41
E value
                   128
Match length
                   66
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003_pir__$33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA\overline{4}8706 (X68807)
                   light-regulated gene [Oryza sativa]
                   402550
Seq. No.
                   LIB3431-054-P1-K1-C4
Seq. ID
                   BLASTN
Method
                   q3885891
NCBI GI
                   245
BLAST score
                   1.0e-135
E value
                   245
Match length
                   100
% identity
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                   mRNA, complete cds
                   402551
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-C5
Method
                   BLASTX
                   q2832672
NCBI GI
BLAST score
                   160
                   1.0e-10
E value
                   33
Match length
% identity
                   97
NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]
                   402552
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-C6
Method
                   BLASTN
                   g1835730
NCBI GI
```

51713

```
Match length
                   92
% identity
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                  complete cds
                  402553
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-C7
Method
                  BLASTX
                  g2924520
NCBI GI
BLAST score
                  609
                  3.0e-63
E value
                  159
Match length
                   72
% identity
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                   402554
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-C8
Method
                  BLASTX
NCBI GI
                   g3789954
BLAST score
                   628
E value
                   1.0e-65
                   159
Match length
                   75
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   402555
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-C9
                   BLASTX
Method
NCBI GI
                   g2072555
BLAST score
                   237
                   1.0e-19
E value
Match length
                   44
                   100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   402556
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-D1 -
Method
                   BLASTN
```

Method BLASTN
NCBI GI g2677829
BLAST score 133
E value 2.0e-68
Match length 341
% identity 85

NCBI Description Prunus armeniaca ribosomal protein L12 mRNA, complete cds

Seq. No. 402557

Seq. ID LIB3431-054-P1-K1-D10

Method BLASTX
NCBI GI g1778095
BLAST score 452
E value 4.0e-45
Match length 122
% identity 71



NCBI Description (U64903) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No. 402558

Seq. ID LIB3431-054-P1-K1-D2

Method BLASTN
NCBI GI g4138289
BLAST score 192
E value 1.0e-104
Match length 251
% identity 94

NCBI Description Oryza sativa mRNA for thioredoxin M

Seq. No. 402559

Seq. ID LIB3431-054-P1-K1-D3

Method BLASTX
NCBI GI g115796
BLAST score 571
E value 1.0e-64
Match length 127
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I

CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza

sativa]

Seq. No. 402560

Seq. ID LIB3431-054-P1-K1-D4

Method BLASTX
NCBI GI g3075488
BLAST score 518
E value 1.0e-52
Match length 117

% identity 85

NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No. 402561

Seq. ID LIB3431-054-P1-K1-D5

Method BLASTX
NCBI GI g3789948
BLAST score 709
E value 5.0e-75
Match length 149
% identity 91

NCBI Description (AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No. 402562

Seq. ID LIB3431-054-P1-K1-D7

Method BLASTX
NCBI GI g4239845
BLAST score 205
E value 6.0e-16
Match length 113
% identity 42

NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

```
Seq. No.
                  LIB3431-054-P1-K1-D8
Seq. ID
                  BLASTX
Method
                  g2191138
NCBI GI
                  152
BLAST score
                  8.0e-10
E value
                  108
Match length
% identity
                   41
                  (AF007269) A_IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
                   402564
Seq. No.
                  LIB3431-054-P1-K1-D9
Seq. ID
                  BLASTX
Method
                  g3776005
NCBI GI
                   746
BLAST score
                   2.0e-79
E value
Match length
                  163
% identity
                   89
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   402565
                   LIB3431-054-P1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4205079
                   436
BLAST score
E value
                   4.0e-43
Match length
                   154
                   55
% identity
                  (U70425) ankyrin repeat-containing protein 2 [Arabidopsis
NCBI Description
                   thaliana]
                   402566
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-E3
                   BLASTX
Method
NCBI GI
                   g320618
BLAST score
                   380
                   7.0e-37
E value
Match length
                   96
                   84
% identity
```

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi 218172 dbj BAA00536 (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza satīva]

Seq. No. 402567

Seq. ID LIB3431-054-P1-K1-E4

Method BLASTX
NCBI GI g1928981
BLAST score 337
E value 1.0e-31
Match length 107
% identity 59

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

```
402568
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-E5
                  BLASTX
Method
                  g2072555
NCBI GI
                  237
BLAST score
                  1.0e-19
E value
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  402569
Seq. No.
                  LIB3431-054-P1-K1-E7
Seq. ID
                  BLASTX
Method
                  g3075488
NCBI GI
BLAST score
                  749
E value
                  1.0e-79
                  143
Match length
                  100
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  402570
Seq. No.
                  LIB3431-054-P1-K1-F11
Seq. ID
Method
                  BLASTX
                  q2760834
NCBI GI
                  422
BLAST score
                  2.0e-41
E value
Match length
                  122
                  67
% identity
                  (AC003105) putative nitrate transporter [Arabidopsis
NCBI Description
                  thaliana]
                  402571
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-F12
                  BLASTX
Method
NCBI GI
                  q2072555
BLAST score
                  237
E value
                  9.0e-20
                  44
Match length
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >qi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  402572
Seq. No.
                  LIB3431-054-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
                  632
BLAST score
                  4.0e-66
E value
Match length
                  121
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
```

Seq. No. 402573

subunit [Oryza sativa]



LIB3431-054-P1-K1-F3 Seq. ID Method BLASTX NCBI GI g115815 454 BLAST score 1.0e-45 E value Match length 84 % identity CHLOROPHYLL A-B BINDING PROTEIN M9 PRECURSOR (LHCII TYPE I NCBI Description CAB-M9) (LHCP) >gi 100866 pir S13098 chlorophyll a/b-binding protein precursor - maize >gi 22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays] 402574 Seq. No. LIB3431-054-P1-K1-F4 Seq. ID BLASTX Method g3345477 NCBI GI BLAST score 404 E value 2.0e-39 Match length 127 % identity 64 NCBI Description (AB016283) carbonic anhydrase [Oryza sativa] 402575 Seq. No. LIB3431-054-P1-K1-F7 Seq. ID BLASTX Method NCBI GI g417260 BLAST score 421 3.0e-41 E value Match length 128 66 % identity LIGHT REGULATED PROTEIN PRECURSOR >gi 422003_pir__S33632 NCBI Description lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa] 402576 Seq. No. Seq. ID LIB3431-054-P1-K1-F9 BLASTX Method NCBI GI g3885886 BLAST score 710 3.0e-75 E value 138 Match length % identity NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa] 402577 Seq. No. LIB3431-054-P1-K1-G10 Seq. ID Method BLASTX NCBI GI g1071913 BLAST score 367

6.0e-35 E value 120 Match length % identity 62

NCBI Description cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial

- spinach >gi 1066153 dbj BAA07177 (D37963) cysteine

synthase [Spinacia oleracea]



```
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g3757521
BLAST score
                   567
E value
                   2.0e-58
                   169
Match length
% identity
                   58
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                   402579
Seq. No.
                   LIB3431-054-P1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   550
E value
                   1.0e-56
Match length
                   122
                   93
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   402580
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-G4
                   BLASTX
Method
NCBI GI
                   q1707657
BLAST score
                   538
                   5.0e-55
E value
Match length
                   167
% identity
                   62
NCBI Description (Z71640) DnaJ homologue [Pisum sativum]
                   402581
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-G5
                   BLASTX
Method
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
% identity
                   100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   402582
Seq. ID
                   LIB3431-054-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q729478
BLAST score
                   794
E value
                   5.0e-85
Match length
                   153
% identity
                   98
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
```

51719

a region of the predicted gene.; similar to

ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

(AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to

```
Seq. No.
                  402583
Seq. ID
                  LIB3431-054-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g3912968
BLAST score
                  172
                  3.0e-12
E value
                  123
Match length
% identity
                  30
NCBI Description ALPHA-ADAPTIN HOMOLOG >gi_1890329 emb_CAA71991_ (Y11104)
                  alpha-adaptin [Drosophila melanogaster]
                  402584
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g629670
BLAST score
                  348
E value
                  6.0e-33
                  94
Match length
% identity
                  68
NCBI Description hypothetical protein - tomato
Seq. No.
                  402585
Seq. ID
                  LIB3431-054-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3885894
BLAST score
                  398
E value
                  7.0e-39
Match length
                  90
% identity
                  87
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                  402586
Seq. ID
                  LIB3431-054-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  g22380
BLAST score
                  512
E value
                  6.0e-52
Match length
                  127
% identity
                  80
NCBI Description (X59714) CAAT-box DNA binding protein subunit B (NF-YB)
                   [Zea mays]
Seq. No.
                  402587
Seq. ID
                  LIB3431-054-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  335
E value
                  3.0e-32
Match length
                  88
% identity
                  83
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
```

[Oryza sativa]

>qi 227611 prf 1707316A chlorophyll a/b binding protein 1



Seq. No. 402588 Seq. ID LIB343

LIB3431-054-P1-K1-H9

Method BLASTX
NCBI GI g132105
BLAST score 635
E value 1.0e-66
Match length 116
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir _RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402589

Seq. ID LIB3431-054-P1-N1-A10

Method BLASTX
NCBI GI g3913426
BLAST score 300
E value 2.0e-33
Match length 118
% identity 69

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi 1532048 emb CAA69074 (Y07766)

S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No. 402590

Seq. ID LIB3431-054-P1-N1-A3

Method BLASTX
NCBI GI g1173347
BLAST score 276
E value 1.0e-48
Match length 116
% identity 77

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 402591

Seq. ID LIB3431-054-P1-N1-A5

Method BLASTX
NCBI GI g6093830
BLAST score 155
E value 4.0e-10
Match length 37
% identity 81

NCBI Description PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)

[CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;

putative photosytem II peptide [Spinacia oleracea]

```
Seq. No.
                  LIB3431-054-P1-N1-A6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g5091597
BLAST score
                  134
                  4.0e-69
E value
                  225
Match length
                  27
% identity
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
                  402593
Seq. No.
                  LIB3431-054-P1-N1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115787
BLAST score
                  405
E value
                  1.0e-60
                  122
Match length
                  88
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   402594
Seq. No.
Seq. ID
                  LIB3431-054-P1-N1-A9
Method
                  BLASTX
                   q517500
NCBI GI
BLAST score
                   374
                   6.0e-36
E value
                   90
Match length
                   81
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein [Zea mays] >gi_444338 prf 1906386A photosystem II
                   OE17 protein [Pisum sativum]
Seq. No.
                   402595
                   LIB3431-054-P1-N1-B10
Seq. ID
                   BLASTX
Method
                   q4972093
NCBI GI
BLAST score
                   196
E value
                   6.0e-27
Match length
                   96
% identity
                  (AL078468) putative protein [Arabidopsis thaliana]
NCBI Description
                   402596
Seq. No.
Seq. ID
                   LIB3431-054-P1-N1-B11
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   430
E value
                   0.0e+00
Match length
                   484
                   98
% identity
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
```

402592

51722

```
402597
Seq. No.
                  LIB3431-054-P1-N1-B12
Seq. ID
                  BLASTX
Method
                  g347451
NCBI GI
                  248
BLAST score
                  4.0e-21
E value
                  48
Match length
                  100
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
                  402598
Seq. No.
                  LIB3431-054-P1-N1-B2
Seq. ID
Method
                  BLASTX
                  g2435519
NCBI GI
BLAST score
                  183
                  3.0e-13
E value
                  62
Match length
                  58
% identity
                  (AF024504) similar to mouse MEM3 (GB:U47024 and S.
NCBI Description
                  cerevisiae vacuolar sorting protein 35 (SW; P34110)
                  [Arabidopsis thaliana]
                  402599
Seq. No.
                  LIB3431-054-P1-N1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q404688
BLAST score
                  242
                  3.0e-20
E value
Match length
                  69
% identity
                  55
                 (L19074) cytochrome P450 [Catharanthus roseus]
NCBI Description
                  402600
Seq. No.
                  LIB3431-054-P1-N1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115802
                  205
BLAST score
                  4.0e-16
E value
Match length
                  39
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
Seq. No.
                  402601
                  LIB3431-054-P1-N1-B5
Seq. ID
Method
                  BLASTX
                  g687677
NCBI GI
BLAST score
                  221
E value
                  4.0e-18
Match length
                  51
                  82
% identity
NCBI Description (U19925) unknown [Arabidopsis thaliana]
```

51723

% identity

NCBI Description

45

thaliana]



```
Seq. No.
                  402602
                  LIB3431-054-P1-N1-B6
Seq. ID
Method
                  BLASTX
                  g2696804
NCBI GI
BLAST score
                  333
                  3.0e-52
E value
                  117
Match length
                  92
% identity
                  (AB009665) water channel protein [Oryza sativa]
NCBI Description
                  402603
Seq. No.
                  LIB3431-054-P1-N1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2407279
BLAST score
                  315
                  3.0e-30
E value
Match length
                  69
                  93
% identity
NCBI Description (AF017362) aldolase [Oryza sativa]
                  402604
Seq. No.
                  LIB3431-054-P1-N1-B9
Seq. ID
Method
                  BLASTX
                  g3789954
NCBI GI
BLAST score
                  328
                  2.0e-30
E value
Match length
                  63
% identity
                  95
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  402605
Seq. No.
                  LIB3431-054-P1-N1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132166
BLAST score
                  156
E value
                  2.0e-10
Match length
                  31
% identity
                  84
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >qi 81660 pir S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >qi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -
                   473) [Arabidopsis thaliana]
                  402606
Seq. No.
                  LIB3431-054-P1-N1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2651310
BLAST score
                  163
                  3.0e-11
E value
Match length
                  69
```

51724

(AC002336) putative PTR2-B peptide transporter [Arabidopsis

```
402607
Seq. No.
                   LIB3431-054-P1-N1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g551047
BLAST score
                   268
                   2.0e-23
E value
Match length
                   52
                   96
% identity
                   (X79277) type II LHCI [Lolium temulentum]
NCBI Description
                   402608
Seq. No.
                   LIB3431-054-P1-N1-C3
Seq. ID
Method
                   BLASTX
                   g417260
NCBI GI
                   288
BLAST score
                   1.0e-25
E value
                   127
Match length
                   55
% identity
                   LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
                   402609
Seq. No.
                   LIB3431-054-P1-N1-C4
Seq. ID
                   BLASTN
Method
                   g3885891
NCBI GI
BLAST score
                   241
                   1.0e-133
E value
Match length
                   245
% identity
                   100
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                   mRNA, complete cds
                   402610
Seq. No.
                   LIB3431-054-P1-N1-C5
Seq. ID
Method
                   BLASTX
                   g2832672
NCBI GI
BLAST score
                   587
E value
                   1.0e-60
Match length
                   135
% identity
                   81
                   (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                   402611
Seq. No.
                   LIB3431-054-P1-N1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q131400
BLAST score
                   284
                   1.0e-34
E value
Match length
                   130
% identity
                   63
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi_81471_pir__S00409 photosystem II 10K protein precursor
- spinach >gi_170127 (J03887) 10kd polypeptide precursor
```

[Spinacia oleracea]



```
402612
Seq. No.
                  LIB3431-054-P1-N1-C7
Seq. ID
                  BLASTX
Method
                  g3158476
NCBI GI
BLAST score
                  356
                  1.0e-33
E value
                  96
Match length
                  72
% identity
                  (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
                  402613
Seq. No.
                  LIB3431-054-P1-N1-C8
Seq. ID
                  BLASTX
Method
                  g3789954
NCBI GI
BLAST score
                  341
E value
                  8.0e-32
Match length
                  118
% identity
                   62
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   402614
Seq. No.
                  LIB3431-054-P1-N1-C9
Seq. ID
Method
                  BLASTN
                   g2072554
NCBI GI
BLAST score
                   440
                   0.0e+00
E value
Match length
                   483
% identity
                   98
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
                   402615
Seq. No.
                   LIB3431-054-P1-N1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4371282
BLAST score
                   541
                   3.0e-55
E value
Match length
                   119
% identity
                   87
                   (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                   thaliana]
                   402616
Seq. No.
                   LIB3431-054-P1-N1-D3
Seq. ID
Method
                   BLASTX
                   g3126854
NCBI GI
                   296
BLAST score
                   5.0e-53
E value
Match length
                   108
                   99
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
```

Seq. No. 402617

Seq. ID LIB3431-054-P1-N1-D4

Method BLASTX NCBI GI g3075488



```
BLAST score
                  2.0e-53
E value
Match length
                  111
                  91
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  402618
                  LIB3431-054-P1-N1-D5
Seq. ID
                  BLASTX
Method
                  q124226
NCBI GI
BLAST score
                  385
                  9.0e-59
E value
                  127
Match length
% identity
                  INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 100278 pir S21059 translation initiation factor
                  eIF-5A.2 - curled-leaved tobacco >gi 19702 emb CAA45104
                  (X63542) eukaryotic initiation factor 5A (2) [Nicotiana
                  plumbaginifolia]
                  402619
Seq. No.
Seq. ID
                  LIB3431-054-P1-N1-D8
Method
                  BLASTX
NCBI GI
                  q2191138
BLAST score
                  241
                  1.0e-21
E value
Match length
                  92
% identity
                  (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  402620
                  LIB3431-054-P1-N1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6093830
BLAST score
                  160
E value
                  7.0e-11
Match length
                  62
% identity
                  31
                  PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
NCBI Description
                  [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                  PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
                  putative photosytem II peptide [Spinacia oleracea]
                  402621
Seq. No.
                  LIB3431-054-P1-N1-E2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3819352
BLAST score
                  58
```

9.0e-24 E value Match length 82 % identity 93

NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0813.rev

Seq. No.

LIB3431-054-P1-N1-E3 Seq. ID

402622

Method BLASTX

51727



```
g115787
NCBI GI
BLAST score
                  356
                  3.0e-61
E value
                  123
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  402623
Seq. No.
                  LIB3431-054-P1-N1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3695375
BLAST score
                  288
                  7.0e-26
E value
Match length
                  67
% identity
                  73
                  (AF096370) contains similarity to the major intrinsic
NCBI Description
                  protein domain (Pfam: PF00230 MIP, E-value: 5.7e-111)
                  [Arabidopsis thaliana]
                  402624
```

Seq. No. LIB3431-054-P1-N1-E5 Seq. ID BLASTX

Method q2072555 NCBI GI BLAST score 237 1.0e-19 E value Match length 44 100 % identity

(AF001396) metallothionein-like protein [Oryza sativa] NCBI Description >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402625

LIB3431-054-P1-N1-E6 Seq. ID

Method BLASTX NCBI GI q1835731 424 BLAST score E value 1.0e-55 126 Match length % identity 86

(U86018) photosystem II 10 kDa polypeptide [Oryza sativa] NCBI Description

402626 Seq. No.

LIB3431-054-P1-N1-E7 Seq. ID

Method BLASTX NCBI GI q4741954 296 BLAST score E value 2.0e-49 Match length 111 % identity 80

(AF134127) Lhcb4.2 protein [Arabidopsis thaliana] NCBI Description

Seq. No. 402627

LIB3431-054-P1-N1-F12 Seq. ID



```
Method BLASTX
NCBI GI g2072555
BLAST score 222
E value 6.0e-18
Match length 41
% identity 100
```

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402628

Seq. ID LIB3431-054-P1-N1-F2

Method BLASTX
NCBI GI g132105
BLAST score 396
E value 1.0e-38
Match length 74
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208 dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402629

Seq. ID LIB3431-054-P1-N1-F3

Method BLASTX
NCBI GI g115787
BLAST score 332
E value 6.0e-55
Match length 115
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 402630

Seq. ID LIB3431-054-P1-N1-F4

Method BLASTX
NCBI GI g606817
BLAST score 182
E value 3.0e-28
Match length 69
% identity 78

NCBI Description (U08404) carbonic anhydrase [Oryza sativa]

>gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic

anhydrase 3 [Oryza sativa]

Seq. No. 402631

Seq. ID LIB3431-054-P1-N1-F6

Method BLASTX



NCBI GI g132105 BLAST score 747 E value 2.0e-79 Match length 158 % identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402632

Seq. ID LIB3431-054-P1-N1-F7

Method BLASTN
NCBI GI g20262
BLAST score 361
E value 0.0e+00
Match length 361
% identity 100

NCBI Description O.sativa light-induced mRNA

Seq. No. 402633

Seq. ID LIB3431-054-P1-N1-F8

Method BLASTX
NCBI GI g4982480
BLAST score 184
E value 2.0e-13
Match length 43
% identity 74

NCBI Description (AF069441) hypothetical protein [Arabidopsis thaliana]

Seq. No. 402634

Seq. ID LIB3431-054-P1-N1-F9

Method BLASTX
NCBI GI g3885886
BLAST score 219
E value 5.0e-33
Match length 67
% identity 85

NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 402635

Seq. ID LIB3431-054-P1-N1-G1

Method BLASTN
NCBI GI g218209
BLAST score 116
E value 1.0e-58
Match length 211
% identity 96

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS2106



```
402636
Seq. No.
                  LIB3431-054-P1-N1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2118307
BLAST score
                   166
                   4.0e-24
E value
                   91
Match length
                   55
% identity
                   cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
NCBI Description
                   >gi 804950_emb_CAA58893_ (X84097) cysteine synthase
                   [Arabidopsis thaliana] >gi_1096196_prf__2111276A Ser(Ac)
                   thiol lyase [Arabidopsis thaliana]
                   402637
Seq. No.
Seq. ID
                   LIB3431-054-P1-N1-G5
Method
                   BLASTX
                   q2072555
NCBI GI
                   230
BLAST score
                   7.0e-19
E value
Match length
                   44
% identity
                   98
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   402638
                   LIB3431-054-P1-N1-G6
Seq. ID
Method
                   BLASTX
                   q6015059
NCBI GI
                   320
BLAST score
                   9.0e-51
E value
                   104
Match length
                   97
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
                   402639
Seq. No.
                   LIB3431-054-P1-N1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729478
BLAST score
                   429
                   1.0e-73
E value
Match length
                   152
% identity
                   93
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
                   (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                   a region of the predicted gene.; similar to
```

ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

402640 Seq. No.

LIB3431-054-P1-N1-H3 Seq. ID

Method BLASTX NCBI GI q3885894 BLAST score 253



```
9.0e-22
E value
Match length
                  64
                  80
% identity
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                  402641
Seq. No.
                  LIB3431-054-P1-N1-H4
Seq. ID
                  BLASTX
Method
                  g115802
NCBI GI
BLAST score
                  191
                  1.0e-14
E value
Match length
                  37
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-36) (LHCP) >gi 100311 pir__S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
Seq. No.
                  402642
Seq. ID
                  LIB3431-054-P1-N1-H6
Method
                  BLASTX
NCBI GI
                  g115840
BLAST score
                  322
E value
                  1.0e-29
Match length
                  81
% identity
                  75
                  CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y
NCBI Description
                  PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN
                  SUBUNIT B)
Seq. No.
                  402643
                  LIB3431-054-P1-N1-H7
Seq. ID
                  BLASTX
Method
                  g115787
NCBI GI
                  410
BLAST score
E value
                  2.0e-70
                  144
Match length
% identity
                  96
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   402644
Seq. No.
                  LIB3431-054-P1-N1-H8
Seq. ID
                  BLASTX
Method
                  g517500
NCBI GI
                   389
BLAST score
                  7.0e-49
E value
Match length
                  126
```

% identity 83

NCBI Description

(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II

OE17 protein [Pisum sativum]

```
Seq. No.
                  402645
                  LIB3431-055-P1-N1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1644427
BLAST score
                  248
E value
                  3.0e-21
                  59
Match length
% identity
                  (U74610) glyoxalase II [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402646
                  LIB3431-055-P1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  360
E value
                  3.0e-34
Match length
                  87
% identity
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  402647
Seq. No.
Seq. ID
                  LIB3431-055-P1-N1-A2
                  BLASTX
Method
NCBI GI
                  q131225
BLAST score
                  216
                  2.0e-17
E value
                  56
Match length
% identity
                  73
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >qi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  402648
Seq. No.
                  LIB3431-055-P1-N1-A6
Seq. ID
Method
                  BLASTX
                  g693920
NCBI GI
BLAST score
                  414
E value
                  2.0e-40
Match length
                  80
% identity
                   97
                  (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                  tuberosum]
                   402649
Seq. No.
                  LIB3431-055-P1-N1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21699
```

BLAST score 317 3.0e-29 E value

Match length 71 83 % identity

(X66013) cathepsin B [Triticum aestivum] NCBI Description

Seq. No. 402650

51733

```
LIB3431-055-P1-N1-B1
Seq. ID
                  BLASTX
Method
                  g1168537
NCBI GI
BLAST score
                  254
E value
                  6.0e-22
Match length
                  46
                  100
% identity
                  ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
NCBI Description
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi 218143 dbj BAA02242 (D12777) aspartic proteinase
                  [Oryza sativa]
                  402651
Seq. No.
                  LIB3431-055-P1-N1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2072554
BLAST score
                  388
E value
                  0.0e+00
Match length
                  388
                  100
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                  402652
Seq. ID
                  LIB3431-055-P1-N1-B11
```

Method BLASTX
NCBI GI g1617197
BLAST score 183
E value 9.0e-20
Match length 71
% identity 61

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Seq. No. 402653

Seq. ID LIB3431-055-P1-N1-B2

Method BLASTX
NCBI GI g3068705
BLAST score 203
E value 6.0e-16
Match length 62
% identity 56

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 402654

Seq. ID LIB3431-055-P1-N1-B3

Method BLASTX
NCBI GI g1173346
BLAST score 189
E value 1.0e-28
Match length 105
% identity 62

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)

>gi 515618 emb CAA52439 (X74418)

sedoheptulose-bisphosphatase [Chlamydomonas reinhardtii]

Seq. No. 402655

NCBI GI

E value

BLAST score

g2570511

3.0e-22

163

```
LIB3431-055-P1-N1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3738261
BLAST score
                  340
E value
                  4.0e-50
Match length
                  122
% identity
                  89
                  (AB018412) chloroplast phosphoglycerate kinase [Populus
NCBI Description
                  nigra]
Seq. No.
                  402656
                  LIB3431-055-P1-N1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  688
E value
                  2.0e-72
Match length
                  131
% identity
                  96
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  satival
Seq. No.
                  402657
Seq. ID
                  LIB3431-055-P1-N1-C1
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  303
E value
                  4.0e-47
Match length
                  101
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  402658
                  LIB3431-055-P1-N1-C10
Seq. ID
                  BLASTX
Method
                  g3075488
NCBI GI
                  200
BLAST score
E value
                  5.0e-30
Match length
                  69
% identity
                  93
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  402659
                  LIB3431-055-P1-N1-C11
Seq. ID
                  BLASTX
Method
                  g3885886
NCBI GI
BLAST score
                  439
E value
                  2.0e-43
Match length
                  79
% identity
                  96
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
Seq. No.
                  402660
                  LIB3431-055-P1-N1-C2
Seq. ID
                  BLASTX
Method
```

51735



```
Match length
                    78
% identity
NCBI Description
                    (AF022738) chlorophyll a-b binding protein [Oryza sativa]
                    402661
Seq. No.
                    LIB3431-055-P1-N1-C6
Seq. ID
Method
                    BLASTX
NCBI GI
                    q485518
                    288
BLAST score
                    6.0e-26
E value
Match length
                    53
                    100
% identity
                    ubiquitin / ribosomal protein CEP52 - rice
NCBI Description
                    >gi 303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal
                    polyprotein [Oryza sativa]
Seq. No.
                    402662
                    LIB3431-055-P1-N1-C7
Seq. ID
                    BLASTN
Method
NCBI GI
                    g5714761
BLAST score
                    50
                    7.0e-19
E value
Match length
                    78
% identity
                    91
                    Oryza sativa subsp. indica serine/threonine protein
NCBI Description
                    phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete
                    cds
Seq. No.
                    402663
                    LIB3431-055-P1-N1-C8
Seq. ID
                    BLASTX
Method
                    q4115925
NCBI GI
BLAST score
                    166
                    2.0e-15
E value
Match length
                    67
% identity
                    64
                    (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
NCBI Description
                    >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
[Arabidopsis thaliana] >gi_4959384_gb_AAD34325.1_
                     (AF109721) RNA-binding protein [Arabidopsis thaliana]
                    402664
Seq. No.
                    LIB3431-055-P1-N1-D11
Seq. ID
Method
                    BLASTN
NCBI GI
                    g6016845
BLAST score
                    354
E value
                    0.0e+00
Match length
                    404
```

% identity 100

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

402665 Seq. No.

LIB3431-055-P1-N1-D2 Seq. ID

Method BLASTX NCBI GI g3789952 BLAST score 320



```
2.0e-29
E value
                  62
Match length
                  97
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  402666
Seq. No.
                  LIB3431-055-P1-N1-D5
Seq. ID
                  BLASTX
Method
                  g671740
NCBI GI
                  541
BLAST score
                  3.0e-55
E value
                  99
Match length
                  99
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  402667
Seq. No.
                  LIB3431-055-P1-N1-D7
Seq. ID
                  BLASTX
Method
                  g3861104
NCBI GI
BLAST score
                  251
                  3.0e-21
E value
                  117
Match length
% identity
                  46
                  (AJ235272) HEMOLYSIN (tlyA) [Rickettsia prowazekii]
NCBI Description
                  402668
Seq. No.
                  LIB3431-055-P1-N1-D8
Seq. ID
                  BLASTX
Method
                  g115787
NCBI GI
                  368
BLAST score
                  2.0e-63
E value
                  129
Match length
                  98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  402669
Seq. No.
                  LIB3431-055-P1-N1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5802955
BLAST score
                  235
                  2.0e-19
E value
                  58
Match length
                  74
% identity
                 (AF178990) stress related protein [Vitis riparia]
NCBI Description
                  402670
Seq. No.
```

Seq. ID LIB3431-055-P1-N1-E12

Method BLASTX
NCBI GI g2130069
BLAST score 320
E value 6.0e-45



Match length % identity 85

NCBI Description catalase (EC 1.11.1.6) catA - rice

>qi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]

402671 Seq. No.

LIB3431-055-P1-N1-E2 Seq. ID

Method BLASTN NCBI GI g3789951 BLAST score 403 0.0e + 00E value 480 Match length % identity 96

Oryza sativa chlorophyll a/b-binding protein presursor NCBI Description

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

402672 Seq. No.

LIB3431-055-P1-N1-E3 Seq. ID

Method BLASTX NCBI GI g4507769 257 BLAST score 7.0e-37 E value Match length 98

74 % identity

NCBI Description ubiquitin-conjugating enzyme E2A (RAD6 homolog)

> >gi 1351346 sp P49459 UBCA HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN

CARRIER PROTEIN) (HR6A) >gi_108016_pir__A41222

ubiquitin-conjugating enzyme HHR6A - human >gi 184044 (M74524) HHR6A (Human homologue of yeast RAD 6); putative

[Homo sapiens]

402673 Seq. No.

LIB3431-055-P1-N1-E9 Seq. ID

Method BLASTX NCBI GI g4335763 BLAST score 333 E value 6.0e-31 Match length 122 55 % identity

(AC006284) unknown protein [Arabidopsis thaliana] NCBI Description

402674 Seq. No.

LIB3431-055-P1-N1-F10 Seq. ID

Method BLASTX g4337175 NCBI GI 168 BLAST score 5.0e-25 E value Match length 114 % identity 58

(AC006416) ESTs gb T20589, gb T04648, gb AA597906, NCBI Description

> gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 402675



```
Seq. ID
                  LIB3431-055-P1-N1-F2
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  362
                  3.0e-50
E value
Match length
                  107
                  98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  402676
Seq. ID
                  LIB3431-055-P1-N1-F3
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  211
                  2.0e-26
E value
Match length
                  66
% identity
                  98
                 (AF017362) aldolase [Oryza sativa]
NCBI Description
                  402677
Seq. No.
Seq. ID
                  LIB3431-055-P1-N1-F5
Method
                  BLASTX
NCBI GI
                  g1321661
BLAST score
                  427
                  5.0e-42
E value
Match length
                  83
% identity
                  98
NCBI Description
                 (D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.
                  402678
                  LIB3431-055-P1-N1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036951
BLAST score
                  343
E value
                  2.0e-61
Match length
                  122
% identity
                  98
NCBI Description
                  (AB012639) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]
                  402679
Seq. No.
Seq. ID
                  LIB3431-055-P1-N1-F8
Method
                  BLASTN
NCBI GI
                  g2624325
```

BLAST score 227 1.0e-124 E value Match length 239 99 % identity

NCBI Description Oryza sativa mRNA for glycine-rich RNA-binding protein

(OsGRP1)

Seq. No. 402680

Seq. ID LIB3431-055-P1-N1-F9

```
Method
                  BLASTX
NCBI GI
                  q4038663
BLAST score
                  163
                  8.0e-24
E value
Match length
                  66
                  69
% identity
                  (AB020929) ribulose-1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                  small subunit [Aeqilops speltoides]
                  402681
Seq. No.
                  LIB3431-055-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score
                  294
                  2.0e-26
E value
Match length
                  89
                  56
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  402682
Seq. No.
                  LIB3431-055-P1-N1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  479
                  5.0e-48
E value
                  93
Match length
% identity
                  99
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  402683
                  LIB3431-055-P1-N1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  180
E value
                  3.0e-13
Match length
                  36
% identity
                  92
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  402684
Seq. No.
                  LIB3431-055-P1-N1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  169
                  7.0e-90
E value
Match length
                  188
% identity
                  97
NCBI Description O.sativa light-induced mRNA
Seq. No.
                  402685
Seq. ID
                  LIB3431-055-P1-N1-G4
```

Method BLASTX NCBI GI g3075488 BLAST score 452 E value 7.0e-45 Match length 88

```
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  402686
Seq. No.
                  LIB3431-055-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  261
                  2.0e-22
E value
Match length
                  71
                  66
% identity
                 (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
Seq. No.
                  402687
                  LIB3431-055-P1-N1-G6
Seq. ID
Method
                  BLASTX
                  g131225
NCBI GI
                  309
BLAST score
                  3.0e-28
E value
Match length
                  75
                  79
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  402688
                  LIB3431-055-P1-N1-G8
Seq. ID.
Method
                  BLASTX
NCBI GI
                  g1076724
                  233
BLAST score
                  1.0e-31
E value
Match length
                  77
                  88
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  402689
Seq. ID
                  LIB3431-055-P1-N1-G9
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  204
E value
                  7.0e-16
Match length
                  47
% identity
                  79
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  402690
Seq. No.
                  LIB3431-055-P1-N1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3063523
BLAST score
                  117
                  4.0e-59
E value
                  281
Match length
% identity
                  86
NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small
```



subunit mRNA, complete cds

Seq. No. 402691 LIB3431-055-P1-N1-H11 Seq. ID Method BLASTX q3004565 NCBI GI 255 BLAST score 9.0e-22 E value 94 Match length % identity 55 (AC003673) putative protein kinase [Arabidopsis thaliana] NCBI Description 402692 Seq. No.

LIB3431-055-P1-N1-H2 Seq. ID Method BLASTN NCBI GI g2773153

371 BLAST score 0.0e + 00E value 375 Match length 100 % identity

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

402693 Seq. No.

LIB3431-055-P1-N1-H3 Seq. ID

Method BLASTX g548605 NCBI GI BLAST score 420 E value 4.0e-56 Match length 131 % identity 91

PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR NCBI Description

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi 539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

402694 Seq. No.

LIB3431-055-P1-N1-H4 Seq. ID

Method BLASTX NCBI GI g115813 BLAST score 432 1.0e-42 E value 104 Match length % identity 81

CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III NCBI Description

CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402695

Seq. ID LIB3431-055-P1-N1-H5

Method BLASTX NCBI GI g132105 BLAST score 521 E value 6.0e-53 Match length 99 % identity 97

51742



RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 402696 Seq. No. LIB3431-055-P1-N1-H6 Seq. ID Method BLASTX NCBI GI q671740 BLAST score 458 E value 1.0e-45 Match length 86 99 % identity (X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description construct] 402697 Seq. No. LIB3431-055-P1-N1-H7 Seq. ID Method BLASTX g4325041 NCBI GI BLAST score 632 E value 6.0e-66 Match length 140 % identity 90 (AF117339) FtsH-like protein Pftf precursor [Nicotiana NCBI Description tabacum] 402698 Seq. No. LIB3431-055-P1-N1-H8 Seq. ID Method BLASTX NCBI GI g3126854 BLAST score 251 E value 1.0e-29 Match length 69 % identity 100 (AF061577) chlorophyll a/b binding protein [Oryza sativa] NCBI Description 402699 Seq. No. LIB3431-055-P1-N1-H9 Seq. ID Method BLASTX NCBI GI g131225 BLAST score 495 7.0e-50 E value Match length 125 % identity 78

PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT NCBI Description

V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

402700 Seq. No.

LIB3431-055-P2-K1-A9 Seq. ID

```
BLASTX
Method
NCBI GI
                  g3650033
BLAST score
                  293
E value
                  2.0e-42
Match length
                  153
% identity
                  61
                 (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402701
Seq. ID
                  LIB3431-055-P2-K1-B1
Method
                  BLASTN
NCBI GI
                  q218142
BLAST score
                  77
                  2.0e-35
E value
                  225
Match length
% identity
                  85
NCBI Description Rice mRNA for aspartic proteinase, complete cds
                  402702
Seq. No.
Seq. ID
                  LIB3431-055-P2-K1-B10
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  233
E value
                  6.0e-20
Match length
                  44
                  98
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  402703
Seq. ID
                  LIB3431-055-P2-K1-B5
Method
                  BLASTX
NCBI GI
                  g3328122
BLAST score
                  150
                  1.0e-09
E value
Match length
                  41
                  78
% identity
                  (AF073473) phosphoglycerate kinase precursor [Solanum
NCBI Description
                  tuberosum]
Seq. No.
                  402704
                  LIB3431-055-P2-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  668
E value
                  2.0e-70
```

Match length 135 93 % identity

(AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description

subunit [Oryza sativa]

Seq. No.

402705

LIB3431-055-P2-K1-B9 Seq. ID

Method BLASTX NCBI GI g3914005 BLAST score 237



7.0e-34 E value Match length 90 % identity 90

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586

(U85494) LON1 protease [Zea mays]

Seq. No. 402706

Seq. ID LIB3431-055-P2-K1-C1

Method BLASTX NCBI GI g3126854 BLAST score 443 E value 5.0e-44Match length 119 84 % identity

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.

402707

Seq. ID LIB3431-055-P2-K1-C11

Method BLASTN NCBI GI q3885885 BLAST score 32 E value 3.0e-09 Match length 32 100 % identity

NCBI Description Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,

complete cds

Seq. No. 402708

Seq. ID LIB3431-055-P2-K1-C6

Method BLASTN g303856 NCBI GI BLAST score 139 4.0e-72 E value Match length 227 93 % identity

NCBI Description Rice mRNA for ubiquitin protein fused to a ribosomal

protein, complete cds

402709 Seq. No.

LIB3431-055-P2-K1-C7 Seq. ID

Method BLASTX NCBI GI g517500 BLAST score 160 1.0e-10 E value Match length 61 57 % identity

NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa

protein [Zea mays] >gi_444338_prf__1906386A photosystem II

OE17 protein [Pisum sativum]

Seq. No. 402710

Seq. ID LIB3431-055-P2-K1-D11

Method BLASTN NCBI GI q6016845 BLAST score 66 E value 1.0e-28 Match length 108

51745

% identity 90

NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 402711

Seq. ID LIB3431-055-P2-K1-E11

Method BLASTX
NCBI GI g2129512
BLAST score 207
E value 7.0e-17
Match length 56

% identity 75
NCBI Description glycerate dehydrogenase (EC 1.1.1.29) splice form HPR2 -

cucurbit >gi 1304044_dbj_BAA08411_ (D49433) hydroxypyruvate

reductase [Cucurbita sp.]

Seq. No. 402712

Seq. ID LIB3431-055-P2-K1-E4

Method BLASTX
NCBI GI g6041808
BLAST score 258
E value 5.0e-27
Match length 92
% identity 66

NCBI Description (AC009755) unknown protein [Arabidopsis thaliana]

Seq. No. 402713

Seq. ID LIB3431-055-P2-K1-F3

Method BLASTN
NCBI GI g2407278
BLAST score 56
E value 9.0e-23
Match length 208
% identity 82

NCBI Description Oryza sativa aldolase mRNA, complete cds

Seq. No. 402714

Seq. ID LIB3431-055-P2-K1-F6

Method BLASTX
NCBI GI g1661160
BLAST score 441
E value 1.0e-43
Match length 104
% identity 80

NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402715

Seq. ID LIB3431-055-P2-K1-F7

Method BLASTN
NCBI GI g2407282
BLAST score 57
E value 6.0e-24
Match length 73
% identity 95

NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 402716



```
LIB3431-055-P2-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  645
E value
                  1.0e-67
Match length
                  122
% identity
                  97
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  402717
                  LIB3431-055-P2-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3075487
BLAST score
                  99
E value
                  1.0e-48
Match length
                  123
% identity
                  95
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  402718
                  LIB3431-055-P2-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  227
E value
                  1.0e-125
Match length
                  231
% identity
                  100
NCBI Description O.sativa light-induced mRNA
Seq. No.
                  402719
                  LIB3431-055-P2-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3004565
BLAST score
                  340
                  4.0e-32
E value
Match length
                  97
                  66
% identity
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  402720
Seq. No.
                  LIB3431-055-P2-K1-H12
Seq. ID
Method
                  BLASTX
                  g4678920
NCBI GI
BLAST score
                  227
                  1.0e-18
E value
Match length
                  102
% identity
                  48
                  (AL049711) putative heat shock transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                  402721
Seq. No.
                  LIB3431-055-P2-K1-H2
Seq. ID
```

Method BLASTN NCBI GI g2773153 BLAST score 171

```
3
                  2.0e-91
E value
Match length
                  186
% identity
                  98
NCBI Description
                  Oryza sativa abscisic acid- and stress-inducible protein
                  (Asr1) mRNA, complete cds
                  402722
Seq. No.
                  LIB3431-055-P2-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  575
E value
                  2.0e-59
Match length
                  113
% identity
                  96
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
                  402723
Seq. No.
                  LIB3431-055-P2-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3808101
BLAST score
                  211
E value
                  2.0e-26
Match length
                  95
% identity
                  74
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
                  402724
Seq. ID
                  LIB3431-055-P2-K1-H8
Method
                  BLASTN
NCBI GI
                  g2570512
BLAST score
                  51
                  2.0e-20
E value
                  55
Match length
% identity
                  98
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete
                  cds
Seq. No.
                  402725
                  LIB3431-056-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5690431
BLAST score
                  241
                  2.0e-20
E value
Match length
                  97
% identity
                  48
NCBI Description (AF165883) prefoldin subunit 2 [Homo sapiens]
                  402726
Seq. No.
                  LIB3431-056-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
```

Method BLASTX
NCBI GI g132105
BLAST score 609
E value 2.0e-63
Match length 131
% identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

Match length

% identity

107

53

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 402727 Seq. ID LIB3431-056-P1-K1-A11 Method BLASTX NCBI GI g1519251 BLAST score 673 E value 7.0e-71 Match length 150 % identity 91 NCBI Description (U65957) GF14-c protein [Oryza sativa] Seq. No. 402728 Seq. ID LIB3431-056-P1-K1-A2 Method BLASTX NCBI GI q3126854 BLAST score 488 E value 3.0e-49 Match length 114 % identity 85 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa] Seq. No. 402729 LIB3431-056-P1-K1-A3 Seq. ID Method BLASTN NCBI GI q4959460 BLAST score 36 E value 1.0e-10 Match length 36 % identity 100 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds Seq. No. 402730 LIB3431-056-P1-K1-A4 Seq. ID Method BLASTN NCBI GI q4959460 BLAST score 35 E value 6.0e-10 Match length 35 % identity 100 NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds 402731 Seq. No. Seq. ID LIB3431-056-P1-K1-A5 BLASTX Method NCBI GI g5734634 BLAST score 318 E value 3.0e-29



```
NCBI Description
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
                   sativa]
                   402732
Seq. No.
                  LIB3431-056-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3288821
BLAST score
                  259
E value
                  2.0e-47
                  110
Match length
                  87
% identity
```

(AF063901) alanine:glyoxylate aminotransferase; NCBI Description

transaminase [Arabidopsis thaliana]

>gi 4733989 gb AAD28669.1 AC007209 5 (AC007209)

alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

402733 Seq. No.

LIB3431-056-P1-K1-A8 Seq. ID

Method BLASTN NCBI GI g1245938 BLAST score 35 5.0e-10 E value Match length 35 100 % identity

rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, NCBI Description

heart atrium, mRNA, 2998 nt]

Seq. No. 402734

Seq. ID LIB3431-056-P1-K1-B1

BLASTX Method NCBI GI q132096 BLAST score 500 8.0e-60 E value Match length 125 % identity 94

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR

(RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6

ribulose-bisphosphate carboxylase ($\overline{\text{EC}}$ 4.1.1.39) small chain precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_

(D00644) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa]

Seq. No. 402735

LIB3431-056-P1-K1-B10 Seq. ID

Method BLASTX NCBI GI g4678311 BLAST score 272 6.0e-24 E value Match length 77 % identity 68

NCBI Description (AL049655) aquaporin/MIP-like protein [Arabidopsis

thaliana]

402736 Seq. No.

LIB3431-056-P1-K1-B11 Seq. ID

Method BLASTX NCBI GI g1076724



```
BLAST score 451
E value 4.0e-66
Match length 141
% identity 87
```

NCBI Description LHCI-680, photosystem I antenna protein - barley

>gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I

antenna protein [Hordeum vulgare]

Seq. No. 402737

Seq. ID LIB3431-056-P1-K1-B12

Method BLASTX
NCBI GI g3789952
BLAST score 652
E value 2.0e-68
Match length 132
% identity 96

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

satival

Seq. No. 402738

Seq. ID LIB3431-056-P1-K1-B2

Method BLASTN
NCBI GI g433216
BLAST score 115
E value 6.0e-58
Match length 118
% identity 99

NCBI Description Rice mRNA for ascorbate peroxidase (gene name SS622),

partial cds

Seq. No. 402739

Seq. ID LIB3431-056-P1-K1-B4

Method BLASTX
NCBI GI g1173347
BLAST score 326
E value 2.0e-39
Match length 103
% identity 87

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_(X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 402740

Seq. ID LIB3431-056-P1-K1-B6

Method BLASTX
NCBI GI g2407281
BLAST score 673
E value 6.0e-71
Match length 133
% identity 94

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 402741



```
LIB3431-056-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  193
                  1.0e-14
E value
                  35
Match length
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  402742
Seq. No.
                  LIB3431-056-P1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4585882
BLAST score
                  469
                  7.0e-51
E value
Match length
                  145
% identity
                  66
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  402743
Seq. No.
                  LIB3431-056-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2264373
BLAST score
                  355
E value
                  9.0e-34
Match length
                  103
% identity
                  63
NCBI Description
                  (AC002354) putative NAM/no apical meristem protein
                   [Arabidopsis thaliana]
                  402744
Seq. No.
Seq. ID
                  LIB3431-056-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g4079798
BLAST score
                  231
                  6.0e-30
E value
Match length
                  93
% identity
                  78
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  402745
Seq. No.
                  LIB3431-056-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885896
BLAST score
                  524
                  2.0e-53
E value
Match length
                  100
% identity
                  100
```

NCBI Description

402746

Seq. No. Seq. ID LIB3431-056-P1-K1-C12

Method BLASTX

51752

(AF093636) plastocyanin precursor [Oryza sativa]



NCBI GI g132105 BLAST score 537 E value 6.0e-55 Match length 111 % identity 91

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402747

Seq. ID LIB3431-056-P1-K1-C2

Method BLASTX
NCBI GI g2073375
BLAST score 459
E value 2.0e-54
Match length 110
% identity 90

NCBI Description (D85317) farnesyl pyrophosphate synthase [Oryza sativa]

>gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate

synthase [Oryza sativa]

Seq. No. 402748

Seq. ID LIB3431-056-P1-K1-C3

Method BLASTX
NCBI GI g417260
BLAST score 421
E value 3.0e-41
Match length 128
% identity 66

NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir \$33632

lir1 protein - rice >gi_20263_emb_CAA48706 (X68807)

light-regulated gene [Oryza sativa]

Seq. No. 402749

Seq. ID LIB3431-056-P1-K1-C4

Method BLASTX
NCBI GI g2407281
BLAST score 650
E value 3.0e-68
Match length 125
% identity 94

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 402750

Seq. ID LIB3431-056-P1-K1-C5

Method BLASTX
NCBI GI g2191151
BLAST score 170
E value 4.0e-17
Match length 87

BLAST score

E value

606

5.0e-63

```
% identity
NCBI Description
                  (AF007269) contains similarity to membrane associated
                  salt-inducible protein [Arabidopsis thaliana]
Seq. No.
                  402751
                  LIB3431-056-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  541
E value
                  2.0e-55
Match length
                  118
% identity
                  91
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  402752
Seq. ID
                  LIB3431-056-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q871931
BLAST score
                  416
E value
                  1.0e-40
Match length
                  108
% identity
                  78
NCBI Description (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  402753
                  LIB3431-056-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2688828
BLAST score
                  169
                  7.0e-12
E value
Match length
                  82
% identity
                  43
                  (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
NCBI Description
                  armeniaca]
Seq. No.
                  402754
Seq. ID
                  LIB3431-056-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  402755
Seq. ID
                  LIB3431-056-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q671740
```

51754



Match length 111 % identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 402756

Seq. ID LIB3431-056-P1-K1-D3

Method BLASTX
NCBI GI g1076660
BLAST score 219
E value 9.0e-20
Match length 126
% identity 45

NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122

(S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes,

leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 402757

Seq. ID LIB3431-056-P1-K1-D4

Method BLASTN
NCBI GI g6015437
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402758

Seq. ID LIB3431-056-P1-K1-D5

Method BLASTN
NCBI GI g218209
BLAST score 135
E value 9.0e-70
Match length 246
% identity 93

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

pOSSS2106

Seq. No. 402759

Seq. ID LIB3431-056-P1-K1-D6

Method BLASTX
NCBI GI g3738261
BLAST score 209
E value 9.0e-17
Match length 48
% identity 92

NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus

nigra]

Seq. No. 402760

Seq. ID LIB3431-056-P1-K1-D7

MethodBLASTXNCBI GIg320618BLAST score648E value6.0e-68



Match length 140 % identity 89

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 402761

Seq. ID LIB3431-056-P1-K1-D8

Method BLASTX
NCBI GI g3885892
BLAST score 557
E value 3.0e-57
Match length 104
% identity 100

NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.

402762

Seq. ID LIB3431-056-P1-K1-D9

Method BLASTN
NCBI GI g3885891
BLAST score 114
E value 2.0e-57
Match length 188
% identity 98

NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)

mRNA, complete cds

Seq. No. 402763

Seq. ID LIB3431-056-P1-K1-E1

Method BLASTX
NCBI GI g3789954
BLAST score 515
E value 2.0e-52
Match length 96
% identity 100

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 402764

Seq. ID LIB3431-056-P1-K1-E10

Method BLASTX
NCBI GI g1458245
BLAST score 261
E value 1.0e-22
Match length 130
% identity 44

NCBI Description (U64834) coded for by C. elegans cDNA cml7al; coded for by

C. elegans cDNA cm7g1; coded for by C. elegans cDNA

CEMSE26F; similar to methyltransferases [Caenorhabditis

elegans]

Seq. No. 402765

Seq. ID LIB3431-056-P1-K1-E11

Method BLASTX NCBI GI g1076724



BLAST score 581 E value 4.0e-60 Match length 121 % identity 86

NCBI Description LHCI-680, photosystem I antenna protein - barley

>gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I

antenna protein [Hordeum vulgare]

Seq. No. 402766

Seq. ID LIB3431-056-P1-K1-E12

Method BLASTX
NCBI GI g1084461
BLAST score 212
E value 5.0e-17
Match length 79
% identity 56

NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No. 402767

Seq. ID LIB3431-056-P1-K1-E2

Method BLASTX
NCBI GI g82080
BLAST score 336
E value 1.0e-32
Match length 113
% identity 68

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 402768

Seq. ID LIB3431-056-P1-K1-E4

Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 5.0e-12
Match length 38
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402769

Seq. ID LIB3431-056-P1-K1-E7

Method BLASTX
NCBI GI g5733872
BLAST score 457
E value 2.0e-45
Match length 119
% identity 74

NCBI Description (AC007932) Similar to gi_4982048 ribosomal protein L18 from

Thermotoga maritima genome gb_AE001798. ESTs gb_Z35613, gb_T75951, gb_T22182, gb_T45962, gb_H76281 and gb_AI100025

come from this gene. [Arabidopsis thaliana]

Seq. No. 402770

Seq. ID LIB3431-056-P1-K1-E9

Method BLASTX NCBI GI g3789952



```
BLAST score
                  2.0e-19
E value
Match length
                  44
                  100
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  402771
Seq. No.
                  LIB3431-056-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  636
                  2.0e-74
E value
Match length
                  142
% identity
                  95
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  402772
Seq. No.
                  LIB3431-056-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  605
E value
                  4.0e-63
Match length
                  117
% identity
                  95
NCBI Description
                 SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                  402773
Seq. No.
                  LIB3431-056-P1-K1-F12
Seq. ID
Method
                  BLASTX
                  g3913808
NCBI GI
BLAST score
                  477
                  6.0e-48
E value
Match length
                  102
% identity
                  88
NCBI Description
                  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
                  SYNTHETASE) >gi 2429618 dbj BAA22284 (AB007120)
                  ferrochelatase [Oryza sativa]
                  402774
Seq. No.
                  LIB3431-056-P1-K1-F2
Seq. ID
```

Method BLASTX NCBI GI q585350 BLAST score 384 E value 3.0e-37 Match length 109 % identity 68

NCBI Description CASEIN KINASE II, ALPHA CHAIN 2 (CK II)

>gi_419753_pir__S31099 casein kinase II (EC 2.7.1.-) alpha-type chain (clone ATCKA2) - Arabidopsis thaliana >gi_391605_dbj_BAA01091_ (D10247) casein kinase II

catalytic subunit [Arabidopsis thaliana]

Seq. No. 402775

Seq. ID LIB3431-056-P1-K1-F3

Method BLASTX
NCBI GI g115787
BLAST score 529
E value 4.0e-54
Match length 121
% identity 88

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 402776

Seq. ID LIB3431-056-P1-K1-F5

Method BLASTX
NCBI GI g2506826
BLAST score 328
E value 2.0e-30
Match length 90
% identity 74

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)

(PAPI) >gi_1619604_emb_CAA69949.1_ (Y08691) lipid transfer protein [Oryza sativa] >gi 1667590 (U77295) lipid transfer

protein [Oryza sativa]

Seq. No. 402777

Seq. ID LIB3431-056-P1-K1-F6

Method BLASTX
NCBI GI g5689238
BLAST score 341
E value 2.0e-32
Match length 73
% identity 86

NCBI Description (AB024292) histidine-containing phosphotransfer protein

[Zea mays]

Seq. No. 402778

Seq. ID LIB3431-056-P1-K1-F7

Method BLASTN
NCBI GI g2062705
BLAST score 37
E value 3.0e-11
Match length 37
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 402779

Seq. ID LIB3431-056-P1-K1-F9

Method BLASTX NCBI GI g4836892



```
BLAST score
                  2.0e-42
E value
                  138
Match length
% identity
                  58
NCBI Description
                  (AC007369) Putative RNA helicase [Arabidopsis thaliana]
                  402780
Seq. No.
                  LIB3431-056-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335349
BLAST score
                  416
E value
                  1.0e-40
Match length
                  155
% identity
                  54
NCBI Description
                  (AC004512) Similar to gb U46691 putative chromatin
                  structure regulator (SUPT6H) from Homo sapiens. ESTs
                  gb T42908, gb AA586170 and gb AA395125 come from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  402781
Seq. ID -
                  LIB3431-056-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g5326825
BLAST score
                  164
E value
                  3.0e-11
Match length
                  90
% identity
NCBI Description
                  (AF044953) NADH: ubiquinone oxidoreductase PGIV subunit
                  [Homo sapiens]
                  402782
Seq. No.
Seq. ID
                  LIB3431-056-P1-K1-G12
Method
                  BLASTX
                  g320618
NCBI GI
BLAST score
                  512
E value
                  4.0e-52
Match length
                  114
% identity
                  85
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  402783
                  LIB3431-056-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
```

237 BLAST score E value 1.0e-19 Match length 44 % identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402784



```
LIB3431-056-P1-K1-G3
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
                  532
BLAST score
E value
                  2.0e-54
Match length
                  117
                  86
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi 218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  402785
                  LIB3431-056-P1-K1-G4
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
                  292
BLAST score
                  2.0e-26
E value
                  73
Match length
                  74
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  402786
Seq. No.
                  LIB3431-056-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548605
BLAST score
                  588
E value
                  7.0e-61
Match length
                  130
% identity
                  90
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  402787
Seq. No.
                  LIB3431-056-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  526
                  7.0e-54
E value
Match length
                  105
```

% identity 97

HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock NCBI Description

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

402788 Seq. No.

Seq. ID LIB3431-056-P1-K1-G7

Method BLASTN



```
g1261857
NCBI GI
BLAST score
                  54
                  2.0e-21
E value
Match length
                  54
                  100
% identity
NCBI Description Rice CatA gene for catalase, complete cds
                  402789
Seq. No.
                  LIB3431-056-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678338
                  202
BLAST score
                  1.0e-15
E value
Match length
                  48
% identity
                  73
NCBI Description (AL049658) putative protein [Arabidopsis thaliana]
                  402790
Seq. No.
                  LIB3431-056-P1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3345476
BLAST score
                  132
E value
                  7.0e-68
Match length
                  241
% identity
                  96
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
Seq. No.
                  402791
Seq. ID
                  LIB3431-056-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g2570512
BLAST score
                  112
E value
                  3.0e-56
Match length
                  212
% identity
                  100
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete
                  cds
Seq. No.
                  402792
                  LIB3431-056-P1-K1-H12
Seq. ID
                                                              à. '
Method
                  BLASTN
NCBI GI
                  g20191
BLAST score
                  279
E value
                  1.0e-156
Match length
                  279
% identity
                  100
NCBI Description O.sativa mRNA for catalase
Seq. No.
                  402793
Seq. ID
                  LIB3431-056-P1-K1-H2
Method
                  BLASTX
```

g133867 NCBI GI BLAST score 558 E value 2.0e-57 124 Match length % identity 85

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal





protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
ribosomal protein S11 [Zea mays]

Seq. No. 402794

Seq. ID LIB3431-056-P1-K1-H3

Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 5.0e-12
Match length 38
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 402795

Seq. ID LIB3431-056-P1-K1-H4

Method BLASTX
NCBI GI g2624326
BLAST score 294
E value 8.0e-27
Match length 61
% identity 93

NCBI Description (AJ002893) OsGRP1 [Oryza sativa]

Seq. No. 402796

Seq. ID LIB3431-056-P1-K1-H5

Method BLASTX
NCBI GI g1173347
BLAST score 663
E value 9.0e-70
Match length 129
% identity 95

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_(X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 402797

Seq. ID LIB3431-056-P1-K1-H6

Method BLASTX
NCBI GI g3128206
BLAST score 143
E value 2.0e-09
Match length 47
% identity 45

NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No. 402798

Seq. ID LIB3431-056-P1-K1-H9

Method BLASTX
NCBI GI g132105
BLAST score 547
E value 4.0e-56
Match length 119
% identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 402799 Seq. ID LIB3431-056-P1-N1-A10 Method BLASTX NCBI GI g671740 BLAST score 443 E value 7.0e-44 Match length 80 % identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 402800

Seq. ID LIB3431-056-P1-N1-A11

Method BLASTN
NCBI GI g2331130
BLAST score 100
E value 8.0e-49
Match length 148
% identity 92

NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete

cds

Seq. No. 402801

Seq. ID LIB3431-056-P1-N1-A12

Method BLASTX
NCBI GI g131225
BLAST score 203
E value 7.0e-16
Match length 71
% identity 58

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi 167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 402802

Seq. ID LIB3431-056-P1-N1-A2

Method BLASTX
NCBI GI g3126854
BLAST score 349
E value 9.0e-33
Match length 66
% identity 100

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.

Seq. ID LIB3431-056-P1-N1-A6

402803

Method BLASTX

```
q2754849
NCBI GI
BLAST score
                  284
E value
                  3.0e-25
Match length
                  63
% identity
                  87
NCBI Description
                  (AF039000) putative serine-glyoxylate aminotransferase
                  [Fritillaria agrestis]
Seq. No.
                  402804
Seq. ID
                  LIB3431-056-P1-N1-B1
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  234
                  2.0e-19
E value
Match length
                  47
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  402805
Seq. ID
                  LIB3431-056-P1-N1-B10
Method
                  BLASTX
NCBI GI
                  g886100
BLAST score
                  265
E value
                  6.0e-23
Match length
                  63
% identity
                  (U27347) putative water channel protein; plasmalemma
NCBI Description
                  intrinsic protein; similar to Arabidopsis Pip2a gene
                  product, PIR Accession Number S44084 [Glycine max]
Seq. No.
                  402806
                  LIB3431-056-P1-N1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076724
BLAST score
                  477
E value
                  8.0e-48
Match length
                  90
% identity
                  96
NCBI Description
                  LHCI-680, photosystem I antenna protein - barley
                  >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
                  402807
Seq. No.
                  LIB3431-056-P1-N1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789952
BLAST score
                  269
                  2.0e-23
E value
```

Match length 51 % identity 100

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

402808 Seq. No.

Seq. ID LIB3431-056-P1-N1-B3

Method BLASTN

51765



```
NCBI GI g304219
BLAST score 51
E value 1.0e-19
Match length 71
% identity 93
NCBI Description Hordeum
```

NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit

mRNA, complete cds

Seq. No. 402809

Seq. ID LIB3431-056-P1-N1-B4

Method BLASTX
NCBI GI g1173347
BLAST score 405
E value 2.0e-39
Match length 86
% identity 97

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_(X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 402810

Seq. ID LIB3431-056-P1-N1-B6

Method BLASTX
NCBI GI g671740
BLAST score 301
E value 3.0e-27
Match length 57
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 402811

Seq. ID LIB3431-056-P1-N1-B7

Method BLASTN
NCBI GI g2072554
BLAST score 269
E value 1.0e-150
Match length 269
% identity 100

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 402812

Seq. ID LIB3431-056-P1-N1-B8

Method BLASTX
NCBI GI g115813
BLAST score 165
E value 2.0e-11
Match length 38
% identity 79

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi 19182 emb CAA33330 (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

```
Seq. No.
                  402813
                  LIB3431-056-P1-N1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  414
                  2.0e-40
E value
Match length
                  81
                  99
% identity
NCBI Description
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  402814
Seq. No.
                  LIB3431-056-P1-N1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885896
BLAST score
                  524
E value
                  2.0e-53
Match length
                  100
                  100
% identity
                  (AF093636) plastocyanin precursor [Oryza sativa]
NCBI Description
                  402815
Seq. No.
                  LIB3431-056-P1-N1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                  37
E value
                  3.0e-11
Match length
                  53
% identity
                  92
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
                  402816
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-C2
Method
                  BLASTX
NCBI GI
                  g2073375
BLAST score
                  576
                  2.0e-59
E value
Match length
                  107
% identity
                  100
NCBI Description
                  (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
                  >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate
                  synthase [Oryza sativa]
Seq. No.
                  402817
                  LIB3431-056-P1-N1-C3
Seq. ID
```

Method BLASTX
NCBI GI g417260
BLAST score 321
E value 1.0e-29
Match length 106
% identity 61

NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632

lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)

light-regulated gene [Oryza sativa]



```
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-C4
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  361
E value
                  3.0e-34
Match length
                  70
                  97
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  402819
Seq. ID
                  LIB3431-056-P1-N1-C6
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  599
E value
                  5.0e-62
Match length.
                  131
% identity
                  91
                 PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
Seq. No.
                  402820
                  LIB3431-056-P1-N1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g871931
BLAST score
                  161
                  5.0e-11
E value
Match length
                  44
                  75
% identity
NCBI Description (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  402821
Seq. ID
                  LIB3431-056-P1-N1-D1
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  228
E value
                  1.0e-18
Match length
                  42
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  402822
Seq. ID
                  LIB3431-056-P1-N1-D12
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  433
```

1.0e-42 E value Match length 78 % identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]



Seq. No. 402823

Seq. ID LIB3431-056-P1-N1-D3

Method BLASTX
NCBI GI g1076660
BLAST score 222
E value 6.0e-18
Match length 89
% identity 57

NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122

(S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes,

leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 402824

Seq. ID LIB3431-056-P1-N1-D5

Method BLASTN
NCBI GI g218209
BLAST score 39
E value 2.0e-12
Match length 55
% identity 93

NCBI Description Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

posss2106

Seq. No. 402825

Seq. ID LIB3431-056-P1-N1-D7

Method BLASTX
NCBI GI g115787
BLAST score 409
E value 6.0e-40
Match length 77
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi 20182 emb CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 402826

Seq. ID LIB3431-056-P1-N1-D8

Method BLASTX
NCBI GI g3885892
BLAST score 544
E value 9.0e-56
Match length 102
% identity 100

NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No. 402827

Seq. ID LIB3431-056-P1-N1-D9

Method BLASTX
NCBI GI g3885892
BLAST score 286
E value 2.0e-25
Match length 57

- 1. ·

```
% identity
NCBI Description
                 (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                  402828
                  LIB3431-056-P1-N1-E1
Seq. ID
                  BLASTX
Method
                  q3789954
NCBI GI
BLAST score
                  611
                  2.0e-63
E value
Match length
                  113
% identity
                  100
                 (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  402829
Seq. ID
                  LIB3431-056-P1-N1-E11
Method
                  BLASTX
NCBI GI
                  q1076724
BLAST score
                  374
E value
                  8.0e-36
Match length
                  72
% identity
                  94
NCBI Description LHCI-680, photosystem I antenna protein - barley
                  >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  402830
                  LIB3431-056-P1-N1-E12
Seq. ID
Method
                  BLASTX
                  g1084461
NCBI GI
BLAST score
                  287
E value
                  1.0e-25
                  98
Match length
% identity
                  60
NCBI Description RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                  402831
                  LIB3431-056-P1-N1-E2
Seq. ID
Method
                  BLASTX -
NCBI GI
                  g115813
                  234
BLAST score
E value
                  2.0e-19
                  56
Match length
                  80
% identity
                 CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  402832
Seq. No.
                  LIB3431-056-P1-N1-E7
Seq. ID
Method
                  BLASTX
                  g5733872
NCBI GI
BLAST score
                  182
                  2.0e-13
E value
Match length
                  57
% identity
                  60
NCBI Description (AC007932) Similar to gi 4982048 ribosomal protein L18 from
```

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Thermotoga maritima genome gb AE001798. ESTs gb Z35613, gb_T75951, gb_T22182, gb_T45962, gb_H76281 and gb_AI100025

402833 Seq. No.

LIB3431-056-P1-N1-E8 Seq. ID

Method BLASTX NCBI GI q6093830 BLAST score 218 2.0e-17 E value Match length 97 51 % identity

PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) NCBI Description

come from this gene. [Arabidopsis thaliana]

[CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;

putative photosytem II peptide [Spinacia oleracea]

402834 Seq. No.

LIB3431-056-P1-N1-E9 Seq. ID

Method BLASTN g3789951 NCBI GI BLAST score 127 6.0e-65 E value 372 Match length 91 % identity

Oryza sativa chlorophyll a/b-binding protein presursor NCBI Description

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

402835 Seq. No.

LIB3431-056-P1-N1-F1 Seq. ID

Method BLASTX NCBI GI q115772 273 BLAST score 5.0e-24 E value Match length 57

91 % identity

CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I NCBI Description

CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding

protein 1R precursor - rice >gi_20178_emb_CAA32108

(X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)

[Oryza sativa]

Seq. No.

402836

LIB3431-056-P1-N1-F10 Seq. ID

Method BLASTX NCBI GI q1173347 BLAST score 401 6.0e-39 E value Match length 85 % identity 96

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

> (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

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402837
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  g2244734
BLAST score
                  166
                  2.0e-11
E value
Match length
                  32
% identity
                  97
                  (D88414) actin [Gossypium hirsutum]
NCBI Description
                  402838
Seq. No.
                  LIB3431-056-P1-N1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585350
BLAST score
                  496
                  5.0e-50
E value
Match length
                  110
% identity
                  83
NCBI Description
                  CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
                  >gi 419753 pir S31099 casein kinase II (EC 2.7.1.-)
                  alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
                  >gi_391605_dbj_BAA01091_ (D10247) casein kinase II
                  catalytic subunit [Arabidopsis thaliana]
Seq. No.
                  402839
Seq. ID
                  LIB3431-056-P1-N1-F3
Method
                  BLASTX
NCBI GI
                  q3036951
BLAST score
                  427
E value
                  6.0e-42
Match length
                  80
                  100
% identity
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
                  402840
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-F5
Method
                  BLASTN
                  g1619603
NCBI GI
BLAST score
                  370
                  0.0e + 00
E value
Match length
                  414
                  97
% identity
NCBI Description
                  O.sativa mRNA for lipid transfer protein
                  >gi_1667589_gb_U77295_OSU77295 Oryza sativa lipid transfer .
                  protein (LTP) mRNA, complete cds
                  402841
Seq. No.
                  LIB3431-056-P1-N1-F9
Seq. ID
Method
                  BLASTX
                  q2673917
NCBI GI
BLAST score
                  305
                  1.0e-27
E value
Match length
                  80
% identity
                  66
NCBI Description (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
```



thaliana]

402842 Seq. No. LIB3431-056-P1-N1-G1 Seq. ID Method BLASTX q3335349 NCBI GI BLAST score 170 5.0e-12 E value Match length 108 38 % identity NCBI Description (AC004512) Similar to gb_U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb T42908, gb AA586170 and gb AA395125 come from this gene. [Arabidopsis thaliana] 402843 Seq. No. LIB3431-056-P1-N1-G10 Seq. ID Method BLASTX NCBI GI g5326825 BLAST score 153 8.0e-10 E value Match length 87 31 % identity (AF044953) NADH: ubiquinone oxidoreductase PGIV subunit NCBI Description [Homo sapiens] Seq. No. 402844 LIB3431-056-P1-N1-G11 Seq. ID Method BLASTX NCBI GI q136640 BLAST score 514 E value 3.0e-52 Match length 102 93 % identity NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720) ubiquitin carrier protein [Triticum aestivum] Seq. No. 402845 Seq. ID LIB3431-056-P1-N1-G12 Method BLASTN g20177 NCBI GI BLAST score 204 1.0e-111 E value Match length 219 % identity 99 Rice cab1R gene for light harvesting chlorophyll NCBI Description a/b-binding protein Seq. No. 402846 Seq. ID LIB3431-056-P1-N1-G2 Method BLASTX NCBI GI q2072555 BLAST score 228

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1.0e-18

42

100

E value

Match length

% identity

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa]

Seq. No. 402847

Seq. ID LIB3431-056-P1-N1-G3

Method BLASTX
NCBI GI g115787
BLAST score 676
E value 4.0e-71
Match length 130
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 402848

Seq. ID LIB3431-056-P1-N1-G4

Method BLASTX
NCBI GI g3036951
BLAST score 650
E value 4.0e-68
Match length 124
% identity 98

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No. 402849

Seq. ID LIB3431-056-P1-N1-G5

Method BLASTX
NCBI GI g548605
BLAST score 301
E value 2.0e-27
Match length 64
% identity 92

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 402850

Seq. ID LIB3431-056-P1-N1-G6

Method BLASTX
NCBI GI g417154
BLAST score 392
E value 7.0e-38
Match length 93
% identity 85

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 402851

Match length

96

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LIB3431-056-P1-N1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006881
BLAST score
                  585
E value
                  2.0e-60
Match length
                  139
% identity
                  79
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                  402852
                  LIB3431-056-P1-N1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3345476
BLAST score
                  342
E value
                  0.0e + 00
Match length
                  386
% identity
                  97
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                  402853
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-H2
Method
                  BLASTN
NCBI GI
                  g22469
BLAST score
                  34
E value
                  1.0e-09
Match length
                  38
% identity
                  97
NCBI Description Maize mRNA for cytoplasmic ribosomal protein S11
Seq. No.
                  402854
                  LIB3431-056-P1-N1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g14264
BLAST score
                  67
                  3.0e-29
E value
Match length
                  115
% identity
                  90
NCBI Description T.aestivum gene for sedoheptulose-1,7-bisphoshatase
Seq. No.
                   402855
                  LIB3431-056-P1-N1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  546
                   6.0e-56
E value
Match length
                   99
% identity
                  100
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                   402856
Seq. ID
                  LIB3431-058-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q3355468
BLAST score
                  355
E value
                  1.0e-33
```

```
% identity
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  402857
                  LIB3431-058-P1-K1-A10
Seq. ID
Method
                  BLASTX
                  g2244749
NCBI GI
BLAST score
                  383
E value
                  7.0e-37
Match length
                  112
% identity
                  66
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
                  402858
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  214
E value
                  4.0e-17
Match length
                  41
% identity
                  95
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                  402859
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-A2
Method
                  BLASTX
NCBI GI
                   g1514643
BLAST score
                  180
                   4.0e-26
E value
                  102
Match length
% identity
                   63
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                   402860
Seq. No.
                  LIB3431-058-P1-K1-A3
Seq. ID
Method
                  BLASTN
                   g1159878
NCBI GI
                   52
BLAST score
E value
                   3.0e-20
Match length
                   64
                   95
% identity
NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF2)
                   402861
Seq. No.
                   LIB3431-058-P1-K1-A4
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g2072555
BLAST score 165
E value 3.0e-11
Match length 32
% identity 94

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441 gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402862

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LIB3431-058-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462760
BLAST score
                  143
                  8.0e-09
E value
Match length
                  75
                  39
% identity
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402863
                  LIB3431-058-P1-K1-A6
Seq. ID
Method
                  BLASTX
                  g3402713
NCBI GI
BLAST score
                  379
E value
                  2.0e-36
Match length
                  123
% identity
                  60
                 (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402864
Seq. ID
                  LIB3431-058-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  494
                  6.0e-50
E value
Match length
                  109
% identity
                  83
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208 dbj_BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  402865
Seq. ID
                  LIB3431-058-P1-K1-A8
Method
                  BLASTX
                  g3046693
NCBI GI
BLAST score
                  573
E value
                  3.0e-59
Match length
                  136
% identity
                  (AL022140) receptor like protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  402866
```

Seq. ID LIB3431-058-P1-K1-A9

Method BLASTX
NCBI GI g3550983
BLAST score 358
E value 5.0e-34
Match length 98
% identity 68

NCBI Description (AB010690) mutM homologue-2 [Arabidopsis thaliana]

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>gi_3820622 (AF099971) putative formamidopyrimidine-DNA glycosylase 2 [Arabidopsis thaliana] >gi_5903054_gb_AAD55613.1_AC008016_23 (AC008016) Identical to gb_AB010690 mutM homologue-2 (formamidopyrimidine-DNA glycosylase 1) from Arabidopsis thaliana. EST gb_Z18192 comes from this gene

402867 Seq. No. LIB3431-058-P1-K1-B10 Seq. ID Method BLASTX g3885886 NCBI GI 748 BLAST score 1.0e-79 E value Match length 144 % identity 100

NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 402868

Seq. ID LIB3431-058-P1-K1-B11

Method BLASTX
NCBI GI g2582381
BLAST score 458
E value 4.0e-46
Match length 87
% identity 93

NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana

tabacum]

Seq. No. 402869

Seq. ID LIB3431-058-P1-K1-B12

Method BLASTX
NCBI GI g2570511
BLAST score 485
E value 5.0e-49
Match length 92
% identity 99

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 402870

Seq. ID LIB3431-058-P1-K1-B2

Method BLASTX
NCBI GI g3850566
BLAST score 236
E value 1.0e-22
Match length 156
% identity 40

NCBI Description (AC005278) F15K9.3 [Arabidopsis thaliana]

Seq. No. 402871

Seq. ID LIB3431-058-P1-K1-B3

Method BLASTN
NCBI GI g5730046
BLAST score 35
E value 3.0e-10
Match length 35
% identity 100

NCBI Description Homo sapiens solute carrier family 17 (sodium phosphate),



member 3 (SLC17A3) mRNA >gi_2062691_gb_U90545_HSU90545 Human sodium phosphate transporter (NPT4) mRNA, complete cds

 Seq. No.
 402872

 Seq. ID
 LIB3431-058-P1-K1-B5

 Method
 BLASTX

 NCBI GI
 g430947

 BLAST score
 360

 E value
 3.0e-34

 Match length
 102

 % identity
 71

% identity 71
NCBI Description (U01103) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 402873

 Seq. ID
 LIB3431-058-P1-K1-B6

 Method
 BLASTX

 NCBI GI
 g132105

 BLAST score
 468

 E value
 4.0e-52

 Match length
 101

Match length 101 % identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >qi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402874

Seq. ID LIB3431-058-P1-K1-B7

Method BLASTX
NCBI GI g21839
BLAST score 734
E value 5.0e-78
Match length 148
% identity 93

NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 402875

Seq. ID LIB3431-058-P1-K1-B8

Method BLASTX
NCBI GI g82080
BLAST score 152
E value 4.0e-10
Match length 68
% identity 51

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi_226872_prf__1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 402876

Seq. ID LIB3431-058-P1-K1-B9



```
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  588
E value
                  5.0e-61
Match length
                  108
                  100
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
Seq. No.
                  402877
                  LIB3431-058-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191138
BLAST score
                  310
E value
                  3.0e-28
Match length
                  136
```

% identity 53
NCBI Description (AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

 Seq. No.
 402878

 Seq. ID
 LIB3431-058-P1-K1-C10

 Method
 BLASTX

NCBI GI g1001355
BLAST score 228
E value 7.0e-19
Match length 119
% identity 42

NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

Seq. No. 402879

Seq. ID LIB3431-058-P1-K1-C12

Method BLASTN
NCBI GI g606816
BLAST score 229
E value 1.0e-126
Match length 229
% identity 100

NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete

cds

Seq. No. 402880

Seq. ID LIB3431-058-P1-K1-C2

Method BLASTX
NCBI GI g1698548
BLAST score 664
E value 8.0e-70
Match length 155
% identity 78

NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No. 402881

Seq. ID LIB3431-058-P1-K1-C3

Method BLASTN
NCBI GI g2570512
BLAST score 283
E value 1.0e-158



Match length 367 % identity 94

NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete

cds

Seq. No. 402882

Seq. ID LIB3431-058-P1-K1-C4

Method BLASTN
NCBI GI g3789951
BLAST score 66
E value 1.0e-28
Match length 162
% identity 85

NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 402883

Seq. ID LIB3431-058-P1-K1-C5

Method BLASTX
NCBI GI g4678949
BLAST score 517
E value 1.0e-52
Match length 123
% identity 79

NCBI Description (AL049711) dihydrolipoamide S-acetyltransferase precursor

[Arabidopsis thaliana]

Seq. No. 402884

Seq. ID LIB3431-058-P1-K1-C6

Method BLASTX
NCBI GI g4531444
BLAST score 482
E value 2.0e-48
Match length 142
% identity 66

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 402885

Seq. ID LIB3431-058-P1-K1-C7

Method BLASTX
NCBI GI g1421730
BLAST score 753
E value 3.0e-80
Match length 146
% identity 95

NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 402886

Seq. ID LIB3431-058-P1-K1-C8

Method BLASTX
NCBI GI g1698548
BLAST score 302
E value 2.0e-32
Match length 131
% identity 54

NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

```
Seq. No.
                  402887
                  LIB3431-058-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5816996
BLAST score
                  325
                  4.0e-30
E value
Match length
                  88
% identity
                  73
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  402888
Seq. No.
                  LIB3431-058-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587563
BLAST score
                  301
                  2.0e-27
E value
Match length
                  81
                  77
% identity
                  (AC006550) Similar to gb U51990 pre-mRNA-splicing factor
NCBI Description
                  hPrp18 from Homo sapiens. ESTs gb T46391 and gb AA721815
                  come from this gene. [Arabidopsis thaliana]
                  402889
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  38
                  7.0e-12
E value
Match length
                  50
                  67
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  402890
Seq. No.
                  LIB3431-058-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115796
BLAST score
                  482
                  4.0e-55
E value
Match length
                  112
% identity
                  96
                  CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB) (LHCP) >gi 218174 dbj BAA00537 (D00642) type II
                  light-harvesting chlorophyll a/b-binding protein [Oryza
                  sativa]
                  402891
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q6016151
BLAST score
                  492
E value
                  9.0e-50
Match length
                  128
```

IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT SHOCK PROTEIN 70 HOMOLOG 3) >gi_1575130 (U58209) lumenal

77

% identity

NCBI Description



binding protein cBiPe3 [Zea mays]

```
Seq. No.
                  402892
Seq. ID
                  LIB3431-058-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g15961
BLAST score
                  259
                  3.0e-22
E value
                  92
Match length .
% identity
                  48
NCBI Description
                  (Z12621) precursor alliinase [Allium cepa]
                  402893
Seq. No.
                  LIB3431-058-P1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4097337
BLAST score
                  304
E value
                  1.0e-170
Match length
                  368
                  99
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  402894
Seq. No.
                  LIB3431-058-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707998
BLAST score
                  510
                  6.0e-52
E value
Match length
                  117
% identity
                  85
NCBI Description
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >qi 481944 pir S40218 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - potato
                  >gi 438247 emb CAA81082 (Z25863) glycine
                  hydroxymethyltransferase [Solanum tuberosum]
                  402895
Seq. No.
                  LIB3431-058-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  564
                  3.0e-58
E value
Match length
                  110
                  99
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  402896
                  LIB3431-058-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130043
BLAST score
                  600
                  3.0e-62
E value
Match length
                  145
% identity
                  82
```



(U26545) Mg-chelatase subunit [Hordeum vulgare]

```
Seq. No.
                  402897
Seq. ID
                  LIB3431-058-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  679
E value
                  1.0e-71
                  152
Match length
                  89
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  402898
Seq. ID
                  LIB3431-058-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q482311
BLAST score
                  551
                  8.0e-57
E value
                  109
Match length
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  402899
Seq. ID
                  LIB3431-058-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g20243
BLAST score
                  145
E value
                  1.0e-75
Match length
                  169
% identity
                  95
NCBI Description O.sativa GP28 gene (partial)
                  402900
Seq. No.
                  LIB3431-058-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q543711
BLAST score
                  191
                  2.0e-18
E value
Match length
                  86
                  70
% identity
                  14-3-3-LIKE PROTEIN S94 >gi 419796 pir S30927 14-3-3
NCBI Description
                  protein homolog - rice >gi 303859 dbj BAA03711 (D16140)
                  brain specific protein [Oryza sativa]
                  402901
Seq. No.
                  LIB3431-058-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  479
E value
                  3.0e-48
Match length
                  109
```

% identity NCBI Description

85

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No.

402902

Seq. ID

LIB3431-058-P1-K1-E5

Method BLASTX
NCBI GI g132105
BLAST score 372
E value 8.0e-36
Match length 90
% identity 82

NCBI Description

on RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No.

402903

Seq. ID

LIB3431-058-P1-K1-E7

Method BLASTX
NCBI GI g2570511
BLAST score 244
E value 7.0e-21
Match length 86
% identity 57

NCBI Description

escription (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.

402904

Seq. ID

LIB3431-058-P1-K1-E8

Method BLASTX
NCBI GI g132105
BLAST score 396
E value 2.0e-59
Match length 133
% identity 86
NCBI Description RIBULOS

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

51785

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Seq. No.

Seq. ID

402910

LIB3431-058-P1-K1-F9



```
402905
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2245020
BLAST score
                  212
E value
                  7.0e-17
Match length
                  137
% identity
                  40
NCBI Description
                  (Z97341) growth regulator like protein [Arabidopsis
                  402906
Seq. No.
                  LIB3431-058-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885894
BLAST score
                  447
E value
                  2.0e-44
Match length
                  101
% identity
                  87
NCBI Description
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
                  402907
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  313
E value
                  3.0e-43
Match length
                  107
% identity
                  88
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thil-1
                  - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  402908
Seq. ID
                  LIB3431-058-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2924520
BLAST score
                  486
E value
                  6.0e-49
Match length
                  151
% identity
                  63
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  402909
Seq. ID
                  LIB3431-058-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  713
E value
                  1.0e-75
Match length
                  133
% identity
                  98
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```



```
BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  34
E value
                  2.0e-09
Match length
                  34
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  402911
Seq. No.
                  LIB3431-058-P1-K1-G1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20262
BLAST score
                  300
E value
                  1.0e-168
Match length
                  328
% identity
                  98
NCBI Description O.sativa light-induced mRNA
                  402912
Seq. No.
                  LIB3431-058-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4581207
BLAST score
                  570
E value
                  6.0e-61
Match length
                  145
% identity
                  81
NCBI Description (Y17914) cyclic nucleotide and calmodulin-regulated ion
                  channel [Arabidopsis thaliana]
                  402913
Seq. No.
                  LIB3431-058-P1-K1-G12
Seq. ID
Method
                  BLASTX
                  g417260
NCBI GI
BLAST score
                  416
E value
                  1.0e-40
Match length
                  127
% identity
                  66
                  LIGHT REGULATED PROTEIN PRECURSOR >qi 422003 pir $33632
NCBI Description
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  402914
                  LIB3431-058-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538934
BLAST score
                  275
                  4.0e-24
E value
Match length
                  102
% identity
                  53
NCBI Description
                  (AL049483) putative leucine-rich-repeat protein
```

[Arabidopsis thaliana]

402915 Seq. No.

Seq. ID LIB3431-058-P1-K1-G4

Method BLASTN NCBI GI g3885891 BLAST score 118



9.0e-60 E value Match length 163 % identity 99

NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)

mRNA, complete cds

Seq. No. 402916

LIB3431-058-P1-K1-G5 Seq. ID

Method BLASTX NCBI GI g2407279 BLAST score 277 E value 6.0e-25 Match length 78 71 % identity

NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 402917

Seq. ID LIB3431-058-P1-K1-G7

Method BLASTX NCBI GI q136636 BLAST score 197 E value 9.0e-20 Match length 54 % identity

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >qi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >qi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 402918

LIB3431-058-P1-K1-G9 Seq. ID

Method BLASTX NCBI GI g3004565 BLAST score 230 E value 6.0e-25 Match length 143 % identity 48

(AC003673) putative protein kinase [Arabidopsis thaliana] NCBI Description

Seq. No.

402919

LIB3431-058-P1-K1-H11 Seq. ID

Method BLASTX NCBI GI g132105 BLAST score 550 E value 2.0e-56 Match length 113 % identity 91

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

402920 Seq. No. LIB3431-058-P1-K1-H12 Seq. ID Method BLASTX NCBI GI q5916444 BLAST score 240 E value 4.0e-20 Match length 120 % identity 40

NCBI Description (AC007633) putative protein [Arabidopsis thaliana]

Seq. No. 402921

Seq. ID LIB3431-058-P1-K1-H2

Method BLASTX NCBI GI q3789954 BLAST score 607 E value 3.0e-63 Match length 120 % identity

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 402922

Seq. ID LIB3431-058-P1-K1-H6

Method BLASTX NCBI GI q4585882 BLAST score 446 E value 2.0e-44 Match length 117 % identity 74

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 402923

LIB3431-058-P1-K1-H8 Seq. ID

Method BLASTX NCBI GI q132105 BLAST score 455 E value 2.0e-45 Match length 106 % identity 84

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

carboxylase S [Oryza sativa]

402924 Seq. No.

LIB3431-058-P1-K1-H9 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  585
E value
                  1.0e-60
Match length
                  118
                  100
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  402925
Seq. No.
Seq. ID
                  LIB3431-058-P1-N1-A1
Method
                  BLASTX
NCBI GI
                  g3355468
BLAST score
                  324
E value
                  2.0e-38
Match length
                  106
% identity
                  85
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
                  402926
Seq. No.
                  LIB3431-058-P1-N1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2274988
BLAST score
                  281
E value
                  8.0e-25
Match length
                  96
% identity
                  55
NCBI Description
                  (AJ000226) partial sequence, homology to serine
                  hydroxymethyltransferases [Hordeum vulgare]
                  402927
Seq. No.
                  LIB3431-058-P1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g517500
BLAST score
                  311
E value
                  1.0e-28
Match length
                  77
% identity
                  81
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  402928
Seq. ID
                  LIB3431-058-P1-N1-A12
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  216
                  2.0e-17
E value
```

Match length 40 % identity 100

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.

Seq. ID LIB3431-058-P1-N1-A2

402929

Method BLASTX

```
g1514643
NCBI GI
BLAST score
                  168
                  3.0e-26
E value
                  144
Match length
                  45
% identity
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
                  402930
Seq. No.
                  LIB3431-058-P1-N1-A3
Seq. ID
                  BLASTN
```

Method g1159878 NCBI GI 50 BLAST score 7.0e-19 E value Match length 82

% identity 90

NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF2)

402931 Seq. No.

LIB3431-058-P1-N1-A4 Seq. ID

Method BLASTN g2072554 NCBI GI BLAST score 313 1.0e-175 E value 313 Match length % identity 100

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

402932 Seq. No.

LIB3431-058-P1-N1-A5 Seq. ID

Method BLASTN NCBI GI g2570510 131 BLAST score 2.0e-67 E value Match length 267 88 % identity

NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete

402933 Seq. No.

LIB3431-058-P1-N1-A7 Seq. ID

Method BLASTX NCBI GI g671740 BLAST score 431 E value 2.0e-42 Match length 80 % identity 96

(X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description

construct]

Seq. No. 402934

LIB3431-058-P1-N1-B10 Seq. ID

Method BLASTX NCBI GI q3885886 244 BLAST score E value 1.0e-22 Match length



% identity 86
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No. 402935
Seq. ID LIB3431-058-P1-N1-B11

Method BLASTX
NCBI GI g2582381
BLAST score 144
E value 1.0e-08
Match length 31
% identity 87

NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana

tabacum]

Seq. No. 402936

Seq. ID LIB3431-058-P1-N1-B12

Method BLASTX
NCBI GI g115793
BLAST score 396
E value 2.0e-38
Match length 78
% identity 95

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR

(CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein

type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum

vulgare]

Seq. No. 402937

Seq. ID LIB3431-058-P1-N1-B2

Method BLASTX
NCBI GI g3924605
BLAST score 227
E value 8.0e-19
Match length 53
% identity 72

NCBI Description (AF069442) putative inhibitor of apoptosis [Arabidopsis

thaliana]

Seq. No. 402938

Seq. ID LIB3431-058-P1-N1-B5

Method BLASTX
NCBI GI g115813
BLAST score 201
E value 2.0e-15
Match length 46
% identity 83

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi 19182 emb CAA33330 (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402939

Seq. ID LIB3431-058-P1-N1-B6

Method BLASTX
NCBI GI 94038663
BLAST score 282
E value 4.0e-38



84

Match length 77 % identity

(AB020929) ribulose-1,5-bisphosphate carboxylase/oxygenase NCBI Description

small subunit [Aegilops speltoides]

Seq. No.

402940 LIB3431-058-P1-N1-B7 Seq. ID

Method BLASTN NCBI GI g21838 BLAST score 67 3.0e-29 E value Match length 207

NCBI Description T.aestivum PRK gene for ribulose-5-phosphate kinase

Seq. No.

% identity

402941

LIB3431-058-P1-N1-B8 Seq. ID Method BLASTX NCBI GI q115813 BLAST score 265 E value 6.0e-23

Match length 97 % identity 61

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III

CAB-8) >gi 19182 emb CAA33330 (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 402942

LIB3431-058-P1-N1-B9 Seq. ID

Method BLASTX NCBI GI q132105 BLAST score 396 E value 2.0e-38 Match length 73 99 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402943

Seq. ID LIB3431-058-P1-N1-C1

Method BLASTX NCBI GI g2191138 390 BLAST score 1.0e-37 E value Match length 91 % identity 78

(AF007269) A IG002N01.18 gene product [Arabidopsis NCBI Description

thaliana]

Seq. No. 402944



```
LIB3431-058-P1-N1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3345476
BLAST score
                  86
                  1.0e-40
E value
                  220
Match length
                  83
% identity
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                  402945
Seq. No.
                  LIB3431-058-P1-N1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g483410
BLAST score
                  216
                  1.0e-21
E value
                  76
Match length
                  79
% identity
                 (L01496) calmodulin-binding protein [Zea mays]
NCBI Description
                  402946
Seq. No.
                  LIB3431-058-P1-N1-C3
Seq. ID
Method
                  BLASTX
                  g115802
NCBI GI
BLAST score
                  249
E value
                  3.0e-21
Match length
                  48
                  98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-36) (LHCP) >gi 100311 pir S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
                  402947
Seq. No.
Seq. ID
                  LIB3431-058-P1-N1-C4
Method
                  BLASTN
NCBI GI
                  g3789951
BLAST score
                  153
                  2.0e-80
E value
Match length
                  233
% identity
                  92
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  402948
Seq. No.
                  LIB3431-058-P1-N1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678949
BLAST score
                  428
E value
                  5.0e-42
```

Match length 104 % identity

NCBI Description (AL049711) dihydrolipoamide S-acetyltransferase precursor

[Arabidopsis thaliana]

402949 Seq. No.



```
LIB3431-058-P1-N1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5816996
BLAST score
                  514
                  4.0e-52
E value
Match length
                  116
% identity
                  85
NCBI Description
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  402950
                  LIB3431-058-P1-N1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  264
                  7.0e-23
E value
Match length
                  71
% identity
                  68
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  402951
Seq. No.
                  LIB3431-058-P1-N1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  249
E value
                  9.0e-38
Match length
                  85
% identity
                  96
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  402952
Seq. No.
                  LIB3431-058-P1-N1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2267005
BLAST score
                  269
E value
                  1.0e-149
Match length
                  341
% identity
                  98
NCBI Description Oryza sativa endosperm lumenal binding protein (BiP) mRNA,
                  complete cds
                  402953
Seq. No.
                  LIB3431-058-P1-N1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g166341
BLAST score
                  266
E value
                  5.0e-23
Match length
                  88
% identity
                  56
                  (M98267) alliinase [Allium cepa] >gi 1044969 (L48614)
NCBI Description
                  allinase [Allium cepa]
```

Seq. No. 402954

Seq. ID LIB3431-058-P1-N1-D3

Method BLASTN
NCBI GI g4097337
BLAST score 487

```
0.0e+00
E value
Match length
                  495
% identity
                  100
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  402955
Seq. No.
                  LIB3431-058-P1-N1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g438246
BLAST score
                  57
                  5.0e-23
E value
Match length
                  77
                  94
% identity
NCBI Description S.tuberosum mRNA for glycine hydroxymethyltransferase
                  402956
Seq. No.
                  LIB3431-058-P1-N1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131400
BLAST score
                  276
E value
                  2.0e-35
Match length
                  113
% identity
                  62
NCBI Description
                 PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi 81471 pir S00409 photosystem II 10K protein precursor
                  - spinach >gi 170127 (J03887) 10kd polypeptide precursor
                  [Spinacia oleracea]
Seq. No.
                  402957
Seq. ID
                  LIB3431-058-P1-N1-D7
Method
                  BLASTX
NCBI GI
                  g3334149
BLAST score
                  206
E value
                  4.0e-22
Match length
                  64
% identity
                  91
                  MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
NCBI Description
                   (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2323329 (AF014053) Mg
                  protoporphyrin chelatase subunit [Nicotiana tabacum]
Seq. No.
                  402958
Seq. ID
                  LIB3431-058-P1-N1-D8
Method
                  BLASTX
NCBI GI
                  q693920
BLAST score
                  416
```

E value 1.0e-40 Match length 80 % identity

NCBI Description (U21113) chlorophyll a/b binding protein [Solanum

tuberosum]

Seq. No. 402959

Seq. ID LIB3431-058-P1-N1-E1

Method BLASTX NCBI GI g400989 BLAST score 544



E value 1.0e-55
Match length 137
% identity 73
NCBI Description 50S RIB

ption 50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24)

>gi_322771_pir__A45113 ribosomal protein L24 precursor
common tobacco >gi_170273 (M87838) ribosomal protein L24

[Nicotiana tabacum] >gi_170324 (M87839) ribosomal protein

L24 [Nicotiana tabacum]

Seq. No. 402960

Seq. ID LIB3431-058-P1-N1-E10

Method BLASTX
NCBI GI g482311
BLAST score 502
E value 1.0e-50
Match length 99
% identity 99

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice

(strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 402961

Seq. ID LIB3431-058-P1-N1-E12

Method BLASTN
NCBI GI g20243
BLAST score 145
E value 1.0e-75
Match length 169
% identity 95

NCBI Description O.sativa GP28 gene (partial)

Seq. No. 402962

Seq. ID LIB3431-058-P1-N1-E2

Method BLASTN
NCBI GI g303858
BLAST score 68
E value 9.0e-30
Match length 147
% identity 87

NCBI Description Rice mRNA for brain specific protein (S94 gene), complete

cds

Seq. No. 402963

Seq. ID LIB3431-058-P1-N1-E4

Method BLASTX
NCBI GI g132105
BLAST score 289
E value 4.0e-49
Match length 97
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

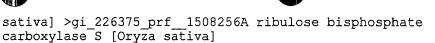
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza





402964 Seq. No. LIB3431-058-P1-N1-E5 Seq. ID Method BLASTX NCBI GI g132105 BLAST score 325 E value 2.0e-47 Match length 94 % identity 99 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 402965 Seq. No. Seq. ID LIB3431-058-P1-N1-E7 Method BLASTX NCBI GI g115794 BLAST score 439 E value 1.0e-66 Match length 134 % identity 92 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato >gi 19277 emb CAA42818 (X60275) LHCII type III [Lycopersicon esculentum] Seq. No. 402966 Seq. ID LIB3431-058-P1-N1-F11 Method BLASTX NCBI GI q2245106 BLAST score 328 E value 2.0e-30 Match length 80 % identity 70 NCBI Description (Z97343) thioesterase like protein [Arabidopsis thaliana] 402967 Seq. No. Seq. ID LIB3431-058-P1-N1-F12 Method BLASTX NCBI GI q3885894 BLAST score 517 E value 2.0e-52 Match length 115

Seq. No. 402968

% identity

NCBI Description

Seq. ID LIB3431-058-P1-N1-F2

(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]



Method BLASTX
NCBI GI g2501190
BLAST score 325
E value 6.0e-30
Match length 85
% identity 81

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR

>gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
- maize >gi_596080 (U17351) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 402969

Seq. ID LIB3431-058-P1-N1-F3

Method BLASTX
NCBI GI g115871
BLAST score 236
E value 2.0e-31
Match length 103
% identity 60

NCBI Description [Segment 2 of 2] SERINE CARBOXYPEPTIDASE II CHAINS A AND B

(CARBOXYPEPTIDASE D) (CPDW-II) (CP-WII)

>gi_82623_pir__B29639 serine-type carboxypeptidase (EC
3.4.16.1) II B chain - wheat >gi_1421108_pdb_1BCR_B Chain
B, Complex Of The Wheat Serine Carboxypeptidase, Cpdw-Ii,
With The Microbial Peptide Aldehyde Inhibitor, Antipain,
And Arginine At Room Temperature >gi_1421113_pdb_1BCS_B
Chain B, Complex Of The Wheat Serine Carboxypeptidase,
Cpdw-Ii, With The Microbial Peptide Aldehyde Inhibitor,

Chymostatin, And Arginine At 100 Degrees Kelvin

>gi_226041_prf__1408164B CPase II B [Triticum aestivum]

Seq. No. 402970

Seq. ID LIB3431-058-P1-N1-F4

Method BLASTX
NCBI GI g3158476
BLAST score 217
E value 8.0e-31
Match length 89
% identity 78

NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 402971

Seq. ID LIB3431-058-P1-N1-F5

Method BLASTX
NCBI GI g4960154
BLAST score 318
E value 4.0e-29
Match length 73
% identity 85

NCBI Description (AF153283) putative progesterone-binding protein homolog

[Arabidopsis thaliana]

Seq. No. 402972

Seq. ID LIB3431-058-P1-N1-F6

Method BLASTN
NCBI GI g505134
BLAST score 209

```
E value 1.0e-114
Match length 305
% identity 93
NCBI Description Rice mRNA for ferredoxin, complete cds
```

 Seq. No.
 402973

 Seq. ID
 LIB3431-058-P1-N1-F8

 Method
 BLASTX

 NCBI GI
 g3126854

NCBI GI g3126854
BLAST score 411
E value 4.0e-54
Match length 113
% identity 96

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 402974

Seq. ID LIB3431-058-P1-N1-G1

Method BLASTX
NCBI GI g417260
BLAST score 255
E value 1.0e-24
Match length 79
% identity 69

NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632

lir1 protein - rice >gi 20263 emb CAA48706 (X68807)

light-regulated gene [Oryza sativa]

Seq. No. 402975

Seq. ID LIB3431-058-P1-N1-G10

Method BLASTX
NCBI GI g517500
BLAST score 301
E value 2.0e-27
Match length 89
% identity 70

NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa

protein [Zea mays] >gi_444338_prf__1906386A photosystem II

OE17 protein [Pisum sativum]

Seq. No. 402976

Seq. ID LIB3431-058-P1-N1-G12

Method BLASTX
NCBI GI g417260
BLAST score 411
E value 5.0e-40
Match length 128
% identity 66

NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632

lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)

light-regulated gene [Oryza sativa]

Seq. No. 402977

Seq. ID LIB3431-058-P1-N1-G4

MethodBLASTXNCBI GIg3885892BLAST score513E value4.0e-52



Match length 96 % identity 100

NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.

402978

Seq. ID

LIB3431-058-P1-N1-G8

Method NCBI GI BLASTX g548603

BLAST score E value 543 1.0e-55

Match length % identity

108 95

NCBI Description

PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

>gi_478404_pir__JQ2247 photosystem I chain D precursor barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.

402979

Seq. ID

LIB3431-058-P1-N1-G9

Method NCBI GI BLASTX g3004565

BLAST score E value 188

Match length

2.0e-18 94

% identity

52

NCBI Description

(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.

402980

Seq. ID

LIB3431-058-P1-N1-H11

Method NCBI GI BLASTX g132105

BLAST score E value

234 4.0e-21

Match length % identity

70 81

% identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor (clone posssili39) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No.

402981

Seq. ID

LIB3431-058-P1-N1-H2

Method NCBI GI BLASTX q3789954

BLAST score

339

E value Match length 1.0e-54 110

% identity

95

NCBI Description

(AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No.

402982

Seq. ID LIB3431-058-P1-N1-H8

Method BLASTX
NCBI GI g132105
BLAST score 482
E value 2.0e-48
Match length 99
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402983

Seq. ID LIB3431-058-P1-N1-H9

Method BLASTX
NCBI GI g2407279
BLAST score 206
E value 4.0e-16
Match length 43
% identity 98

NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 402984

Seq. ID LIB3431-059-P1-K1-A10

Method BLASTX
NCBI GI g115787
BLAST score 571
E value 4.0e-59
Match length 111
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 402985

Seq. ID LIB3431-059-P1-K1-A11

Method BLASTX
NCBI GI g6006871
BLAST score 333
E value 4.0e-31
Match length 126
% identity 52

NCBI Description (AC009540) hypothetical protein [Arabidopsis thaliana]

>gi_6091753_gb_AAF03463.1_AC009327_2 (AC009327)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 402986

Seq. ID LIB3431-059-P1-K1-A12

Method BLASTX NCBI GI g3789952

% identity

87

```
BLAST score
E value
                   1.0e-58
Match length
                   114
% identity
                   98
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
Seq. No.
                   402987
Seq. ID
                  LIB3431-059-P1-K1-A2
Method
                  BLASTX
NCBI GI
                   g1001355
BLAST score
                  144
E value
                   6.0e-09
Match length
                  60
% identity
                  45
NCBI Description
                  (D64006) auxin-induced protein [Synechocystis sp.]
                   402988
Seq. No.
Seq. ID
                  LIB3431-059-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  578
                  7.0e-60
E value
Match length
                  109
% identity
                  99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  402989
Seq. No.
                  LIB3431-059-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548774
BLAST score
                  464
E value
                  2.0e-46
Match length
                  109
% identity
                  83
NCBI Description
                  60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__$38360 ribosomal
                  protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                  402990
Seq. ID
                  LIB3431-059-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g4469021
BLAST score
                  312
E value
                  2.0e-28
Match length
                  85
% identity
                  71
NCBI Description
                  (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  402991
Seq. ID
                  LIB3431-059-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  643
E value
                  2.0e-67
Match length
                  142
```



NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 402992

Seq. ID LIB3431-059-P1-K1-B1

Method BLASTX NCBI GI g3860277 BLAST score 423 E value 1.0e-41 Match length 96

% identity 84

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 402993

Seq. ID LIB3431-059-P1-K1-B10

Method BLASTX NCBI GI g2736155 BLAST score 476 E value 9.0e-48 Match length 122 % identity 75

(AF022082) sulfolipid biosynthesis protein [Arabidopsis NCBI Description

thaliana] >gi_3688184 emb CAA21212 (AL031804) sulfolipid

biosynthesis protein SQD1 [Arabidopsis thaliana]

Seq. No. 402994

Seq. ID LIB3431-059-P1-K1-B11

Method BLASTX NCBI GI g2072555 BLAST score 237 E value 8.0e-20 Match length 44 % identity 100

(AF001396) metallothionein-like protein [Oryza sativa] NCBI Description

>gi_6103441 gb AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402995

Seq. ID LIB3431-059-P1-K1-B12

Method BLASTX NCBI GI g1352461 BLAST score 178 E value 4.0e-15 Match length 93 % identity 49

NCBI Description IN2-2 PROTEIN

Seq. No.

402996

Seq. ID LIB3431-059-P1-K1-B2 Method BLASTX

NCBI GI g6041833 BLAST score 200

```
E value
                   2.0e-15
Match length
                   123
% identity
                   38
NCBI Description
                  (AC009853) unknown protein [Arabidopsis thaliana]
Seq. No.
                  402997
Seq. ID
                  LIB3431-059-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q131192
                  297
BLAST score
E value
                   6.0e-27
Match length
                  97
% identity
                   65
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
                   (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 100606 pir S20937
                  photosystem I chain V precursor - barley
                  >gi_19091 emb CAA42727 (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
Seq. No.
                  402998
Seq. ID
                  LIB3431-059-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3618310
BLAST score
                  334
                  3.0e-31
E value
Match length
                  97
% identity
                  67
NCBI Description (AB001883) zinc finger protein [Oryza sativa]
                  402999
Seq. No.
Seq. ID
                  LIB3431-059-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g1881585
BLAST score
                  231
E value
                  4.0e-19
Match length
                  117
% identity
                  45
NCBI Description (U72489) remorin [Solanum tuberosum]
Seq. No.
                  403000
Seq. ID
                  LIB3431-059-P1-K1-B6
Method
                  BLASTX
                 g2293480
NCBI GI
BLAST score
                  168
E value
                  2.0e-12
Match length
                  48
% identity
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  403001
Seq. ID
                  LIB3431-059-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q3885894
BLAST score
                  402
E value
                  3.0e-39
Match length
                  91
% identity
                  87
```

Method

BLASTN

```
NCBI Description
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                  403002
Seq. ID
                  LIB3431-059-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q1351270
BLAST score
                  562
                  7.0e-58
E value
Match length
                  123
% identity
                  89
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                  >gi 478410 pir JQ2255 triose-phosphate isomerase (EC
                  5.3.1.1) - rice >gi 169821 (M87064) triosephosphate
                  isomerase [Oryza sativa]
Seq. No.
                  403003
                  LIB3431-059-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4732091
BLAST score
                  254
E value
                  7.0e-22
Match length
                  69
% identity
                  67
NCBI Description
                 (AF126742) bundle sheath defective protein 2 [Zea mays]
Seq. No.
                  403004
Seq. ID
                  LIB3431-059-P1-K1-C1
Method
                  BLASTN
                  g3617841
NCBI GI
BLAST score
                  190
E value
                  1.0e-103
Match length
                  190
% identity
                  100
NCBI Description Oryza sativa clone F14605 calmodulin (CaM1) mRNA, complete
                  cds
Seq. No.
                  403005
Seq. ID
                  LIB3431-059-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  614
E value
                  6.0e-64
Match length
                  132
% identity
                  88
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403006
Seq. ID
                  LIB3431-059-P1-K1-C11
```

```
NCBI GI
                  q4218534
BLAST score
                  34
E value
                  2.0e-09
Match length
                   46
                  93
% identity
                  Triticum sp. mRNA for GRAB1 protein
NCBI Description
Seq. No.
                  403007
                  LIB3431-059-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885891
BLAST score
                  141
E value
                  1.0e-73
Match length
                  141
% identity
                  100
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                  mRNA, complete cds
                  403008
Seq. No.
                  LIB3431-059-P1-K1-C3
Seq. ID
Method
                  BLASTX
                  g5734720
NCBI GI
BLAST score
                  231
E value
                   4.0e-19
                  138
Match length
% identity
                   43
                   (AC008075) Contains PF 01426 BAH (bromo-adjacent homology)
NCBI Description
                   domain. ESTs gb N96349, gb T42710, gb H77084, gb AA395147
                   and gb AA605500 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   403009
                  LIB3431-059-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1848214
BLAST score
                  197
                   4.0e-15
E value
Match length
                   49
                  73
% identity
NCBI Description
                  (Y11210) uracil phosphoribosyltransferase [Nicotiana
                  tabacum]
                   403010
Seq. No.
                  LIB3431-059-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2570511
BLAST score
                   625
E value
                   2.0e-65
Match length
                  123
                   95
% identity
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   403011
Seq. No.
                  LIB3431-059-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  q3885894
NCBI GI
BLAST score
                   436
E value
                  3.0e-43
```

```
Match length
% identity
                  88
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                  403012
Seq. No.
                  LIB3431-059-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3138799
BLAST score
                  603
E value
                  1.0e-62
                  125
Match length
                  92
% identity
NCBI Description
                  (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]
Seq. No.
                  403013
                  LIB3431-059-P1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2072555
BLAST score
                  237
                  8.0e-20
E value
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  403014
                  LIB3431-059-P1-K1-D11
Seq. ID
Method
                  BLASTX
                  g671740
NCBI GI
BLAST score
                   695
E value
                  2.0e-73
Match length
                  128
                  99
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                   403015
                  LIB3431-059-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  q3915826
NCBI GI
BLAST score
                   309
E value
                   2.0e-28
Match length
                   67
% identity
                   93
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
```

Seq. No. 403016

Seq. ID LIB3431-059-P1-K1-D3

Method BLASTX
NCBI GI g548605
BLAST score 386
E value 3.0e-37
Match length 80
% identity 95

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)



>gi_539055_pir A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No. 403017 Seq. ID LIB3431-059-P1-K1-D4

Method BLASTX
NCBI GI g2407281
BLAST score 567
E value 2.0e-58
Match length 109
% identity 98

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 403018

Seq. ID LIB3431-059-P1-K1-D5

Method BLASTX
NCBI GI g132105
BLAST score 576
E value 1.0e-59
Match length 124
% identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403019

Seq. ID LIB3431-059-P1-K1-D7

Method BLASTX
NCBI GI g3894170
BLAST score 174
E value 2.0e-12
Match length 41
% identity 80

NCBI Description (AC005312) putative glutathione s-transferase [Arabidopsis

thaliana]

Seq. No. 403020

Seq. ID LIB3431-059-P1-K1-D8

Method BLASTX
NCBI GI g132105
BLAST score 609
E value 2.0e-63
Match length 131
% identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate



carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

 Seq. No.
 403021

 Seq. ID
 LIB3431-059-P1-K1-D9

 Method
 BLASTX

 NCBI GI
 g3914466

 BLAST score
 307

E value 5.0e-28 Match length 63 % identity 92

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN

subunit precursor [Zea mays]

Seq. No. 403022

Seq. ID LIB3431-059-P1-K1-E1

Method BLASTX
NCBI GI g3738329
BLAST score 237
E value 9.0e-20
Match length 61
% identity 74

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 403023

Seq. ID LIB3431-059-P1-K1-E10

Method BLASTN
NCBI GI g169133
BLAST score 60
E value 4.0e-25
Match length 156
% identity 85

NCBI Description Zea mays precursor of the oxygen evolving complex 17 kDa

protein mRNA, complete cds

Seq. No. 403024

Seq. ID LIB3431-059-P1-K1-E11

Method BLASTX
NCBI GI g2407281
BLAST score 642
E value 2.0e-67
Match length 121
% identity 98

NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small

subunit [Oryza sativa]

Seq. No. 403025

Seq. ID LIB3431-059-P1-K1-E2

Method BLASTX
NCBI GI g548603
BLAST score 271
E value 5.0e-28
Match length 115
% identity 65



NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

>gi 478404 pir JQ2247 photosystem I chain D precursor barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 403026

Seq. ID LIB3431-059-P1-K1-E4

Method BLASTX NCBI GI q2198851 BLAST score 794 5.0e-85 E value Match length 155 % identity 97

NCBI Description (AF007785) cystathionine gamma-synthase [Zea mays]

Seq. No. 403027

Seq. ID LIB3431-059-P1-K1-E5

Method BLASTX NCBI GI q1235664 BLAST score 631 E value 6.0e-66 Match length 131 % identity 59

NCBI Description (U37936) novel calmodulin-like protein [Oryza sativa]

>gi_3171148 (AF064456) calmodulin-like protein [Oryza

satīva subsp. indica]

Seq. No. 403028

Seq. ID LIB3431-059-P1-K1-E6

Method BLASTX NCBI GI q133999 BLAST score 378 E value 2.0e-36 Match length 79 97

% identity

CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_70904_pir__R3RZ7 NCBI Description

ribosomal protein S7 - rice chloroplast
>gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7
[Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal protein S7 [Oryza sativa] >gi 226657 prf 1603356CH

ribosomal protein S7 [Oryza sativa]

Seq. No. 403029

Seq. ID LIB3431-059-P1-K1-E7

Method BLASTX NCBI GI g1835731 BLAST score 520 E value 4.0e-53 99 Match length % identity 99

(U86018) photosystem II 10 kDa polypeptide [Oryza sativa] NCBI Description

Seq. No. 403030

Seq. ID LIB3431-059-P1-K1-E9

Method BLASTX NCBI GI g733454 BLAST score 519

4.182

```
E value
                  8.0e-53
Match length
                  121
% identity
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                  403031
Seq. ID
                  LIB3431-059-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q1173347
BLAST score
                  593
E value
                  2.0e-61
Match length
                  130
% identity
                  91
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  403032
Seq. ID
                  LIB3431-059-P1-K1-F10
Method
                  BLASTX
                  g3288821
NCBI GI
BLAST score
                  484
                  9.0e-49
E value
Match length
                  132
% identity
                  72
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  >gi_4733989 gb AAD28669.1 AC007209 5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                  403033
Seq. ID
                  LIB3431-059-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  35
E value
                  4.0e-10
Match length
                  35
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  403034
Seq. ID
                  LIB3431-059-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g1245938
BLAST score
                  35
E value
                  4.0e-10
Match length
                  35
                  100
% identity
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
NCBI Description
                  heart atrium, mRNA, 2998 nt]
```

51812

403035

LIB3431-059-P1-K1-F3

Seq. No. Seq. ID

```
BLASTX
Method
NCBI GI
                   q1800227
                   246
BLAST score
                   6.0e-21
E value
Match length
                   67
% identity
                   60
NCBI Description
                   (U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]
Seq. No.
                   403036
                   LIB3431-059-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   519
E value
                   7.0e-53
Match length
                   120
                   87
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi 82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   403037
Seq. No.
Seq. ID
                   LIB3431-059-P1-K1-F5
Method
                   BLASTX
                   g132105
NCBI GI
                   395
BLAST score
E value
                   2.0e-38
                   73
Match length
% identity
                   99
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403038
                   LIB3431-059-P1-K1-F6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3819345
BLAST score
                   60
E value
                   7.0e-25
```

Match length 168

84

NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0803

Seq. No. 403039 Seq. ID LIB3431-059-P1-K1-G2 Method BLASTX

NCBI GI g132105 BLAST score 429 E value 2.0e-42 Match length 104

% identity

```
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403040
Seq. ID
                   LIB3431-059-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q3450889
BLAST score
                   207
E value
                   2.0e-16
Match length
                   96
% identity
                   69
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.
                   403041
Seq. ID
                  LIB3431-059-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q3264767
BLAST score
                  183
E value
                  2.0e-13
Match length
                   59
% identity
                  54
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                  403042
Seq. ID
                  LIB3431-059-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q100796
BLAST score
                   650
E value
                   3.0e-68
Match length
                  132
% identity
                  92
NCBI Description phosphoribulokinase (EC 2.7.1.19) - wheat
Seq. No.
                  403043
Seq. ID
                  LIB3431-059-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q3345477
BLAST score
                  179
E value
                  2.0e-13
Match length
                  63
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  403044
Seq. ID
                  LIB3431-059-P1-K1-H11
Method
                  BLASTX
NCBI GI
```

g21693

9.0e-29

308

BLAST score

E value

```
Match length
% identity
                  82
                  (X66012) cathepsin B [Triticum aestivum]
NCBI Description
Seq. No.
                  403045
Seq. ID
                  LIB3431-059-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q4567283
BLAST score
                  270
E value
                  8.0e-24
Match length
                  125
% identity
                  46
NCBI Description
                  (AC006841) unknown protein [Arabidopsis thaliana]
                  403046
Seq. No.
Seq. ID
                  LIB3431-059-P1-K1-H2
Method
                  BLASTX
                  g2582822
NCBI GI
BLAST score
                  213
                  6.0e-17
E value
Match length
                  53
                  74
% identity
NCBI Description
                  (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
                  Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                  403047
Seq. ID
                  LIB3431-059-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q115772
BLAST score
                  298
E value
                  1.0e-34
Match length
                  96
                  83
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                  CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
                  protein 1R precursor - rice >gi_20178_emb_CAA32108
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
Seq. No.
                  403048
Seq. ID
                  LIB3431-059-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g871931
BLAST score
                  281
E value
                  4.0e-25
Match length
                  77
% identity
                  78
NCBI Description
                  (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  403049
Seq. ID
                  LIB3431-059-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g131773
BLAST score
                  583
E value
                  2.0e-60
Match length
                  122
% identity
                  97
```

```
40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                  >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                  maize
Seq. No.
                  403050
                  LIB3431-059-P1-K1-H8
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
BLAST score
                  38
E value
                  9.0e-12
Match length
                  49
                  66
% identity
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
                  403051
Seq. No.
                  LIB3431-059-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3894197
BLAST score
                  346
                  1.0e-32
E value
Match length
                  139
                  49
% identity
NCBI Description
                  (AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  403052
Seq. ID
                  LIB3431-059-P1-N1-A1
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  257
E value
                  3.0e-22
Match length
                  61
% identity
                  82
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  403053
                  LIB3431-059-P1-N1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421916
BLAST score
                  190
E value
                  2.0e-14
Match length
                  36
                  97
% identity
NCBI Description
                  chlorophyll a/b-binding protein - English ivy (fragment)
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                  403054
Seq. ID
                  LIB3431-059-P1-N1-A12
Method
                  BLASTN
NCBI GI
                  q3789951
BLAST score
                  160
E value
                  1.0e-84
Match length
                  362
% identity
                  99
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
```

Seq. No.

403060

```
complete cds
Seq. No.
                  403055
                  LIB3431-059-P1-N1-A2
Seq. ID
Method
                  BLASTX
                  g1001355
NCBI GI
BLAST score
                  192
E value
                  1.0e-14
                  57
Match length
% identity
                  61
                  (D64006) auxin-induced protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  403056
                  LIB3431-059-P1-N1-A3
Seq. ID
                  BLASTX
Method
                  g3126854
NCBI GI
BLAST score
                  211
                  1.0e-19
E value
Match length
                  66
                  79
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  403057
Seq. No.
                  LIB3431-059-P1-N1-A4
Seq. ID
Method
                  BLASTX
                  g548774
NCBI GI
BLAST score
                  267
E value
                  2.0e-23
Match length
                  69
% identity
                  80
                  60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi_303855_dbj_BAA02156 (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                  403058
                  LIB3431-059-P1-N1-A6
Seq. ID
Method
                  BLASTX
                  g4469021
NCBI GI
BLAST score
                  287
E value
                  1.0e-25
Match length
                  71
                  76
% identity
NCBI Description
                  (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  403059
                  LIB3431-059-P1-N1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  329
E value
                  1.0e-30
Match length
                  63
% identity
                  100
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
```

(Cab27) mRNA, nuclear gene encoding chloroplast protein,



```
LIB3431-059-P1-N1-B1
Seq. ID
Method
                  BLASTX
                  g3860277
NCBI GI
BLAST score
                  167
                  1.0e-11
E value
                  32
Match length
                  100
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                   403061
                  LIB3431-059-P1-N1-B11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2072554
BLAST score
                  321
                   0.0e + 00
E value
Match length
                   321
% identity
                  100
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
                   403062
Seq. No.
                  LIB3431-059-P1-N1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g6041833
BLAST score
                   151
E value
                   9.0e-10
Match length
                   85
% identity
                   42
                  (AC009853) unknown protein [Arabidopsis thaliana]
NCBI Description
                   403063
Seq. No.
                   LIB3431-059-P1-N1-B3
Seq. ID
                   BLASTN
Method
                   g19090
NCBI GI
BLAST score
                   45
E value
                   5.0e-16
Match length
                   65
% identity
                   92
NCBI Description H.vulgare PsaG mRNA
                   403064
Seq. No.
                   LIB3431-059-P1-N1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3618310
BLAST score
                   317
                   3.0e-29
E value
Match length
                   61
% identity
                   100
NCBI Description
                  (AB001883) zinc finger protein [Oryza sativa]
Seq. No.
                   403065
Seq. ID
                   LIB3431-059-P1-N1-B6
```

NCBI GI g2624325 BLAST score 224

BLASTN

Method

E value

3.0e-23

```
1.0e-123
E value
Match length
                  248
% identity
                  Oryza sativa mRNA for glycine-rich RNA-binding protein
NCBI Description
                  (OsGRP1)
                  403066
Seq. No.
Seq. ID
                  LIB3431-059-P1-N1-B7
Method
                  BLASTX
                  g3885894
NCBI GI
BLAST score
                  193
                  1.0e-14
E value
Match length
                  53
% identity
                  75
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                  403067
Seq. No.
                  LIB3431-059-P1-N1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351270
BLAST score
                  195
                  6.0e-15
E value
Match length
                  48
                  85
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                  >gi 478410 pir JQ2255 triose-phosphate isomerase (EC
                  5.3.1.1) - rice >gi_169821 (M87064) triosephosphate
                  isomerase [Oryza sativa]
Seq. No.
                  403068
                  LIB3431-059-P1-N1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3617841
BLAST score
                  186
E value
                  1.0e-100
Match length
                  190
% identity
                  99
                  Oryza sativa clone F14605 calmodulin (CaM1) mRNA, complete
NCBI Description
                  cds
                  403069
Seq. No.
                  LIB3431-059-P1-N1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  197
                  3.0e-15
E value
Match length
                  37
                  100
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  403070
Seq. ID
                  LIB3431-059-P1-N1-C12
Method
                  BLASTX
NCBI GI
                  q3885892
BLAST score
                  266
```

```
Match length
% identity
                  100
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                  403071
Seq. No.
                  LIB3431-059-P1-N1-C2
Seq. ID
Method
                  BLASTN
                  g4079797
NCBI GI
BLAST score
                  39
                  2.0e-12
E value
Match length
                  71
                  89
% identity
NCBI Description
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
                  complete cds
                  403072
Seq. No.
Seq. ID
                  LIB3431-059-P1-N1-C6
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  163
                  3.0e-22
E value
                  67
Match length
                  78
% identity
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                  403073
Seq. No.
                  LIB3431-059-P1-N1-C7
Seq. ID
Method
                  BLASTN
                  g20262
NCBI GI
BLAST score
                  126
                  2.0e-64
E value
                  194
Match length
% identity
                  91
NCBI Description O.sativa light-induced mRNA
                  403074
Seq. No.
Seq. ID
                  LIB3431-059-P1-N1-C8
Method
                  BLASTX
NCBI GI
                  g3885894
BLAST score
                  193
E value
                  1.0e-14
Match length
                  53
% identity
                  75
NCBI Description
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                  403075
                  LIB3431-059-P1-N1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3138799
BLAST score
                  263
                  7.0e-23
E value
```

Match length 60 % identity

NCBI Description (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]

Seq. No. 403076

LIB3431-059-P1-N1-D10 Seq. ID



Method BLASTN
NCBI GI g2072554
BLAST score 380
E value 0.0e+00
Match length 380
% identity 100

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 403077

Seq. ID LIB3431-059-P1-N1-D11

Method BLASTX
NCBI GI g671740
BLAST score 243
E value 1.0e-20
Match length 47
% identity 100

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 403078

Seq. ID LIB3431-059-P1-N1-D12

Method BLASTX
NCBI GI g3915826
BLAST score 202
E value 9.0e-16
Match length 41
% identity 100

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 403079

Seq. ID LIB3431-059-P1-N1-D3

Method BLASTX
NCBI GI g548605
BLAST score 386
E value 2.0e-37
Match length 80
% identity 95

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 403080

Seq. ID LIB3431-059-P1-N1-D4

Method BLASTX
NCBI GI g132105
BLAST score 526
E value 1.0e-53
Match length 95
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

E value

Match length

2.0e-36

91



carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 403081 LIB3431-059-P1-N1-D5 Seq. ID Method BLASTX NCBI GI g347451 BLAST score 248 E value 4.0e-21 Match length 48 % identity 100 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa] Seq. No. 403082 Seq. ID LIB3431-059-P1-N1-D7 Method BLASTX NCBI GI q3894171 BLAST score 252 E value 1.0e-21 Match length 67 70 % identity NCBI Description (AC005312) putative glutathione s-transferase [Arabidopsis thaliana] 403083 Seq. No. Seq. ID LIB3431-059-P1-N1-D8 Method BLASTX g347451 NCBI GI BLAST score 248 E value 4.0e-21 Match length 48 % identity 100 NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza sativa] Seq. No. 403084 Seq. ID LIB3431-059-P1-N1-D9 Method BLASTX NCBI GI q3914466 BLAST score 163 E value 2.0e-11 Match length 46 % identity 67 PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR NCBI Description (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN subunit precursor [Zea mays] Seq. No. 403085 Seq. ID LIB3431-059-P1-N1-E10 Method BLASTX NCBI GI g517500 BLAST score 378

BLAST score

E value

425

7.0e-42

```
% identity
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                   protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                   OE17 protein [Pisum sativum]
Seq. No.
                   403086
Seq. ID
                  LIB3431-059-P1-N1-E11
Method
                  BLASTN
NCBI GI
                  q218209
BLAST score
                  149
                   4.0e-78
E value
Match length
                   316
% identity
                   97
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                  403087
Seq. ID
                  LIB3431-059-P1-N1-E2
Method
                  BLASTX
NCBI GI
                  g548603
BLAST score
                  366
E value
                  5.0e-35
Match length
                  72
% identity
                  96
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir JQ2247 photosystem I chain D precursor -
                  barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  403088
Seq. ID
                  LIB3431-059-P1-N1-E4
Method
                  BLASTX
NCBI GI
                  g2198853
BLAST score
                  355
E value
                  9.0e-34
Match length
                  82
% identity
                  80
NCBI Description
                  (AF007786) cystathionine gamma-synthase [Zea mays]
Seq. No.
                  403089
Seq. ID
                  LIB3431-059-P1-N1-E5
Method
                  BLASTN
NCBI GI
                  g1235663
BLAST score
                  253
E value
                  1.0e-140
Match length
                  261
% identity
                  99
NCBI Description
                  Oryza sativa clone pFDRSC61 novel calmodulin-like protein
                  mRNA, complete cds
Seq. No.
                  403090
Seq. ID
                  LIB3431-059-P1-N1-E6
Method
                  BLASTX
NCBI GI
                  g1173275
```

```
Match length
% identity
                   86
```

CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 NCBI Description

>gi_2119068_pir S58630 ribosomal protein S7 - maize chloroplast >gi 902274 emb CAA60339 (X86563) ribosomal protein S7 [Zea mays] >gi 902298 emb CAA60362 (X86563)

ribosomal protein S7 [Zea mays]

Seq. No. 403091

Seq. ID LIB3431-059-P1-N1-E7

Method BLASTX NCBI GI g1835731 BLAST score 286 E value 1.0e-25 Match length 65 % identity 85

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.

403092

Seq. ID LIB3431-059-P1-N1-E9

Method BLASTX NCBI GI g733454 BLAST score 232 E value 3.0e-19 Match length 48 % identity 94

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 403093

Seq. ID LIB3431-059-P1-N1-F1

Method BLASTX NCBI GI g1173347 BLAST score 216 E value 2.0e-17 Match length 47 % identity 94

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi 14265 emb CAA46507 (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 403094

Seq. ID LIB3431-059-P1-N1-F10

Method BLASTX NCBI GI g2754849 BLAST score 199 E value 2.0e-15 Match length 45 % identity 87

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase

[Fritillaria agrestis]

Seq. No. 403095

Seq. ID LIB3431-059-P1-N1-F4

Seq. No.

Seq. ID

Method

403100

BLASTX

LIB3431-059-P1-N1-G2

```
Method
                   BLASTX
NCBI GI
                   q3036951
BLAST score
                   199
E value
                   9.0e-19
Match length
                   52
% identity
                   98
NCBI Description
                   (AB012639) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                   403096
Seq. ID
                   LIB3431-059-P1-N1-F5
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   336
E value
                   2.0e-31
Match length
                   64
% identity
                   95
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
Seq. No.
                   403097
Seq. ID
                   LIB3431-059-P1-N1-F7
Method
                   BLASTN
NCBI GI
                   q606816
BLAST score
                   306
E value
                   1.0e-172
Match length
                   326
% identity
                   98
NCBI Description
                  Oryza sativa chloroplast carbonic anhydrase mRNA, complete
Seq. No.
                   403098
Seq. ID
                   LIB3431-059-P1-N1-F8
Method
                  BLASTX
NCBI GI
                   q517500
BLAST score
                   378
E value
                   2.0e-36
Match length
                   91
% identity
                   81
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                   403099
Seq. ID
                  LIB3431-059-P1-N1-G11
Method
                  BLASTX
NCBI GI
                  g4079798
BLAST score
                  326
E value
                  3.0e-30
Match length
                  65
% identity
                  97
NCBI Description
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
```

```
NCBI GI
                   q347451
BLAST score
                   248
E value
                   4.0e-21
Match length
                   48
% identity
                   100
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
Seq. No.
                   403101
Seq. ID
                   LIB3431-059-P1-N1-G3
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   329
E value
                   1.0e-30
Match length
                   63
% identity
                  100
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir_ S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  403102
Seq. ID
                  LIB3431-059-P1-N1-G7
Method
                  BLASTX
NCBI GI
                  g3450889
BLAST score
                  279
E value
                  9.0e-25
Match length
                  63
% identity
                  86
NCBI Description
                  (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.
                  403103
Seq. ID
                  LIB3431-059-P1-N1-G9
Method
                  BLASTX
NCBI GI
                  g21839
BLAST score
                  163
E value
                  3.0e-11
Match length
                  35
% identity
                  94
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
Seq. No.
                  403104
Seq. ID
                  LIB3431-059-P1-N1-H1
Method
                  BLASTX
NCBI GI
                  g4455232
BLAST score
                  151
E value
                  9.0e-10
Match length
                  36
% identity
                  75
NCBI Description
                  (AL035523) putative protein [Arabidopsis thaliana]
```

... representation (imposses) pacacive process (Alapidopsis clia

Seq. No. 403105

Seq. ID LIB3431-059-P1-N1-H10

Method BLASTX NCBI GI g3345477 BLAST score 172

```
E value
                   3.0e-12
Match length
                   32
% identity
                   97
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                   403106
Seq. ID
                   LIB3431-059-P1-N1-H11
Method
                   BLASTX
NCBI GI
                   g21699
BLAST score
                   351
E value
                   3.0e-33
Match length
                   76
% identity
                   86
                  (X66013) cathepsin B [Triticum aestivum]
NCBI Description
Seq. No.
                   403107
Seq. ID
                   LIB3431-059-P1-N1-H3
Method
                   BLASTX
NCBI GI
                   q3510256
BLAST score
                   190
E value
                   2.0e-14
Match length
                   40
% identity
                   82
NCBI Description
                  (AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.
                   403108
Seq. ID
                   LIB3431-059-P1-N1-H4
Method
                   BLASTX
NCBI GI
                   g4512125
BLAST score
                   181
E value
                   3.0e-13
Match length
                   34
% identity
                   100
NCBI Description
                   (AF133340) putative chlorophyll a/b-binding protein
                   [Phalaenopsis sp. 'KCbutterfly']
Seq. No.
                   403109
Seq. ID
                  LIB3431-059-P1-N1-H5
Method
                  BLASTX
NCBI GI
                  g871931
BLAST score
                  144
E value
                  2.0e-13
Match length
                  43
% identity
                  95
NCBI Description (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  403110
Seq. ID
                  LIB3431-059-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  g131773
BLAST score
                  246
E value
                  6.0e-21
Match length
                  65
% identity
                  83
NCBI Description
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
                  >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                  maize
```

```
Seq. No.
                  403111
Seq. ID
                  LIB3431-060-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q417260
BLAST score
                  381
E value
                  1.0e-36
Match length
                  121
% identity
                  64
NCBI Description
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  403112
Seq. ID
                  LIB3431-060-P1-K1-A12
Method
                  BLASTX
                  q729668
NCBI GI
BLAST score
                  251
E value
                  2.0e-21
Match length
                  73
% identity
                  62
                  HISTONE H1 >gi_2147479_pir__S65059 histone H1,
NCBI Description
                  drought-inducible - Lycopersicon pennellii >gi 436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
                  403113
Seq. No.
Seq. ID
                  LIB3431-060-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3201632
BLAST score
                  223
E value
                  3.0e-18
Match length
                  112
% identity
                  40
NCBI Description
                  (AC004669) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                  403114
Seq. ID
                  LIB3431-060-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  417
E value
                  5.0e-41
Match length
                  101
% identity
                  79
NCBI Description
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
Seq. No.
                  403115
Seq. ID
                  LIB3431-060-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4098250
BLAST score
                  161
E value
                  7.0e-11
Match length
                  69
% identity
                  42
NCBI Description
                  (U76611) similar to Solanum tuberosum ci21A gene product
```

Number U76610 [Solanum tuberosum]

encoded by the sequence presented in GenBank Accession

```
Seq. No.
                   403116
Seq. ID
                   LIB3431-060-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q5262202
BLAST score
                   220
E value
                   8.0e-18
Match length
                   127
% identity
                   39
NCBI Description
                   (AL080252) nodulin-like protein [Arabidopsis thaliana]
Seq. No.
                   403117
Seq. ID
                  LIB3431-060-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                   280
E value
                  8.0e-25
Match length
                   49
                  100
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  403118
Seq. ID
                  LIB3431-060-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q2673914
BLAST score
                  287
E value
                  1.0e-25
Match length
                  122
                  47
% identity
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  403119
Seq. ID
                  LIB3431-060-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3201612
BLAST score
                  153
E value
                  5.0e-10
Match length
                  60
% identity
                  50
NCBI Description
                  (AC004669) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                  403120
Seq. ID
                  LIB3431-060-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  637
E value
                  1.0e-66
Match length
                  120
% identity
                  99
NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                  403121
Seq. ID
                  LIB3431-060-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  481
```



E value 2.0e-48
Match length 112
% identity 86

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding

protein 2R precursor - rice >gi_20182_emb_CAA32109

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 403122

Seq. ID LIB3431-060-P1-K1-B7

Method BLASTX
NCBI GI g320618
BLAST score 510
E value 8.0e-52
Match length 113
% identity 86

NCBI Description chlorophyll a/b-binding protein I precursor - rice

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

[Oryza sativa]

Seq. No. 403123

Seq. ID LIB3431-060-P1-K1-B9

Method BLASTX
NCBI GI g3023816
BLAST score 592
E value 2.0e-61
Match length 115
% identity 98

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 403124

Seq. ID LIB3431-060-P1-K1-C1

Method BLASTX
NCBI GI g3885888
BLAST score 348
E value 8.0e-33
Match length 113
% identity 67

NCBI Description (AF093632) high mobility group protein [Oryza sativa]

Seq. No. 403125

Seq. ID LIB3431-060-P1-K1-C10

Method BLASTX
NCBI GI g5091623
BLAST score 295
E value 1.0e-26
Match length 75
% identity 69

NCBI Description (AC007454) Similar to gb_U93048 somatic embryogenesis

receptor-like kinase from Daucus carota, contains 4 PF_00560 Leucine Rich Repeat domains and a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Method

BLASTX

```
403126
Seq. No.
                  LIB3431-060-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  g2980641
NCBI GI
                  174
BLAST score
E value
                  2.0e-12
Match length
                  76
                  50
% identity
                  (Y11250) multi resistance protein [Arabidopsis thaliana]
NCBI Description
                  403127
Seq. No.
                  LIB3431-060-P1-K1-C12
Seq. ID
Method
                  BLASTX
                  g3789954
NCBI GI
                  610
BLAST score
                  1.0e-63
E value
                  113
Match length
                  100
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  403128
Seq. No.
                  LIB3431-060-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  7.0e-20
E value
                  44
Match length
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  403129
                  LIB3431-060-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                 g3885886
BLAST score
                  632
                  3.0e-66
E value
Match length
                  123
                  100
% identity
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
Seq. No.
                  403130
                  LIB3431-060-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4200165
BLAST score
                   563
                  5.0e-58
E value
Match length
                  134
                  79
% identity
NCBI Description
                  (Y16262) neutral invertase [Daucus carota]
                   403131
Seq. No.
                  LIB3431-060-P1-K1-C8
Seq. ID
```

Ģ.

```
NCBI GI g2244867
BLAST score 261
E value 1.0e-22
Match length 138
% identity 39
NCBI Description (Z97337) hydroxynitrile lyase like protein [Arabidopsis thaliana]

Seq. No. 403132
Seq. ID LIB3431-060-P1-K1-D2
```

Seq. ID LIB3431-060
Method BLASTX
NCBI GI g266567
BLAST score 548
E value 3.0e-56
Match length 144

E value 3.0e
Match length 144
% identity 72

NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)

>gi_421956_pir__S23558 mitochondrial processing peptidase

(EC 3.4.99.41) alpha chain precursor - potato

>gi_21493_emb_CAA46990_ (X66284) mitochondrial processing

peptidase [Solanum tuberosum]

Seq. No. 403133

Seq. ID LIB3431-060-P1-K1-D3

Method BLASTX
NCBI GI g4098647
BLAST score 652
E value 2.0e-68
Match length 131
% identity 88

NCBI Description (U80668) homogentisate 1,2-dioxygenase [Arabidopsis

thaliana]

Seq. No. 403134

Seq. ID LIB3431-060-P1-K1-D4

Method BLASTX
NCBI GI g733454
BLAST score 431
E value 1.0e-42
Match length 103
% identity 81

NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor

[Zea mays]

Seq. No. 403135

Seq. ID LIB3431-060-P1-K1-D5

Method BLASTX
NCBI GI g548605
BLAST score 534
E value 1.0e-54
Match length 133
% identity 82

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir_ A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

51832

[Hordeum vulgare] 403136 Seq. No. LIB3431-060-P1-K1-D7 Seq. ID Method BLASTN NCBI GI g20239 BLAST score 141 3.0e-73 E value Match length 169 96 % identity NCBI Description O.sativa (rice) shoot-specific GOS5 gene for a putative chloroplast transit peptide Seq. No. 403137

Seq. ID LIB3431-060-P1-K1-D8
Method BLASTX
NCBI GI g4587579
BLAST score 251
E value 2.0e-21

E value 2.0e
Match length 143
% identity 35

NCBI Description (AC006550) F1003.1 [Arabidopsis thaliana]

 Seq. No.
 403138

 Seq. ID
 LIB3431-060-P1-K1-D9

 Method
 BLASTN

 NCBI GI
 6015437

NCBI GI g6015437 BLAST score 36 E value 4.0e-11 Match length 44 % identity 64

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403139

Seq. ID LIB3431-060-P1-K1-E1

Method BLASTX
NCBI GI 94559358
BLAST score 341
E value 5.0e-32
Match length 97
% identity 63

NCBI Description (AC006585) putative steroid binding protein [Arabidopsis

thaliana]

Seq. No. 403140

Seq. ID LIB3431-060-P1-K1-E10

Method BLASTX
NCBI GI g1488297
BLAST score 190
E value 3.0e-14
Match length 132
% identity 36

NCBI Description (U63530) osRAD23 [Oryza sativa]

Seq. No. 403141

Seq. ID LIB3431-060-P1-K1-E2

Method BLASTX



```
g115787
NCBI GI
BLAST score
                  498
                  2.0e-50
E value
Match length
                  117
% identity
                  86
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  403142
Seq. No.
                  LIB3431-060-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4127456
BLAST score
                  244
                  1.0e-20
E value
Match length
                  62
% identity
                  76
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403143
                  LIB3431-060-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3288821
BLAST score
                  490
                  2.0e-49
E value
Match length
                  117
% identity
                  79
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  >qi 4733989 gb AAD28669.1 AC007209 5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
                  403144
Seq. No.
                  LIB3431-060-P1-K1-E5
Seq. ID
Method
                  BLASTX
                  g2754849
NCBI GI
BLAST score
                  175
                  1.0e-12
E value
Match length
                  39
                  87
% identity
                   (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                   [Fritillaria agrestis]
Seq. No.
                  403145
                  LIB3431-060-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
                   500
BLAST score
```

E value 1.0e-50 Match length 111 % identity

chlorophyll a/b-binding protein I precursor - rice NCBI Description

>gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

E value

Match length

% identity

1.0e-52

103

98



[Oryza sativa]

```
403146
Seq. No.
                  LIB3431-060-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g2995990
NCBI GI
BLAST score
                  205
                  4.0e-16
E value
Match length
                  102
% identity
                  44
                  (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
Seq. No.
                  403147
                  LIB3431-060-P1-K1-F11
Seq. ID
                  BLASTX
Method
                  g3068713
NCBI GI
                  549
BLAST score
                  2.0e-56
E value
Match length
                  139
                  76
% identity
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                  403148
Seq. No.
                  LIB3431-060-P1-K1-F2
Seq. ID
                  BLASTX
Method
                   g4507223
NCBI GI
                  215
BLAST score
                   2.0e-27
E value
                   95
Match length
                   71
% identity
                  signal recognition particle receptor ('docking protein')
NCBI Description
                   >gi_134892_sp_P08240_SRPR_HUMAN SIGNAL RECOGNITION PARTICLE
                   RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA)
                   (DP-ALPHA) >gi_88607_pir__A29440 signal recognition
                   particle receptor - human >gi_30866_emb_CAA29608_ (X06272)
                   docking protein [Homo sapiens]
Seq. No.
                   403149
Seq. ID
                   LIB3431-060-P1-K1-F4
Method
                   BLASTN
                   g2062705
NCBI GI
                   35
BLAST score
E value
                   5.0e-10
Match length
                   35
                   100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   403150
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   q3789952
BLAST score
                   516
```

```
(AF094775) chlorophyll a/b-binding protein presursor [Oryza
 NCBI Description
                      sativa]
                      403151
 Seq. No.
 Seq. ID
                      LIB3431-060-P1-K1-F6
 Method
                      BLASTX
                      q3386621
 NCBI GI
                      593
 BLAST score
E value
                      2.0e-61
                      141
 Match length
 % identity
                      (AC004665) unknown protein [Arabidopsis thaliana]
 NCBI Description
                      403152
 Seq. No.
                      LIB3431-060-P1-K1-F7
 Seq. ID
 Method
                      BLASTX
 NCBI GI
                      g2281649
 BLAST score
                      198
                      3.0e-15
 E value
                      42
 Match length
 % identity
                      (AF003105) AP2 domain containing protein RAP2.12
 NCBI Description
                       [Arabidopsis thaliana]
                      403153
 Seq. No.
                      LIB3431-060-P1-K1-F8
 Seq. ID
 Method
                      BLASTN
                      q169133
 NCBI GI
                       40
 BLAST score
 E value
                       5.0e-13
                       132
 Match length
                       83
 % identity
                      Zea mays precursor of the oxygen evolving complex 17 kDa
 NCBI Description
                      protein mRNA, complete cds
                       403154
 Seq. No.
                       LIB3431-060-P1-K1-F9
 Seq. ID
 Method
                       BLASTX
 NCBI GI
                       q417103
 BLAST score
                       577
 E value
                       1.0e-59
 Match length
                       115
 % identity
                       100
                      HISTONE H3.2, MINOR >gi 282871 pir S24346 histone
 NCBI Description
                       H3.3-like protein - Arabidopsis thaliana
                       >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
                       [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
                       histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                       (U09458) histone H3.2 [Medicago sativa] >gi_488567 (\overline{U}09460)
                      histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulativa] >gi_510911 emb_CAA58445 (X83422)
                       histone H3 variant H3.3 [Lycopersicon esculentum]
                       >qi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
                       >gi 3273350 dbj BAA31218_ (AB015760) histone H3 [Nicotiana
```

tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana] >gi 6006364 dbj BAA84794.1 (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to histone H3 (AB015760) [Oryza sativa]

403155 Seq. No. LIB3431-060-P1-K1-G1 Seq. ID Method BLASTX NCBI GI g2072555 BLAST score 232 3.0e-19 E value Match length 43 100 % identity

(AF001396) metallothionein-like protein [Oryza sativa] NCBI Description >qi 6103441 gb AAF03603.1 (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 403156

LIB3431-060-P1-K1-G11 Seq. ID

Method BLASTX g3789954 NCBI GI BLAST score 744 E value 3.0e-79 Match length 136 % identity 99

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

403157 Seq. No.

LIB3431-060-P1-K1-G12 Seq. ID

Method BLASTN g5006852 NCBI GI BLAST score 176 E value 3.0e-94 Match length 336 % identity 98

Oryza sativa homeodomain leucine zipper protein (hox4) NCBI Description

mRNA, complete cds

403158 Seq. No.

Seq. ID LIB3431-060-P1-K1-G2

Method BLASTX NCBI GI q131192 BLAST score 209 E value 2.0e-16 Match length 44 % identity

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR

(PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >qi 100606 pir S20937

photosystem I chain V precursor - barley
>gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide

PSI-G precursor [Hordeum vulgare]

```
403159
Seq. No.
                  LIB3431-060-P1-K1-G3
Seq. ID
Method
                  BLASTX
                  g2072555
NCBI GI
                  237
BLAST score
                  9.0e-20
E value
                  44
Match length
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  403160
Seq. No.
                  LIB3431-060-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g2407281
NCBI GI
BLAST score
                  700
                   4.0e-74
E value
                  131
Match length
                   99
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   403161
                  LIB3431-060-P1-K1-G6
Seq. ID
Method
                  BLASTX
                   g2501189
NCBI GI
BLAST score
                   257
E value
                   3.0e-22
                   121
Match length
                   58
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
                   403162
Seq. No.
                   LIB3431-060-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4544428
BLAST score
                   214
                   3.0e-17
E value
Match length
                   51
                   76
% identity
                  (AC006955) unknown protein [Arabidopsis thaliana]
NCBI Description
                   403163
Seq. No.
                   LIB3431-060-P1-K1-G8
Seq. ID
Method
                   BLASTX
                   g1053047
NCBI GI
BLAST score
                   591
                   3.0e-61
E value
                   118
Match length
% identity
                   100
                   (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
NCBI Description
```

[Glycine max]

histone H3 [Glycine max] >gi_1053051 (U38427) histone H3

Seq. No.

Seq. ID

403168

LIB3431-060-P1-K1-H3

```
Seq. No.
                  403164
Seq. ID
                  LIB3431-060-P1-K1-H1
Method
                  BLASTX
                  g6006270
NCBI GI
                   196
BLAST score
                   5.0e-15
E value
Match length
                   66
% identity
                   47
                  (AB022692) TAF-Ibeta2 [Xenopus laevis]
NCBI Description
                   403165
Seq. No.
                  LIB3431-060-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g132105
                   488
BLAST score
                   3.0e-49
E value
                   110
Match length
                   85
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375_prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403166
Seq. No.
                   LIB3431-060-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   293
                   1.0e-26
E value
Match length
                   73
                   77
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   403167
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-H2
Method
                   BLASTX
                   q2344889
NCBI GI
                   297
BLAST score
E value
                   7.0e-27
                   133
Match length
% identity
                   (AC002388) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4895255_gb_AAD32840.1_AC007659_22 (AC007659) unknown
                   protein [Arabidopsis thaliana]
```



```
BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   567
E value
                   2.0e-58
Match length
                   122
                   87
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403169
Seq. No.
                   LIB3431-060-P1-K1-H4
Seq. ID
Method
                   BLASTX
                   g2306981
NCBI GI
BLAST score
                   503
                   5.0e-51
E value
                   90
Match length
                   98
% identity
                  (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
                   403170
Seq. No.
                   LIB3431-060-P1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2501189
                   547
BLAST score
                   3.0e-56
E value
                   111
Match length
                   95
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
                   403171
Seq. No.
                   LIB3431-060-P1-K1-H7
Seq. ID
Method
                   BLASTX
                   q3789952
NCBI GI
                   560
BLAST score
E value
                   1.0e-57
Match length
                   112
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403172
Seq. ID
                   LIB3431-060-P1-K1-H9
Method
                   BLASTN
```

Method BLASTN
NCBI GI g2062705
BLAST score 35
E value 4.0e-10
Match length 35

```
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  403173
Seq. No.
                  LIB3431-060-P1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  327
                  2.0e-30
E value
                  75
Match length
                  83
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir __S33632
NCBI Description
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
                  403174
Seq. No.
                  LIB3431-060-P1-N1-A3
Seq. ID
                  BLASTN
Method
                  g2073379
NCBI GI
BLAST score
                  154
                  3.0e-81
E value
                  173
Match length
                  97
% identity
NCBI Description Rice CP26 mRNA, partial sequence
                  403175
Seq. No.
                  LIB3431-060-P1-N1-A4
Seq. ID
                  BLASTX
Method
                  g4098250
NCBI GI
BLAST score
                  160
                   7.0e-11
E value
                   56
Match length
                   50
% identity
                  (U76611) similar to Solanum tuberosum ci21A gene product
NCBI Description
                   encoded by the sequence presented in GenBank Accession
                   Number U76610 [Solanum tuberosum]
Seq. No.
                   403176
Seq. ID
                  LIB3431-060-P1-N1-A6
Method
                   BLASTN
                   g218207
NCBI GI
                   279
BLAST score
                   1.0e-156
E value
Match length
                   291
                   99
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS1139
                   403177
Seq. No.
Seq. ID
                   LIB3431-060-P1-N1-B4
                   BLASTN
Method
                   q11957
NCBI GI
                   65
BLAST score
```

5.0e-28

84

48

E value Match length

% identity

```
403178
Seq. No.
                  LIB3431-060-P1-N1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q20181
BLAST score
                  163
                  2.0e-86
E value
Match length
                  177
                  98
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  403179
Seq. ID
                  LIB3431-060-P1-N1-B7
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  559
                  2.0e-57
E value
Match length
                  111
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  403180
Seq. No.
                  LIB3431-060-P1-N1-C1
Seq. ID
Method
                  BLASTN
                  g3885887
NCBI GI
BLAST score
                  221
                  1.0e-121
E value
                  296
Match length
% identity
                  93
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                  complete cds
                  403181
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-C10
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  174
E value
                  2.0e-12
Match length
                  48
% identity
                  65
NCBI Description
                  (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                  403182
                  LIB3431-060-P1-N1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2316016
BLAST score
                  150
E value
                  2.0e-09
Match length
                  71
% identity
                  44
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
```

NCBI Description Rice complete chloroplast genome

```
Seq. No.
                  403183
Seq. ID
                  LIB3431-060-P1-N1-C12
Method
                  BLASTN
NCBI GI
                  q3789953
BLAST score
                  298
E value
                  1.0e-167
Match length
                  298
                  100
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein precursor
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  403184
Seq. No.
                  LIB3431-060-P1-N1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885885
BLAST score
                  144
                  3.0e-75
E value
                  167
Match length
% identity
                  Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  403185
                  LIB3431-060-P1-N1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  a2072554
BLAST score
                  186
E value
                  1.0e-100
Match length
                  210
                   97
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                   403186
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-C6
Method
                  BLASTX
NCBI GI
                  q3885886
BLAST score
                   630
E value
                   9.0e-66
Match length
                  112
% identity
                   99
NCBI Description
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.
                   403187
Seq. ID
                  LIB3431-060-P1-N1-C9
Method
                  BLASTX
NCBI GI
                  g3184292
BLAST score
                  287
                  1.0e-25
E value
                  56
Match length
                   86
% identity
                  (AC004136) putative nucleic acid binding protein, 5'
NCBI Description
                  partial [Arabidopsis thaliana]
```

403188

Seq. No.



```
LIB3431-060-P1-N1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913811
                  367
BLAST score
                  4.0e-35
E value
Match length
                  91
% identity
                  GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
NCBI Description
                  >gi 2920320 dbj BAA25003_ (AB011416) glutamyl-tRNA
                  reductase [Oryza sativa]
                  403189
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-D12
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  345
                  1.0e-32
E value
                  65
Match length
% identity
                  100
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  403190
Seq. No.
                  LIB3431-060-P1-N1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266567
BLAST score
                  306
E value
                  8.0e-28
                  87
Match length
% identity
                   66
                  MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
NCBI Description
                   (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
                   >gi_421956_pir__S23558 mitochondrial processing peptidase
                   (EC 3.4.99.41) alpha chain precursor - potato
                   >gi_21493_emb_CAA46990_ (X66284) mitochondrial processing
                   peptidase [Solanum tuberosum]
                   403191
Seq. No.
                  LIB3431-060-P1-N1-D4
Seq. ID
                   BLASTX
Method
                   q733456
NCBI GI
BLAST score
                   352
                 2.0e-33
E value
                   73
Match length
                   95
% identity
NCBI Description
                   (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
                   403192
Seq. No.
Seq. ID
                   LIB3431-060-P1-N1-D8
Method
                   BLASTX
NCBI GI
                   q3850577
```

BLAST score 185 E value 6.0e-16 Match length 120 % identity

(AC005278) This gene may be cut off. [Arabidopsis thaliana] NCBI Description

Method

BLASTN

```
Seq. No.
                  403193
Seq. ID
                  LIB3431-060-P1-N1-E10
Method
                  BLASTX
NCBI GI
                  g5640111
BLAST score
                  305
                  1.0e-27
E value
                  83
Match length
                  72
% identity
NCBI Description (AJ243875) RAD23 protein [Lycopersicon esculentum]
                  403194
Seq. No.
                  LIB3431-060-P1-N1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
                  319
BLAST score
                  2.0e-29
E value
                  61
Match length
                  100
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  403195
Seq. No.
                  LIB3431-060-P1-N1-E8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g218171
                  40
BLAST score
                  3.0e-13
E value
Match length
                  107
                  85
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
                  403196
Seq. No.
                  LIB3431-060-P1-N1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  268
E value
                   1.0e-149
Match length
                   280
% identity
                   99
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
Seq. No.
                   403197
                   LIB3431-060-P1-N1-F2
Seq. ID
                   BLASTN
Method
                   g5106766
NCBI GI
BLAST score
                   38
                   7.0e-12
E value
Match length
                   86
                   86
% identity
NCBI Description Arabidopsis thaliana BAC F17I23
                   403198
Seq. No.
                   LIB3431-060-P1-N1-F5
Seq. ID
```



```
q3789951
NCBI GI
BLAST score
                  186
                  1.0e-100
E value
Match length
                  379
                  98
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  403199
Seq. No.
                  LIB3431-060-P1-N1-F8
Seq. ID
Method
                  BLASTX
                  g517500
NCBI GI
BLAST score
                  530
                  4.0e-54
E value
                  126
Match length
                   83
% identity
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi_444338_prf_ 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                   403200
Seq. No.
                  LIB3431-060-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g70753
BLAST score
                   219
                   9.0e-18
E value
Match length
                   44
% identity
                   100
                  histone H3 - garden pea >gi 82610 pir S00373 histone H3 -
NCBI Description
                  wheat
                   403201
Seq. No.
                   LIB3431-060-P1-N1-G1
Seq. ID
Method
                   BLASTN
                   g2072554
NCBI GI
BLAST score
                   288
E value
                   1.0e-161
Match length
                   292
                   100
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   403202
Seq. No.
                   LIB3431-060-P1-N1-G11
Seq. ID
Method
                   BLASTX
                   g3789954
NCBI GI
BLAST score
                   241
E value
                   2.0e-20
Match length
                   43
% identity
                   100
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
```

403203 Seq. No.

Seq. ID LIB3431-060-P1-N1-G12 BLASTN

sativa]

Method

```
q5006852
NCBI GI
BLAST score
                  225
                  1.0e-123
E value
                  293
Match length
% identity
                  Oryza sativa homeodomain leucine zipper protein (hox4)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  403204
                  LIB3431-060-P1-N1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131192
BLAST score
                  209
                  2.0e-16
E value
Match length
                  44
% identity
                  86
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 100606 pir__S20937
                  photosystem I chain V precursor - barley
                  >gi 19091 emb CAA42727 (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
                  403205
Seq. No.
                  LIB3431-060-P1-N1-G3
Seq. ID
                  BLASTX
Method
                  g2072555
NCBI GI
BLAST score
                  237
                  1.0e-19
E value
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  403206
Seq. No.
                  LIB3431-060-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  186
E value
                  6.0e-14
Match length
                  35
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

403207 Seq. No. Seq. ID

LIB3431-060-P1-N1-G7

Method BLASTX NCBI GI q4544428 BLAST score 294

2.0e-26 E value Match length 81 % identity 69 (AC006955) unknown protein [Arabidopsis thaliana] NCBI Description 403208 Seq. No. Seq. ID LIB3431-060-P1-N1-G8 Method BLASTX NCBI GI q417103 BLAST score 283 E value 4.0e-25 Match length 58 % identity 98 NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] $>gi_4885\overline{7}7$ (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone

[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone
H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)
histone H3 variant H3.3 [Lycopersicon esculentum]
>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

>gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425)
corresponds to a region of the predicted gene.; Similar to

histone H3 (AB015760) [Oryza sativa]

Seq. No. 403209

Seq. ID LIB3431-060-P1-N1-H10

Method BLASTX
NCBI GI g671740
BLAST score 499
E value 2.0e-50
Match length 91
% identity 99

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

Seq. No. 403210

Seq. ID LIB3431-060-P1-N1-H11

Method BLASTX
NCBI GI g3036951
BLAST score 282
E value 3.0e-25
Match length 54
% identity 100

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

```
Seq. No.
                  403211
Seq. ID
                  LIB3431-060-P1-N1-H12
Method
                  BLASTX
                  q3318613
NCBI GI
                  156
BLAST score
E value
                  2.0e-10
                  34
Match length
                  85
% identity
NCBI Description (AB016064) mitochondrial phosphate transporter [Zea mays]
Seq. No.
                  403212
Seq. ID
                  LIB3431-060-P1-N1-H3
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  303
                  1.0e-170
E value
Match length
                  319
% identity
                  99
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
                  403213
Seq. No.
                  LIB3431-060-P1-N1-H4
Seq. ID
Method
                  BLASTX
                  g551047
NCBI GI
                  210
BLAST score
E value
                  9.0e-17
                  41
Match length
                  93
% identity
NCBI Description (X79277) type II LHCI [Lolium temulentum]
Seq. No.
                  403214
Seq. ID
                  LIB3431-060-P1-N1-H7
Method
                  BLASTN
NCBI GI
                  q3789951
BLAST score
                  243
E value
                  1.0e-134
Match length
                  356
% identity
                  91
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  403215
Seq. ID
                  LIB3431-061-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  g2696224
BLAST score
                  41
                  9.0e-14
E value
Match length
                  109
% identity
                  84
NCBI Description Oryza sativa mRNA for chitinase, complete cds
                  403216
Seq. No.
                  LIB3431-061-P1-K1-A10
Seq. ID
```

% identity

100

```
BLASTX
Method
                  g132105
NCBI GI
BLAST score
                   327
                  8.0e-41
E value
                  108
Match length
% identity
                  83
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxy\overline{l}ase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403217
Seq. No.
                  LIB3431-061-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3345477
                   232
BLAST score
                   2.0e-19
E value
Match length
                   85
                   55
% identity
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   403218
Seq. No.
                   LIB3431-061-P1-K1-A12
Seq. ID
Method
                   BLASTX
                   g82080
NCBI GI
BLAST score
                   310
                   1.0e-28
E value
Match length
                   90
                   68
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872_prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   403219
                   LIB3431-061-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455248
BLAST score
                   150
E value
                   1.0e-09
Match length
                   69
% identity
                   51
                  (AL035523) acyl carrier-like protein [Arabidopsis thaliana]
NCBI Description
                   403220
Seq. No.
                   LIB3431-061-P1-K1-A3
Seq. ID
Method
                   BLASTX
                   a3913018
NCBI GI
                   570
BLAST score
                   7.0e-59
E value
Match length
                   115
```

51850

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

```
403221
 Seq. No.
                    LIB3431-061-P1-K1-A4
 Seq. ID
 Method
                    BLASTN
                    q20262
 NCBI GI
 BLAST score
                    330
                    0.0e+00
 E value
 Match length
                    346
                    99
 % identity
 NCBI Description O.sativa light-induced mRNA
                    403222
 Seq. No.
 Seq. ID
                    LIB3431-061-P1-K1-A6
 Method
                    BLASTX
                    g2351846
 NCBI GI
 BLAST score
                    146
                    3.0e-09
E value
                    123
 Match length
 % identity
                    30
                   (U93050) poly(A) binding protein II [Mus musculus]
 NCBI Description
                    403223
 Seq. No.
                    LIB3431-061-P1-K1-A8
 Seq. ID
 Method
                   BLASTN
                    q3063523
 NCBI GI
 BLAST score
                    176
                    2.0e-94
 E value
 Match length
                    219
                    95
 % identity
                    Oryza sativa ribulose 1,5-bisphosphate carboxylase small
 NCBI Description
                    subunit mRNA, complete cds
                    403224
 Seq. No.
                    LIB3431-061-P1-K1-A9
 Seq. ID
 Method
                    BLASTX
                    g1709846
 NCBI GI
 BLAST score
                    163
                    4.0e-11
 E value
 Match length
                    118
 % identity
                    45
                    PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)
 NCBI Description
                    22 kDa component of photosystem II [Lycopersicon
                    esculentum]
                    403225
  Seq. No.
                    LIB3431-061-P1-K1-B10
  Seq. ID
 Method
                    BLASTX
                    g115813
 NCBI GI
 BLAST score
                    243
                    1.0e-20
 E value
                    55
 Match length
                    85
  % identity
                    CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
 NCBI Description
                    CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
```

(ALDP) >gi 218155 dbj_BAA02730_ (D13513) chloroplastic

aldolase [Oryza sativa]

51851

chlorophyll a/b-binding protein [Lycopersicon esculentum]

E value

1.0e-42

```
403226
Seq. No.
                  LIB3431-061-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4165550
                  567
BLAST score
                  1.0e-58
E value
Match length
                  121
% identity
                  88
                  (AJ004915) apgm [Malus domestica]
NCBI Description
                  403227
Seq. No.
                  LIB3431-061-P1-K1-B2
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
                  477
BLAST score
                  5.0e-48
E value
                  106
Match length
                  85
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  403228
Seq. No.
                  LIB3431-061-P1-K1-B3
Seq. ID
Method
                  BLASTX
                  g3913192
NCBI GI
                  142
BLAST score
                  9.0e-09
E value
                  70
Match length
% identity
                  47
                  CYTOCHROME P450 93A1 >gi_2129824_pir__$62899 cytochrome
NCBI Description
                  P450 (CYP93 A1) - soybean >gi_1232111_dbj_BAA12159_
                   (D83968) Cytochrome P-450 (CYP93A1) [Glycine max]
                  >gi_1588679_prf__2209281A cytochrome P450 [Glycine max]
Seq. No.
                  403229
                  LIB3431-061-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q400879
BLAST score
                  202
E value
                   6.0e-16
Match length
                  102
% identity
                   48
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_479690_pir__S35159 photosystem I chain psaN -
                   barley >gi_19095_emb_CAA47056_ (X66428) photosystem I
                   subunit N [Hordeum vulgare]
                   403230
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-B7
                  BLASTX
Method
                  g733454
NCBI GI
BLAST score
                   431
```

% identity

NCBI Description

60

```
Match length
% identity
NCBI Description
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
                  403231
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-C10
Method
                  BLASTX
                  g4586058
NCBI GI
                  209
BLAST score
E value
                  2.0e-17
Match length
                  116
% identity
                  46
                  (AC007020) unknown protein [Arabidopsis thaliana]
NCBI Description
                  403232
Seq. No.
                  LIB3431-061-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  47
                  3.0e-17
E value
Match length
                  199
% identity
                  81
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                  403233
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-C2
Method
                  BLASTX
                  g1052960
NCBI GI
BLAST score
                  748
                  1.0e-79
E value
Match length
                  146
% identity
                  91
NCBI Description
                  (U37437) PNIL34 [Ipomoea nil]
Seq. No.
                   403234
Seq. ID
                  LIB3431-061-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  g1304214
BLAST score
                  51
E value
                  1.0e-19
Match length
                  95
% identity
                  88
NCBI Description
                  Rice mRNA for precursor of 22 kDa protein of photosystem II
                   (PSII-S), complete cds
Seq. No.
                   403235
Seq. ID
                  LIB3431-061-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q729668
BLAST score
                  197
                  3.0e-15
E value
                  58
Match length
```

51853

HISTONE H1 >gi 2147479 pir S65059 histone H1,

drought-inducible - Lycopersicon pennellii >gi 436823

E value

Match length

% identity

9.0e-35

109

64





(U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No. 403236 LIB3431-061-P1-K1-C5 Seq. ID Method BLASTX NCBI GI q417154 BLAST score 370 1.0e-35 E value 98 Match length 85 % identity HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock NCBI Description protein 82 - rice (strain Taichung Native One) >gi 20256 emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa] 403237 Seq. No. LIB3431-061-P1-K1-C6 Seq. ID BLASTN Method g218207 NCBI GI 191 BLAST score 1.0e-103 E value 191 Match length 100 % identity Oryza sativa mRNA for the small subunit of NCBI Description ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139 403238 Seq. No. LIB3431-061-P1-K1-C7 Seq. ID BLASTX Method g4850382 NCBI GI 152 BLAST score 7.0e-10 E value 70 Match length % identity 44 (ACO07357) Similar to gb D38124 EREBP-3 from Nicotiana NCBI Description tabacum and contains PF $\overline{0}0847$ AP2 domain. [Arabidopsis thaliana] Seq. No. 403239 LIB3431-061-P1-K1-C8 Seq. ID Method BLASTX q3126854 NCBI GI 670 BLAST score E value 1.0e-70 126 Match length % identity 100 (AF061577) chlorophyll a/b binding protein [Oryza sativa] NCBI Description 403240 Seq. No. Seq. ID LIB3431-061-P1-K1-C9 Method BLASTX NCBI GI q3158476 BLAST score 310

NCBI Description

```
(AF067185) aquaporin 2 [Samanea saman]
NCBI Description
Seq. No.
                  403241
                  LIB3431-061-P1-K1-D11
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
BLAST score
                  540
E value
                  2.0e-55
                  117
Match length
                  86
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  403242
Seq. No.
                  LIB3431-061-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  591
                  3.0e-61
E value
                  127
Match length
% identity
                  87
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403243
                  LIB3431-061-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2864617
                  154
BLAST score
E value
                  4.0e-10
Match length
                  62
% identity
                  55
                  (AL021811) H+-transporting ATP synthase chain9 - like
NCBI Description
                  protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1_
                   (AJ245574) ATP synthase beta chain precursor (subunit II)
                  [Arabidopsis thaliana]
Seq. No.
                  403244
Seq. ID
                  LIB3431-061-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2293480
BLAST score
                  344
                  2.0e-40
E value
Match length
                  89
% identity
                  96
```

(AF011331) glycine-rich protein [Oryza sativa]

```
Seq. No.
                  403245
Seq. ID
                  LIB3431-061-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  612
                  8.0e-64
E value
Match length
                  114
% identity
                  100
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  403246
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4115913
BLAST score
                  236
                  1.0e-19
E value
                  78
Match length
                  54
% identity
NCBI Description
                  (AF118222) contains similarity to Iron/Ascorbate family of
                  oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88,
                  N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_
                   (AL049524) putative flavanone 3-beta-hydroxylase
                   [Arabidopsis thaliana]
Seq. No.
                  403247
Seq. ID
                  LIB3431-061-P1-K1-D6
Method
                  BLASTN
                  g505134
NCBI GI
BLAST score
                  154
E value
                  5.0e-81
Match length
                  230
% identity
                  92
NCBI Description Rice mRNA for ferredoxin, complete cds
Seq. No.
                  403248
Seq. ID
                  LIB3431-061-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q2407281
BLAST score
                  522
E value
                  3.0e-53
Match length
                  99
                  99
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  403249
Seq. ID
                  LIB3431-061-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3047064
BLAST score
                  293
E value
                  2.0e-26
Match length
                  116
% identity
                   (AF058825) contains similarity to peptidyl-prolyl cis-trans
NCBI Description
                  isomerase (Pfam: pro isomerase.hmm, score: 23.86 and 28.41
```

[Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4803924
BLAST score
                  571
                  6.0e-59
E value
Match length
                  141
                  77
% identity
                  (AC006264) putative ER lumen protein retaining receptor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  403251
Seq. ID
                  LIB3431-061-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2492519
BLAST score
                  401
E value
                  1.0e-45
Match length
                  97
% identity
                  86
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
                  7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                  subunit [Spinacia oleracea]
Seq. No.
                  403252
Seq. ID
                  LIB3431-061-P1-K1-E12
Method
                  BLASTX
                  g3135751
NCBI GI
BLAST score
                  398
E value
                  9.0e-39
Match length
                  79
% identity
                  95
                  (AJ006095) 26S protease regulatory subunit 6 [Cicer
NCBI Description
                  arietinum]
Seq. No.
                  403253
Seq. ID
                  LIB3431-061-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q417260
BLAST score
                  381
E value
                  1.0e-36
Match length
                  121
% identity
NCBI Description
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  403254
Seq. ID
                  LIB3431-061-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q2570511
BLAST score
                  307
```

E value 5.0e-28 Match length 94 % identity 66

NCBI Description (AF022738) chlorophyll a-b binding protein [Oryza sativa]

Seq. No. 403255

```
Seq. ID
                  LIB3431-061-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  552
E value
                  1.0e-56
Match length
                  105
% identity
                  99
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  403256
Seq. No.
                  LIB3431-061-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1881585
BLAST score
                  187
E value
                  5.0e-14
Match length
                  44
% identity
                  80
NCBI Description (U72489) remorin [Solanum tuberosum]
Seq. No.
                  403257
                  LIB3431-061-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q401190
BLAST score
                  669
E value
                  2.0e-70
                  128
Match length
% identity
                  96
                  THAUMATIN-LIKE PROTEIN PRECURSOR >gi_100715_pir__$25551
NCBI Description
                  thaumatin-like protein - rice >gi 20376 emb CAA48278
                  (X68197) thaumatin-like protein [Oryza sativa]
Seq. No.
                  403258
                  LIB3431-061-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3775987
BLAST score
                  430
E value
                  2.0e-42
Match length
                  112
% identity
                  71
NCBI Description
                  (AJ010457) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  403259
Seq. ID
                  LIB3431-061-P1-K1-F11
```

Method BLASTX
NCBI GI g131225
BLAST score 311
E value 1.0e-28
Match length 105
% identity 65

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi 167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

```
Seq. No.
                  403260
                  LIB3431-061-P1-K1-F12
Seq. ID
                  BLASTN
Method
                  q11957
NCBI GI
BLAST score
                  47
                  2.0e-17
E value
Match length
                  87
                  44
% identity
NCBI Description Rice complete chloroplast genome
                  403261
Seq. No.
                  LIB3431-061-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2653558
BLAST score
                  606
                  4.0e-63
E value
Match length
                  124
% identity
                  93
NCBI Description (D50679) ferredoxin-sulfite reductase precursor [Zea mays]
Seq. No.
                  403262
                  LIB3431-061-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  8.0e-20
E value
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  403263
                  LIB3431-061-P1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6006355
                  36
BLAST score
                  1.0e-10
E value
Match length
                  44
                  95
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  403264
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q2315363
BLAST score
                  212
E value
                  7.0e-17
Match length
                  115
% identity
                  (AF016441) No definition line found [Caenorhabditis
NCBI Description
                  elegans]
Seq. No.
                  403265
Seq. ID
                  LIB3431-061-P1-K1-F8
Method
                  BLASTN
```

```
g6015437
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
Match length
                  47
                  65
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  403266
                  LIB3431-061-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
                  40
BLAST score
E value
                  4.0e-13
Match length
                  40
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  403267
Seq. No.
                  LIB3431-061-P1-K1-G1
Seq. ID
Method
                  BLASTN
                  g4138289
NCBI GI
                  300
BLAST score
                  1.0e-168
E value
Match length
                  312
% identity
                  99
NCBI Description Oryza sativa mRNA for thioredoxin M
                  403268
Seq. No.
                  LIB3431-061-P1-K1-G10
Seq. ID
Method
                  BLASTX
                  g4105561
NCBI GI
BLAST score
                  568
                  1.0e-58
E value
Match length
                  127
% identity
                  89
NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
                  403269
Seq. No.
                  LIB3431-061-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  q320618
NCBI GI
                  409
BLAST score
                  5.0e-40
E value
                  98
Match length
% identity
                  80
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  403270
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g3057120
                  256
BLAST score
```

2.0e-22

E value

```
Match length
% identity
                  66
NCBI Description
                  (AF023159) starch synthase DULL1 [Zea mays]
                  403271
Seq. No.
                  LIB3431-061-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3790102
BLAST score
                  594
                  1.0e-61
E value
Match length
                  133
                  84
% identity
                  (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                  alpha subunit [Citrus X paradisi]
Seq. No.
                  403272
                  LIB3431-061-P1-K1-G4
Seq. ID
Method
                  BLASTX
                  g1173275
NCBI GI
BLAST score
                  159
                  4.0e-11
E value
Match length
                  47
                  70
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
NCBI Description
                  >gi_2119068_pir__S58630 ribosomal protein S7 - maize
                  chloroplast >gi 902274 emb CAA60339 (X86563) ribosomal
                  protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
                  ribosomal protein S7 [Zea mays]
                  403273
Seq. No.
                  LIB3431-061-P1-K1-G6
Seq. ID
                  BLASTX
Method
                  q1498315
NCBI GI
BLAST score
                  355
                  1.0e-33
E value
Match length
                  126
% identity
                  58
NCBI Description
                  (U56419) IAP100 [Pisum sativum]
Seq. No.
                  403274
Seq. ID
                  LIB3431-061-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q5931694
BLAST score
                  410
E value
                  3.0e-40
Match length
                  104
% identity
NCBI Description
                  (Y18470) Exportin1 (XPO1) protein [Arabidopsis thaliana]
Seq. No.
                  403275
Seq. ID
                  LIB3431-061-P1-K1-H10
                  BLASTN
Method
NCBI GI
                  g1144509
BLAST score
                  36
E value
                  1.0e-10
                  44
Match length
                  95
% identity
```



```
NCBI Description Oryza sativa wanderer mobile element linked to Xa21
                  403276
Seq. No.
                  LIB3431-061-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g81946
BLAST score
                  453
E value
                  2.0e-45
Match length
                  91
                  92 、
% identity
NCBI Description
                  protochlorophyllide reductase (EC 1.3.1.33) precursor -
                  garden pea
Seq. No.
                  403277
                  LIB3431-061-P1-K1-H12
Seq. ID
Method
                  BLASTN
                  g949979
NCBI GI
BLAST score
                  36
E value
                  1.0e-10
Match length
                  60
                  90
% identity
NCBI Description Z.mays Glossy2 locus DNA
Seq. No.
                  403278
Seq. ID
                  LIB3431-061-P1-K1-H3
Method
                  BLASTX
                  g3789954
NCBI GI
BLAST score
                  559
E value
                  1.0e-57
Match length
                  109
                  96
% identity
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
Seq. No.
                  403279
Seq. ID
                  LIB3431-061-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2435511
BLAST score
                  474
E value
                  1.0e-47
Match length
                  111
% identity
                  (AF024504) contains similarity to prolyl 4-hydroxylase
NCBI Description
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  403280
Seq. ID
                  LIB3431-061-P1-K1-H5
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3947448
BLAST score 212
E value 5.0e-17
Match length 102
% identity 44

NCBI Description (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene; cDNA EST ...

% identity

84

>gi_3947543_emb_CAA88952.1_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene; cDNA EST yk

```
403281
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-H6
Method
                  BLASTN
                  g949979
NCBI GI
BLAST score
                  49
E value
                  1.0e-18
Match length
                  97
% identity
                  88
NCBI Description Z.mays Glossy2 locus DNA
                  403282
Seq. No.
                  LIB3431-061-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  g1483213
NCBI GI
BLAST score
                  308
                  4.0e-28
E value
                  108
Match length
                  56
% identity
NCBI Description
                  (X96480) PAC [Arabidopsis thaliana]
                  >gi 5729705 gb AAD48512.1 AC007927 2 (AC007927) pale cress
                  protein [Arabidopsis thaliana]
Seq. No.
                  403283
Seq. ID
                  LIB3431-061-P1-K1-H9
Method
                  BLASTX
                  g3075488
NCBI GI
BLAST score
                  705
E value
                  1.0e-74
Match length
                  137
% identity
                  99
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  403284
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q3885888
BLAST score
                  321
                  1.0e-29
E value
Match length
                  108
% identity
                  66
                  (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
Seq. No.
                  403285
Seq. ID
                  LIB3431-062-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q3929545
BLAST score
                  425
E value
                  9.0e-42
Match length
                  107
```

51863

NCBI Description (AF067194) S-adenosylmethionine decarboxylase [Oryza

NCBI Description

403291

Seq. No.



sativa]

```
403286
Seq. No.
                  LIB3431-062-P1-K1-A12
Seq. ID
                  BLASTX
Method
                  q5360591
NCBI GI
BLAST score
                   476
                   9.0e-48
E value
Match length
                  149
                   60
% identity
NCBI Description
                  (AB022328) nClpP3 [Arabidopsis thaliana]
Seq. No.
                  403287
                  LIB3431-062-P1-K1-A2
Seq. ID
Method
                  BLASTX
                   g419742
NCBI GI
BLAST score
                   624
E value
                   3.0e-65
Match length
                  127
                  91
% identity
                  protochlorophyllide reductase (EC 1.3.1.33) precursor -
NCBI Description
                   loblolly pine
                   403288
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-A3
Method
                  BLASTX
                   g548603
NCBI GI
BLAST score
                   434
                   7.0e-43
E value
Match length
                   130
% identity
                   70
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                   barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                   403289
Seq. No.
                   LIB3431-062-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   a1835731
BLAST score
                   180
                   9.0e-14
E value
                   44
Match length
                   80
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                   403290
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   648
E value
                   1.0e-73
Match length
                   150
                   93
% identity
```

51864

(AF061577) chlorophyll a/b binding protein [Oryza sativa]



```
LIB3431-062-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4138289
                  228
BLAST score
                  1.0e-125
E value
                  276
Match length
                  96
% identity
NCBI Description Oryza sativa mRNA for thioredoxin M
Seq. No.
                  403292
                  LIB3431-062-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131388
BLAST score
                  250
                  2.0e-21
E value
                  95
Match length
                  65
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
Seq. No.
                  403293
                  LIB3431-062-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4914411
BLAST score
                  363
                  2.0e-34
E value
Match length
                  105
% identity
                  68
NCBI Description
                  (AL050352) putative protein [Arabidopsis thaliana]
Seq. No.
                  403294
Seq. ID
                  LIB3431-062-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q4733937
BLAST score
                  264
E value
                  8.0e-23
Match length
                  146
% identity
                  42
NCBI Description
                  (AF080245) sesquiterpene synthase [Elaeis oleifera]
                  403295
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q1261917
BLAST score
                  339
```

E value 1.0e-31 Match length 96 % identity 62

(X96979) lipid transfer protein 7a2b [Hordeum vulgare] NCBI Description

403296 Seq. No.

LIB3431-062-P1-K1-B5 Seq. ID

```
Method
                   BLASTX
NCBI GI
                   q1617197
BLAST score
                   298
                   7.0e-27
E value
                   76
Match length
% identity
                   75
                   (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                   403297
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g2245015
BLAST score
                   463
                   3.0e-46
E value
Match length
                   107
% identity
                   80
NCBI Description
                   (Z97341) glucosyltransferase like protein [Arabidopsis
                   thaliana]
Seq. No.
                   403298
Seq. ID
                   LIB3431-062-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g2286121
BLAST score
                   521
                   5.0e-53
E value
Match length
                   102
% identity
                   97
NCBI Description (U88068) sec14 like protein [Oryza sativa]
                   403299
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   g871931
BLAST score
                   248
                   6.0e-21
E value
                   75
Match length
                   68
% identity
NCBI Description
                   (D30763) ferredoxin [Oryza sativa]
Seq. No.
                   403300
Seq. ID
                   LIB3431-062-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g115772
BLAST score
                   156
                   6.0e-11
E value
Match length
                   32
                   100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
Seq. No.
                   403301
Seq. ID
                   LIB3431-062-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g5091520
```



BLAST score 204 E value 6.0e-16 Match length 130 % identity 45

NCBI Description (AB023482) ESTs AU058081(E30812), AU058365(E50679),

AU030138(E50679) correspond to a region of the predicted gene.; Similar to Spinacia oleracea mRNA for proteasome

37kD subunit.(X96974) [Oryza sativa]

Seq. No. 403302

Seq. ID LIB3431-062-P1-K1-C5

Method BLASTX
NCBI GI g132105
BLAST score 553
E value 7.0e-57
Match length 120
% identity 87

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403303

Seq. ID LIB3431-062-P1-K1-C6

Method BLASTX
NCBI GI g1854378
BLAST score 252
E value 1.0e-25
Match length 125
% identity 56

NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum

officinarum]

Seq. No. 403304

Seq. ID LIB3431-062-P1-K1-C7

Method BLASTX
NCBI GI g4972111
BLAST score 546
E value 6.0e-56
Match length 151
% identity 62

NCBI Description (AL078579) protein phosphatase homolog (PPH1) [Arabidopsis

thaliana]

Seq. No. 403305

Seq. ID LIB3431-062-P1-K1-C9

Method BLASTN
NCBI GI g2072554
BLAST score 188
E value 1.0e-101
Match length 196
% identity 99

```
Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  403306
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  g2267594
BLAST score
                  49
E value
                  4.0e-19
Match length
                  49
% identity
                  100
NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds
                  403307
Seq. No.
                  LIB3431-062-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  461
E value
                  5.0e-46
Match length
                  95
                  95
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  403308
                  LIB3431-062-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2244965
BLAST score
                  307
E value
                  3.0e-28
Match length
                  85
                  68
% identity
NCBI Description
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  403309
Seq. ID
                  LIB3431-062-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  3.0e-10
Match length
                  35
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  403310
Seq. ID
                  LIB3431-062-P1-K1-D3
Method
                  BLASTX
                  g21695
NCBI GI
BLAST score
                  361
                  3.0e - 34
E value
Match length
                  110
% identity
                  62
                  (X66014) cathepsin B [Triticum aestivum]
NCBI Description
Seq. No.
                  403311
                  LIB3431-062-P1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4585882
```

```
BLAST score
E value
                  2.0e-45
Match length
                  141
                  70
% identity
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  403312
                  LIB3431-062-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3290022
BLAST score
                  434
E value
                  9.0e-43
Match length
                  142
% identity
                  58
                  (AF044173) cysteine synthase; CS-B; O-acetylserine (thiol)
NCBI Description
                  lyase; plastidic isoform [Solanum tuberosum]
                  403313
Seq. No.
                  LIB3431-062-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201969
BLAST score
                  225
E value
                  2.0e-18
Match length
                  43
                  98
% identity
                  (AF068332) submergence induced protein 2A [Oryza sativa]
NCBI Description
                  403314
Seq. No.
                  LIB3431-062-P1-K1-E1
Seq. ID
Method
                  BLASTN
                  g2624325
NCBI GI
                  86
BLAST score
E value
                  9.0e-41
Match length
                  110
                  95
% identity
NCBI Description
                  Oryza sativa mRNA for glycine-rich RNA-binding protein
                   (OsGRP1)
Seq. No.
                  403315
Seq. ID
                  LIB3431-062-P1-K1-E11
Method
                  BLASTN
                  g218209
NCBI GI
                  155
BLAST score
E value
                  1.0e-81
Match length
                  281
% identity
                   96
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                  403316
Seq. ID
                  LIB3431-062-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g3618310
BLAST score
                   331
```

6.0e-31

E value

NCBI GI

E value

BLAST score

g2739375

3.0e-15

197

```
Match length
% identity
                   65
                  (AB001883) zinc finger protein [Oryza sativa]
NCBI Description
Seq. No.
                   403317
                  LIB3431-062-P1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g320618
BLAST score
                   476
                  8.0e-48
E value
                  115
Match length
                  80
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi 218172 dbj BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   403318
Seq. No.
                  LIB3431-062-P1-K1-E4
Seq. ID
Method
                   BLASTX
                   g2832606
NCBI GI
BLAST score
                   214
                   5.0e-17
E value
Match length
                   90
% identity
                   50
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3292810_emb_CAA19800.1_ (AL031018) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   403319
                   LIB3431-062-P1-K1-E5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2306981
BLAST score
                   409
                   2.0e-44
E value
                   98
Match length
                   91
% identity
                  (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
Seq. No.
                   403320
                   LIB3431-062-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4512705
BLAST score
                   483
E value
                   1.0e-48
Match length
                   144
                   69
% identity
                   (AC006569) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   403321
Seq. No.
                   LIB3431-062-P1-K1-E7
Seq. ID
Method
                   BLASTX
```

```
Match length
% identity
                   46
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                   403322
Seq. No.
                   LIB3431-062-P1-K1-E8
Seq. ID
Method
                   BLASTN
                   g5042437
NCBI GI
BLAST score
                   287
                   1.0e-160
E value
                   358
Match length
                   99
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                   403323
Seq. No.
                   LIB3431-062-P1-K1-F1
Seq. ID
                   BLASTX
Method
                   g4079798
NCBI GI
BLAST score
                   227
                   4.0e-20
E value
                   92
Match length
                   60
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   403324
Seq. No.
                   LIB3431-062-P1-K1-F10
Seq. ID
Method
                   BLASTX
                   g132105
NCBI GI
BLAST score
                   270
E value
                   4.0e-24
Match length
                   79
% identity
                   71
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403325
Seq. ID
                   LIB3431-062-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q5042462
BLAST score
                   221
E value
                   9.0e-18
Match length
                   109
% identity
                   (AC007789) putative negatively light-regulated protein
NCBI Description
```

[Oryza sativa]

Seq. No. 403326

Seq. ID LIB3431-062-P1-K1-F12

BLASTX Method



```
q2407281
NCBI GI
BLAST score
                   775
E value
                   7.0e-83
Match length
                   145
                   99
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
                   403327
Seq. No.
                   LIB3431-062-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885894
BLAST score
                   302
E value
                   1.0e-27
Match length
                   90
                   72
% identity
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                   403328
Seq. No.
                   LIB3431-062-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789952
BLAST score
                   290
E value
                   2.0e-26
Match length
                  71
                   86
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
Seq. No.
                   403329
                   LIB3431-062-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2407281
BLAST score
                   614
                   5.0e-64
E value
Match length
                   126
% identity
                   90
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   403330
Seq. ID
                   LIB3431-062-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   391
E value
                   7.0e-38
Match length
                   108
                   75
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
```

carboxylase S [Oryza sativa]

```
Seq. No.
                  403331
Seq. ID
                  LIB3431-062-P1-K1-G1
Method
                  BLASTX
                  g2462834
NCBI GI
                  293
BLAST score
E value
                  3.0e-26
Match length
                  106
                  57
% identity
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
                  403332
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  q1835730
BLAST score
                  156
E value
                  1.0e-82
Match length
                  164
% identity
                  99
NCBI Description
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                  complete cds
                  403333
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-G11
Method
                  BLASTX
                  g3126854
NCBI GI
BLAST score
                  289
E value
                  2.0e-26
Match length
                  57
% identity
                  98
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  403334
Seq. ID
                  LIB3431-062-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q3885892
BLAST score
                  667
E value
                  3.0e-70
Match length
                  136
% identity
                  94
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                  403335
Seq. ID
                  LIB3431-062-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q5031281
BLAST score
                  356
E value
                  1.0e-33
Match length
                  121
% identity
                  60
NCBI Description (AF139499) unknown [Prunus armeniaca]
                  403336
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
```



E value 9.0e-20 Match length 44 % identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 403337

Seq. ID LIB3431-062-P1-K1-G4

Method BLASTX
NCBI GI g5123711
BLAST score 467
E value 1.0e-46
Match length 148
% identity 62

NCBI Description (AL079347) putative protein [Arabidopsis thaliana]

Seq. No. 403338

Seq. ID LIB3431-062-P1-K1-G5

Method BLASTX
NCBI GI g132105
BLAST score 751
E value 6.0e-80
Match length 164
% identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403339

Seq. ID LIB3431-062-P1-K1-G6

Method BLASTX
NCBI GI g4973264
BLAST score 376
E value 4.0e-36
Match length 93
% identity 73

NCBI Description (AF144391) thioredoxin-like 5 [Arabidopsis thaliana]

Seq. No. 403340

Seq. ID LIB3431-062-P1-K1-G7

Method BLASTX
NCBI GI g3913018
BLAST score 515
E value 3.0e-52
Match length 125
% identity 81

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic

aldolase [Oryza sativa]

NCBI GI

```
Seq. No.
                    403341
 Seq. ID
                    LIB3431-062-P1-K1-G8
 Method
                    BLASTN
NCBI GI
                    q20369
 BLAST score
                    388
                    0.0e+00
 E value
 Match length
                    396
 % identity
                    99
                    Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
 NCBI Description
                    synthetase (EC 6.3.1.2) (clone lambda-GS31)
                    >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
                    chloroplast localising glutamine synthetase
                    403342
 Seq. No.
                    LIB3431-062-P1-K1-H2
 Seq. ID
 Method
                    BLASTX
                    g3289002
 NCBI GI
 BLAST score
                    590
 E value
                    4.0e-61
                    170
 Match length
                    42
 % identity
 NCBI Description (AF073522) CRP1 [Zea mays]
                    403343
 Seq. No.
 Seq. ID
                    LIB3431-062-P1-K1-H5
 Method
                    BLASTX
                    g2072555
 NCBI GI
                    237
 BLAST score
                    1.0e-19
 E value
 Match length
                    44
                    100
 % identity
                    (AF001396) metallothionein-like protein [Oryza sativa]
 NCBI Description
                    >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                    protein [Oryza sativa]
 Seq. No.
                    403344
 Seq. ID
                    LIB3431-062-P1-K1-H7
 Method
                    BLASTX
 NCBI GI
                    q132105
 BLAST score
                    606
                    5.0e-63
 E value
 Match length
                    131
                    87
 % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
                    403345
 Seq. No.
 Seq. ID
                    LIB3431-062-P1-K1-H9
 Method
                    BLASTN
```

51875

g6015437

```
BLAST score
E value
                  3.0e-10
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  403346
Seq. No.
                  LIB3431-062-P1-N1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885887
BLAST score
                  465
E value
                  0.0e+00
Match length
                  473
% identity
                  100
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
                  403347
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-A10
Method
                  BLASTX
                  g3913426
NCBI GI
BLAST score
                  362
                  2.0e-34
E value
Match length
                  67
% identity
                  100
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi 1532048 emb CAA69074 (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
Seq. No.
                  403348
Seq. ID
                  LIB3431-062-P1-N1-A2
Method
                  BLASTX
NCBI GI
                  g2598151
BLAST score
                  251
E value
                  2.0e-21
Match length
                  50
                  94
% identity
                  (AF027350) NADPH:protochlorophyllide oxidoreductase porB
NCBI Description
                  [Pinus taeda]
Seq. No.
                  403349
Seq. ID
                  LIB3431-062-P1-N1-A6
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  360
E value
                  3.0e-34
Match length
                  99
                  71
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
```

hydrophobic protein [Hordeum vulgare]

Seq. ID LIB3431-062-P1-N1-A7

403350

Method BLASTN NCBI GI g1835730

Seq. No.

% identity

70

```
BLAST score
                  6.0e-86
E value
Match length
                  282
% identity
                  89
NCBI Description
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                  complete cds
                  403351
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  g2570513
BLAST score
                  172
E value
                  2.0e-12
Match length
                  32
% identity
                  97
NCBI Description
                  (AF022739) chlorophyll a-b binding protein [Oryza sativa]
                  403352
Seq. No.
                  LIB3431-062-P1-N1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4138290
BLAST score
                  313
E value
                  1.0e-28
Match length
                  63
                  97
% identity
NCBI Description
                  (AJ005841) thioredoxin M [Oryza sativa]
Seq. No.
                  403353
                  LIB3431-062-P1-N1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5931625
BLAST score
                  529
E value
                  6.0e-54
Match length
                  111
% identity
                  94
NCBI Description
                  (AB032761) rab5B [Oryza sativa]
                  403354
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-B10
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  398
E value
                  1.0e-38
Match length
                  79
% identity
                  100
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  403355
Seq. ID
                  LIB3431-062-P1-N1-B11
Method
                  BLASTX
NCBI GI
                  g3158476
BLAST score
                  166
E value
                  2.0e-11
Match length
                  43
```

NCBI GI

BLAST score





```
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
                  403356
Seq. No.
                  LIB3431-062-P1-N1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4914411
BLAST score
                  245
E value
                  1.0e-20
Match length
                  85
% identity
                  59
                  (AL050352) putative protein [Arabidopsis thaliana]
NCBI Description
                  403357
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-B3
Method
                  BLASTX
NCBI GI
                  g3108343
BLAST score
                  159
E value
                  1.0e-10
Match length
                  102
% identity
                  29
NCBI Description
                  (AF061285) sesquiterpene cyclase [Capsicum annuum]
                  403358
Seq. No.
                  LIB3431-062-P1-N1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1261917
BLAST score
                  218
E value
                  2.0e-17
Match length
                  59
% identity
                  64
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
Seq. No.
                  403359
Seq. ID
                  LIB3431-062-P1-N1-B5
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  300
                  3.0e-27
E value
Match length
                  71
% identity
                  77
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                  403360
Seq. ID
                  LIB3431-062-P1-N1-B7
Method
                  BLASTX
NCBI GI
                  g2286121
BLAST score
                  534
E value
                  1.0e-54
Match length
                  102
% identity
                  98
NCBI Description
                  (U88068) sec14 like protein [Oryza sativa]
Seq. No.
                  403361
Seq. ID
                  LIB3431-062-P1-N1-B8
Method
                  BLASTN
```

51878

g2305114

```
1.0e-123
   E value
   Match length
                      352
   % identity
                     Oryza sativa ferredoxin mRNA, complete cds
   NCBI Description
                     403362
   Seq. No.
   Seq. ID
                     LIB3431-062-P1-N1-B9
   Method
                     BLASTX
   NCBI GI
                     q132105
   BLAST score
                      411
   E value
                      4.0e-40
   Match length
                     76
   % identity
                     99
                     RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
   NCBI Description
                      (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                     ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                     precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                      (D00643) small subunit of ribulose-1,5-bisphosphate
                      carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                      ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                      sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                     carboxylase S [Oryza sativa]
   Seq. No.
                      403363
                     LIB3431-062-P1-N1-C11
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g115787
   BLAST score
                      403
   E value
                      3.0e-39
   Match length
                      76
   % identity
                      100
                     CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
   NCBI Description
                      CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                     protein 2R precursor - rice >gi_20182_emb_CAA32109
                      (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                      [Oryza sativa]
                      403364
Seq. No.
   Seq. ID
                      LIB3431-062-P1-N1-C12
   Method
                     BLASTN
   NCBI GI
                      q20262
   BLAST score
                      108
   E value
                      1.0e-53
   Match length
                      220
   % identity
                      87
   NCBI Description O.sativa light-induced mRNA
   Seq. No.
                      403365
   Seq. ID
                      LIB3431-062-P1-N1-C5
   Method
                     BLASTN
   NCBI GI
                      g218207
   BLAST score
                      256
                      1.0e-142
   E value
```

Oryza sativa mRNA for the small subunit of

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

284

98

Match length % identity

NCBI Description

Seq. No.

403371



p0SSS1139

```
Seq. No.
                  403366
Seq. ID
                  LIB3431-062-P1-N1-C6
Method
                  BLASTX
NCBI GI
                  q1854378
BLAST score
                  275
                  4.0e-24
E value
                  60
Match length
                  87
% identity
NCBI Description
                  (AB001338) Sucrose-Phosphate Synthase [Saccharum
                  officinarum]
                  403367
Seq. No.
                  LIB3431-062-P1-N1-C7
Seq. ID
Method
                  BLASTX
                  q3643090
NCBI GI
BLAST score
                  337
                  2.0e-31
E value
Match length
                  96
% identity
                  66
                  (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  403368
                  LIB3431-062-P1-N1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g451193
BLAST score
                  397
E value
                  2.0e-38
Match length
                  109
                  72
% identity
NCBI Description
                  (L28008) wali7 [Triticum aestivum]
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
                  403369
Seq. ID
                  LIB3431-062-P1-N1-C9
Method
                  BLASTN
NCBI GI
                  q2072554
BLAST score
                  317
                  1.0e-178
E value
Match length
                  325
% identity
                  99
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
Seq. No.
                  403370
Seq. ID
                  LIB3431-062-P1-N1-D1
Method
                  BLASTN
                  g2267594
NCBI GI
BLAST score
                  43
                  1.0e-15
E value
Match length
                  43
                  100
% identity
NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds
```

51880

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```
LIB3431-062-P1-N1-D11
Seq. ID
Method
                   BLASTX
                   g131400
NCBI GI
                   243
BLAST score
                   3.0e-27
E value
Match length
                   93
% identity
                   67
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi_81471_pir__S00409 photosystem II 10K protein precursor
- spinach >gi_170127 (J03887) 10kd polypeptide precursor
                   [Spinacia oleracea]
Seq. No.
                   403372
                   LIB3431-062-P1-N1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244965
BLAST score
                   157
E value
                   2.0e-10
Match length
                   37
% identity
                   81
                   (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   403373
Seq. No.
Seq. ID
                   LIB3431-062-P1-N1-D3
Method
                   BLASTN
                   g21692
NCBI GI
BLAST score
                   43
E value
                   9.0e-15
Match length
                   75
% identity
                   89
NCBI Description T.aestivum mRNA 1 for cathepsin B (2529)
Seq. No.
                   403374
Seq. ID
                   LIB3431-062-P1-N1-D4
Method
                   BLASTX
NCBI GI
                   q115813
BLAST score
                   280
E value
                   8.0e-25
                   68
Match length
% identity
                   82
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                   403375
Seq. ID
                   LIB3431-062-P1-N1-D5
Method
                   BLASTX
NCBI GI
                   g399333
BLAST score
                   289
E value
                   8.0e-26
Match length
                   66
% identity
                   88
                   CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE
NCBI Description
                   SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                   >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8)
                   precursor - pepper >gi 17944 emb CAA46086 (X64874)
```

O-acetylserine (thiol)-lyase [Capsicum annuum]

% identity

88

```
Seq. No.
                  403376
Seq. ID
                  LIB3431-062-P1-N1-D6
Method
                  BLASTX
NCBI GI
                  q2498397
BLAST score
                  217
E value
                  2.0e-17
Match length
                  48
% identity
                  83
NCBI Description
                  FERREDOXIN-THIOREDOXIN REDUCTASE, VARIABLE CHAIN (FTR-V)
                   (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT A) (FTR-A)
Seq. No.
                  403377
Seq. ID
                  LIB3431-062-P1-N1-D7
Method
                  BLASTN
NCBI GI
                  q3201968
BLAST score
                  235
E value
                  1.0e-129
Match length
                  307
                  94
% identity
NCBI Description Oryza sativa submergence induced protein 2A mRNA, complete
Seq. No.
                  403378
Seq. ID
                  LIB3431-062-P1-N1-E1
Method
                  BLASTN
NCBI GI
                  q2624325
BLAST score
                  179
E value
                  4.0e-96
Match length
                  273
% identity
                  92
NCBI Description Oryza sativa mRNA for glycine-rich RNA-binding protein
                  (OsGRP1)
                  403379
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-E10
Method
                  BLASTX
                  g1173347
NCBI GI
BLAST score
                  184
E value
                  1.0e-13
Match length
                  40
                  95
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  403380
Seq. ID
                  LIB3431-062-P1-N1-E11
Method
                  BLASTN
NCBI GI
                  q218209
BLAST score
                  44
E value
                  1.0e-15
Match length
                  155
```

NCBI Description

```
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
Seq. No.
                   403381
Seq. ID
                   LIB3431-062-P1-N1-E12
Method
                   BLASTX
NCBI GI
                   q3618310
BLAST score
                   378
E value
                   3.0e-36
Match length
                   72
% identity
                   100
NCBI Description
                  (AB001883) zinc finger protein [Oryza sativa]
                   403382
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-E2
Method
                  BLASTX
NCBI GI
                   q1617197
BLAST score
                   274
E value
                   4.0e-24
Match length
                   67
% identity
                  73
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   403383
Seq. ID
                  LIB3431-062-P1-N1-E3
Method
                  BLASTX
NCBI GI
                   q693920
BLAST score
                   386
                   3.0e-37
E value
Match length
                   77
                   95
% identity
NCBI Description
                   (U21113) chlorophyll a/b binding protein [Solanum
                  tuberosum]
Seq. No.
                   403384
Seq. ID
                  LIB3431-062-P1-N1-E5
Method
                  BLASTX
NCBI GI
                  q1076724
BLAST score
                   404
E value
                   3.0e-39
Match length
                   77
% identity
                   95
NCBI Description
                  LHCI-680, photosystem I antenna protein - barley
                  >gi_666054_emb_CAA59049 (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                   403385
Seq. ID
                  LIB3431-062-P1-N1-E7
Method
                  BLASTX
NCBI GI
                  g2739375
BLAST score
                  162
E value
                  6.0e-11
Match length
                  93
% identity
                  42
```

51883

(AC002505) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                   403386
Seq. ID
                   LIB3431-062-P1-N1-E8
Method
                   BLASTN
                   g5042437
NCBI GI
BLAST score
                   283
E value
                   1.0e-158
                   342
Match length
                   100
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                   403387
Seq. No.
Seq. ID
                   LIB3431-062-P1-N1-F1
Method
                   BLASTX
NCBI GI
                   q4079798
BLAST score
                   455
E value
                   3.0e-45
Match length
                   88
% identity
                   100
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   sativa]
Seq. No.
                   403388
Seq. ID
                   LIB3431-062-P1-N1-F12
Method
                   BLASTX
NCBI GI
                   q347451
BLAST score
                   154
E value
                   4.0e-10
Match length
                   29
% identity
                   100
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
Seq. No.
                   403389
Seq. ID
                   LIB3431-062-P1-N1-F3
Method
                   BLASTX
NCBI GI
                   g3885894
BLAST score
                   330
E value
                   1.0e-30
Match length
                   77
                   83
% identity
NCBI Description
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                   403390
Seq. ID
                   LIB3431-062-P1-N1-F6
Method
                   BLASTX
NCBI GI
                   g2997591
BLAST score
                   306
                   8.0e-28
E value
Match length
                   74
                   80
% identity
                   (AF020814) glucose-6-phosphate/phosphate-translocator
NCBI Description
                   precursor [Pisum sativum]
Seq. No.
                   403391
Seq. ID
                   LIB3431-062-P1-N1-F7
Method
                   BLASTX
NCBI GI
                   q3789952
```

```
BLAST score
                   1.0e-14
E value
Match length
                   35
% identity
                   100
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   403392
Seq. No.
                  LIB3431-062-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q132105
BLAST score
                   556
E value
                   3.0e-57
Match length
                   101
% identity
                   100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{\text{lase}} (\overline{\text{EC}} 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403393
Seq. No.
                  LIB3431-062-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2462834
                   244
BLAST score
                   1.0e-20
E value
                   107
Match length
% identity
                   48
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   403394
Seq. ID
                   LIB3431-062-P1-N1-G10
Method
                   BLASTX
NCBI GI
                   q1835731
BLAST score
                   426
                   6.0e-42
E value
Match length
                   92
% identity
                   89
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                   403395
Seq. ID
                   LIB3431-062-P1-N1-G11
Method
                   BLASTX
                   g3126854
NCBI GI
BLAST score
                   370
                   2.0e-35
E value
Match length
                   70
                   100
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   403396
                   LIB3431-062-P1-N1-G12
Seq. ID
```

E value

4.0e-36

```
Method
                  BLASTX
                  q3885892
NCBI GI
BLAST score
                  208
E value
                  1.0e-16
Match length
                  41
% identity
                  100
NCBI Description
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-G2
Method
                  BLASTX
NCBI GI
                  q5031281
BLAST score
                  223
E value
                  4.0e-18
Match length
                  47
                  81
% identity
NCBI Description
                  (AF139499) unknown [Prunus armeniaca]
                  403398
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-G3
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  1.0e-19
E value
Match length
                  44
                  100
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  403399
Seq. ID
                  LIB3431-062-P1-N1-G4
Method
                  BLASTX
NCBI GI
                  g5123711
BLAST score
                  280
E value
                  9.0e-25
Match length
                  90
% identity
                  61
NCBI Description
                  (AL079347) putative protein [Arabidopsis thaliana]
                  403400
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-G5
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  220
                  9.0e-18
E value
Match length
                  65
% identity
                  69
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
Seq. No.
                  403401
Seq. ID
                  LIB3431-062-P1-N1-G6
Method
                  BLASTX
NCBI GI
                  g4973264
BLAST score
                  376
```

% identity

76

```
Match length
% identity
                   73
NCBI Description
                  (AF144391) thioredoxin-like 5 [Arabidopsis thaliana]
Seq. No.
                   403402
                  LIB3431-062-P1-N1-G7
Seq. ID
Method
                  BLASTX
                  g2407279
NCBI GI
BLAST score
                  206
                  4.0e-16
E value
Match length
                  42
% identity
                  100
NCBI Description
                  (AF017362) aldolase [Oryza sativa]
                  403403
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-G8
Method
                  BLASTN
NCBI GI
                  g20369
BLAST score
                  381
E value
                  0.0e+00
Match length
                  385
% identity
                  100
NCBI Description
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi_2170909 dbj E02681 E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
Seq. No.
                  403404
                  LIB3431-062-P1-N1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885887
BLAST score
                  269
E value
                  1.0e-149
Match length
                  397
% identity
                  92
NCBI Description
                  Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
                  403405
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-H11
Method
                  BLASTX
NCBI GI
                  q451193
BLAST score
                  412
E value
                  3.0e-40
Match length
                  114
% identity
                  72
NCBI Description
                  (L28008) wali7 [Triticum aestivum]
                  >gi_1090845_prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
                  403406
Seq. ID
                  LIB3431-062-P1-N1-H3
Method
                  BLASTX
NCBI GI
                  q3250697
BLAST score
                  377
E value
                  3.0e-36
Match length
                  91
```



NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 403407

Seq. ID LIB3431-062-P1-N1-H5

Method BLASTN
NCBI GI g2072554
BLAST score 285

E value 1.0e-159 Match length 301 % identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 403408

Seq. ID LIB3431-062-P1-N1-H7

Method BLASTX
NCBI GI g132105
BLAST score 402
E value 4.0e-39
Match length 73
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403409

Seq. ID LIB3431-062-P1-N1-H9

Method BLASTN
NCBI GI g5051932
BLAST score 200
E value 1.0e-108
Match length 254
% identity 100

NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds

Seq. No. 403410

Seq. ID LIB3431-063-P1-K1-A1

Method BLASTN
NCBI GI g6015437
BLAST score 41
E value 1.0e-13
Match length 41
% identity 100

NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 403411

Seq. ID LIB3431-063-P1-K1-A11

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 7.0e-20

```
Match length
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  403412
Seq. ID
                  LIB3431-063-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  392
E value
                  2.0e-38
Match length
                  74
                  100
% identity
                 (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  403413
Seq. ID
                  LIB3431-063-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  363
                  1.0e-34
E value
Match length
                  101
% identity
                  74
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403414
                  LIB3431-063-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2407281
BLAST score
                  696
E value
                  1.0e-73
Match length
                  144
                  93
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  403415
Seq. ID
                  LIB3431-063-P1-K1-A4
Method
                  BLASTN
```

Method BLASTN
NCBI GI g3819202
BLAST score 51
E value 2.0e-19
Match length 191
% identity 82

NCBI Description Hordeum vulgare partial mRNA; clone cMWG0680.rev

Seq. No. 403416

Seq. ID LIB3431-063-P1-K1-A5



```
Method
                   BLASTX
NCBI GI
                   q548605
BLAST score
                   469
                   5.0e-47
E value
Match length
                   112
                   85
% identity
```

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi 304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

```
403417
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-A7
Method
```

BLASTN NCBI GI g2773153 181 BLAST score 2.0e-97 E value Match length 197 98 % identity

Oryza sativa abscisic acid- and stress-inducible protein NCBI Description

(Asr1) mRNA, complete cds

Seq. No. 403418

Seq. ID LIB3431-063-P1-K1-A8

Method BLASTX NCBI GI q4973254 BLAST score 436 E value 4.0e-43 Match length 100 80 % identity

(AF144386) thioredoxin f2 [Arabidopsis thaliana] NCBI Description

Seq. No. 403419

LIB3431-063-P1-K1-A9 Seq. ID

Method BLASTN g3819198 NCBI GI BLAST score 67 4.0e-29 E value Match length 95 93 % identity

NCBI Description Hordeum vulgare partial mRNA; clone cMWG0676.rev

403420 Seq. No.

Seq. ID LIB3431-063-P1-K1-B1

Method BLASTX NCBI GI q132105 BLAST score 664 E value 8.0e-70 Match length 143 % identity 88

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No. 403421 Seq. ID LIB3431-063-P1-K1-B10 Method BLASTX NCBI GI q4220533 BLAST score 220 2.0e-18 E value Match length 56 % identity 77 (AL035356) putative mitochondrial uncoupling protein NCBI Description [Arabidopsis thaliana] Seq. No. 403422 LIB3431-063-P1-K1-B11 Seq. ID Method BLASTN g6015437 NCBI GI 38 BLAST score 1.0e-12 E value Match length 38 % identity 100 NCBI Description Homo sapiens PEX1 mRNA, complete cds Seq. No. 403423 LIB3431-063-P1-K1-B2 Seq. ID Method BLASTX g3929924 NCBI GI 479 BLAST score 4.0e-48 E value Match length 93 % identity 98 NCBI Description (AB020502) catalase [Oryza sativa] Seq. No. 403424 Seq. ID LIB3431-063-P1-K1-B3 Method BLASTX NCBI GI q4103987 BLAST score 486 E value 6.0e-49 Match length 115 % identity NCBI Description (AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum] >gi_6002383_emb_CAB56756.1_ (AJ011589) 5,10-methylenetetrahydrofolate dehydrogenase: 5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum] Seq. No. 403425 Seq. ID LIB3431-063-P1-K1-B5 Method BLASTX NCBI GI g2570511 BLAST score 256

2.0e-22

57

E value Match length

```
% identity
NCBI Description
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
                  403426
Seq. No.
                  LIB3431-063-P1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q20177
                  47
BLAST score
                  1.0e-17
E value
Match length
                  115
% identity
                  85
NCBI Description
                  Rice cab1R gene for light harvesting chlorophyll
                  a/b-binding protein
Seq. No.
                  403427
                  LIB3431-063-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  434
                  5.0e-43
E value
Match length
                  84
                  98
% identity
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  403428
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-B9
Method
                  BLASTX
                  g5803266
NCBI GI
BLAST score
                  425
                  7.0e-42
E value
Match length
                  84
                  99
% identity
                  (AP000399) ESTs AU078063(S15496), C97608(C60475),
NCBI Description
                  C28255(C60475) correspond to a region of the predicted
                  gene; similar to plastid transketolase 2 (Y15782) [Oryza
                  sativa]
Seq. No.
                  403429
Seq. ID
                  LIB3431-063-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q2245120
BLAST score
                  372
E value
                  1.0e-35
Match length
                  121
% identity
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  403430
Seq. ID
                  LIB3431-063-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2264373
BLAST score
                  163
                  1.0e-11
E value
Match length
                  41
% identity
                  66
                  (ACO02354) putative NAM/no apical meristem protein
NCBI Description
                  [Arabidopsis thaliana]
```

BLAST score

E value

61 7.0e-26

```
Seq. No.
                  403431
                  LIB3431-063-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6015437
                  37
BLAST score
E value
                  2.0e-11
Match length
                  48
% identity
                  66
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  403432
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  q2305114
BLAST score
                  92
E value
                  1.0e-44
Match length
                  108
% identity
                  96
NCBI Description Oryza sativa ferredoxin mRNA, complete cds
                  403433
Seq. No.
                  LIB3431-063-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g132105
NCBI GI
BLAST score
                  271
                  1.0e-40
E value
Match length
                  84
                  95
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403434
Seq. ID
                  LIB3431-063-P1-K1-C5
Method
                  BLASTX
                  g3913018
NCBI GI
BLAST score
                  547
E value
                  3.0e-56
Match length
                  112
% identity
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  403435
Seq. ID
                  LIB3431-063-P1-K1-C8
                  BLASTN
Method
NCBI GI
                  g2570514
```

```
Match length
% identity
                  95
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
Seq. No.
                  403436
Seq. ID
                  LIB3431-063-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q4038695
BLAST score
                  198
E value
                  3.0e-18
Match length
                  63
% identity
                  78
NCBI Description
                  (AB020945) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  small subunit [Avena sativa]
Seq. No.
                  403437
                  LIB3431-063-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  518
E value
                  6.0e-53
Match length
                  99
% identity
                  95
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403438
Seq. ID
                  LIB3431-063-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q5734636
BLAST score
                  238
E value
                  5.0e-20
Match length
                  71
% identity
                  56
NCBI Description
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
                  sativa]
Seq. No.
                  403439
Seq. ID
                  LIB3431-063-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  159
E value
                  3.0e-11
Match length
                  39
% identity
                  79
```

Seq. No. 403440

NCBI Description

Seq. ID LIB3431-063-P1-K1-D6

subunit [Oryza sativa]

(AF017363) ribulose 1,5-bisphosphate carboxylase small



Method BLASTX g6014934 NCBI GI BLAST score 540 3.0e-55 E value 118 Match length 81 % identity NCBI Description DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS AND LEAVES PROTEIN) >gi_1305531 (U55219) defective chloroplasts and leaves; required for chloroplast development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi_1323698 (U55278) DCL [Solanum lycopersicum] Seq. No. 403441 LIB3431-063-P1-K1-D9 Seq. ID BLASTX Method g3549665 NCBI GI BLAST score 175 E value 1.0e-12 37 Match length 81 % identity NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana] 403442 Seq. No. LIB3431-063-P1-K1-E11 Seq. ID Method BLASTX NCBI GI g3738329 257 BLAST score 2.0e-22 E value Match length 65 75 % identity NCBI Description (AC005170) unknown protein [Arabidopsis thaliana] Seq. No. 403443 LIB3431-063-P1-K1-E4 Seq. ID Method BLASTN NCBI GI g451192 BLAST score 47 1.0e-17 E value Match length 119 % identity 85 NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds 403444 Seq. No. Seq. ID LIB3431-063-P1-K1-E6 Method BLASTX NCBI GI q3914423 BLAST score 183 E value 8.0e-14 Match length 37 % identity

NCBI Description PROFILIN 4 >gi 2642324 (AF032370) profilin [Zea mays]

Seq. No. 403445

Seq. ID LIB3431-063-P1-K1-E7

Method BLASTN NCBI GI g6015437

```
BLAST score
E value
                  2.0e-10
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  403446
                  LIB3431-063-P1-K1-E8
Seq. ID
                  BLASTX
Method
                  g2182029
NCBI GI
BLAST score
                  522
E value
                  2.0e-53
Match length
                  99
                  96
% identity
NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]
                  403447
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q473980
BLAST score
                  45
E value
                  1.0e-16
Match length
                  73
% identity
                  89
NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
                  403448
Seq. No.
                  LIB3431-063-P1-K1-F10
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                  788
                  2.0e-84
E value
                  143
Match length
% identity
                  99
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                   403449
Seq. ID
                  LIB3431-063-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2244867
BLAST score
                   314
E value
                   9.0e-29
Match length
                  156
% identity
                   (Z97337) hydroxynitrile lyase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   403450
Seq. ID
                  LIB3431-063-P1-K1-F12
Method
                  BLASTX
                  g2570515
NCBI GI
BLAST score
                   568
                  1.0e-58
E value
Match length
                  121
                  93
% identity
NCBI Description (AF022740) glycolate oxidase [Oryza sativa]
```

```
Seq. No.
                  403451
Seq. ID
                  LIB3431-063-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3953471
BLAST score
                  207
                  3.0e-16
E value
Match length
                  62
% identity
NCBI Description
                  (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                  403452
Seq. ID
                  LIB3431-063-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  q3075488
BLAST score
                  197
E value
                  2.0e-15
Match length
                  58
% identity
                  67
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  403453
Seq. ID
                  LIB3431-063-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q5911907
BLAST score
                  337
E value
                  1.0e-31
Match length
                  118
% identity
                  56
NCBI Description
                  (AL117455) hypothetical protein [Homo sapiens]
Seq. No.
                  403454
Seq. ID
                  LIB3431-063-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g218171
BLAST score
                  90
                  4.0e-43
E value
Match length
                  113
% identity
                  96
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
Seq. No.
                  403455
Seq. ID
                  LIB3431-063-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g1076724
BLAST score
                  586
E value
                  9.0e-61
                  125
Match length
                  84
% identity
NCBI Description
                  LHCI-680, photosystem I antenna protein - barley
                  >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
                  403456
Seq. No.
                  LIB3431-063-P1-K1-F7
Seq. ID
```

```
Method
                  BLASTN
NCBI GI
                  q218154
BLAST score
                  39
                  4.0e-13
E value
Match length
                  59
                  92
% identity
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
NCBI Description
                  clone:Aldp
                  403457
Seq. No.
                  LIB3431-063-P1-K1-F9
```

Seq. NO. 403457
Seq. ID LIB3431-063-P1-F
Method BLASTX
NCBI GI g3126854
BLAST score 388

E value 1.0e-37
Match length 82
% identity 90

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

 Seq. No.
 403458

 Seq. ID
 LIB3431-063-P1-K1-G1

 Method
 BLASTX

 NCBI GI
 g1184774

 BLAST score
 502

BLAST score 502 E value 8.0e-51 Match length 114 % identity 88

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 403459

Seq. ID LIB3431-063-P1-K1-G12

Method BLASTX
NCBI GI g3913018
BLAST score 698
E value 7.0e-74
Match length 139
% identity 99

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No. 403460

Seq. ID LIB3431-063-P1-K1-G3

Method BLASTN
NCBI GI g11957
BLAST score 342
E value 0.0e+00
Match length 362
% identity 99

NCBI Description Rice complete chloroplast genome

Seq. No. 403461

Seq. ID LIB3431-063-P1-K1-G4

Method BLASTX NCBI GI g3695005 BLAST score 386

```
E value
                  2.0e-62
                  145
Match length
% identity
                  89
NCBI Description
                  (AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2
                  [Zea mays]
Seq. No.
                  403462
Seq. ID
                  LIB3431-063-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  534
E value
                  7.0e-55
Match length
                  96
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403463
Seq. ID
                  LIB3431-063-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q1777375
BLAST score
                  527
E value
                  6.0e-54
Match length
                  105
% identity
                  99
NCBI Description
                  (D78573) aspartate kinase-homoserine dehydrogenase [Oryza
Seq. No.
                  403464
Seq. ID
                  LIB3431-063-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q2688828
BLAST score
                  197
E value
                  3.0e-15
Match length
                  81
% identity
NCBI Description
                  (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
                  armeniaca]
Seq. No.
                  403465
Seq. ID
                  LIB3431-063-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  741
E value
                  7.0e-79
Match length
                  140
                  99
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
```

subunit [Oryza sativa]

```
Seq. No.
                    403466
 Seq. ID
                    LIB3431-063-P1-K1-H4
 Method
                    BLASTX
 NCBI GI
                    g3832512
 BLAST score
                    374
 E value
                    5.0e-36
 Match length
                    110
  % identity
                    69
 NCBI Description
                    (AF097922) granule-bound glycogen (starch) synthase
                    [Astragalus membranaceus]
 Seq. No.
                    403467
 Seq. ID
                    LIB3431-063-P1-K1-H5
 Method
                    BLASTX
 NCBI GI
                    q131225
 BLAST score
                    179
 E value
                    2.0e-13
 Match length
                    59
  % identity
                    66
 NCBI Description
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                    V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                    precursor - barley >gi_167087 (M61146) photosystem I
                    hydrophobic protein [Hordeum vulgare]
- Seq. No.
                    403468
 Seq. ID
                    LIB3431-063-P1-N1-A11
 Method
                    BLASTX
 NCBI GI
                    q2072555
 BLAST score
                    237
 E value
                    7.0e-20
 Match length
                    44
                    100
 % identity
 NCBI Description
                    (AF001396) metallothionein-like protein [Oryza sativa]
                    >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                    protein [Oryza sativa]
 Seq. No.
                    403469
 Seq. ID
                    LIB3431-063-P1-N1-A12
 Method
                    BLASTX
 NCBI GI
                    q3126854
 BLAST score
                    393
 E value
                    5.0e-38
                    78
 Match length
 % identity
                    95
 NCBI Description
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
 Seq. No.
                    403470
 Seq. ID
                    LIB3431-063-P1-N1-A2
 Method
                    BLASTX
 NCBI GI
                    q132105
 BLAST score
                    508
 E value
                    2.0e-51
                    91
 Match length
 % identity
                    100
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
 NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

 Seq. No.
 403471

 Seq. ID
 LIB3431-063-P1-N1-A3

 Method
 BLASTX

 NCBI GI
 g132105

 BLAST score
 713

 E value
 2.0e-75

 Match length
 131

 % identity
 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi 226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 403472

Seq. ID LIB3431-063-P1-N1-A4

Method BLASTX
NCBI GI g5541681
BLAST score 202
E value 9.0e-16
Match length 83
% identity 59

NCBI Description (AL096859) putative protein [Arabidopsis thaliana]

Seq. No. 403473

Seq. ID LIB3431-063-P1-N1-A5

Method BLASTX NCBI GI g548605 BLAST score 570 E value 9.0e-59 Match length 127 % identity 89

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

>gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit

[Hordeum vulgare]

Seq. No. 403474

Seq. ID LIB3431-063-P1-N1-A7

Method BLASTN
NCBI GI g2773153
BLAST score 373
E value 0.0e+00
Match length 389
% identity 99

NCBI GI

BLAST score

g1076724

471

```
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
Seq. No.
                   403475
Seq. ID
                   LIB3431-063-P1-N1-A8
Method
                   BLASTX
NCBI GI
                   q4973254
                   396
BLAST score
                   2.0e-38
E value
Match length
                   94
% identity
                   79
NCBI Description (AF144386) thioredoxin f2 [Arabidopsis thaliana]
Seq. No.
                   403476
                   LIB3431-063-P1-N1-A9
Seq. ID
Method
                   BLASTN
                   q3819197
NCBI GI
BLAST score
                   55
                   7.0e-22
E value
Match length
                   200
% identity
                   82
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0676.uni
Seq. No.
                   403477
Seq. ID
                   LIB3431-063-P1-N1-B1
Method
                   BLASTX
                   g132105
NCBI GI
                   426
BLAST score
E value
                   7.0e-42
                   77
Match length
                   100
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403478
Seq. No.
                   LIB3431-063-P1-N1-B10
Seq. ID
Method
                   BLASTX
                   g4544443
NCBI GI
BLAST score
                   172
E value
                   3.0e-12
Match length
                   45
% identity
                   71
                   (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   403479
Seq. No.
Seq. ID
                   LIB3431-063-P1-N1-B11
Method
                   BLASTX
```

E value 4.0e-47 Match length 89 % identity NCBI Description LHCI-680, photosystem I antenna protein - barley >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare] 403480 Seq. No. LIB3431-063-P1-N1-B2 Seq. ID Method BLASTX NCBI GI q3929924 BLAST score 357 E value 8.0e-34 Match length 67 99 % identity NCBI Description (AB020502) catalase [Oryza sativa] 403481 Seq. No. LIB3431-063-P1-N1-B3 Seq. ID Method BLASTX NCBI GI q4103987 BLAST score 486 E value 6.0e-49 Match length 115 % identity 83 NCBI Description (AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum] >gi_6002383_emb_CAB56756.1_ (AJ011589) 5,10-methylenetetrahydrofolate dehydrogenase: 5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum] 403482 Seq. No. Seq. ID LIB3431-063-P1-N1-B5 Method BLASTX NCBI GI q115793 BLAST score 229 3.0e-23E value Match length 65 % identity 91 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR NCBI Description (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare] 403483 Seq. No. Seq. ID LIB3431-063-P1-N1-B8 Method BLASTX NCBI GI q3126854 BLAST score 410 E value 4.0e-40 Match length 78 % identity 99 NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa] Seq. No. 403484

```
Seq. ID
                  LIB3431-063-P1-N1-B9
Method
                  BLASTN
NCBI GI
                  q5803242
BLAST score
                   388
E value
                   0.0e + 00
Match length
                   484
% identity
                  100
NCBI Description
                  Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
Seq. No.
                   403485
Seq. ID
                  LIB3431-063-P1-N1-C12
Method
                  BLASTX
NCBI GI
                  q6103011
BLAST score
                   478
E value
                   5.0e-48
Match length
                  104
% identity
                   46
NCBI Description
                   (X84225) precursor of photosystem II subunit (22KDa)
                   [Nicotiana tabacum]
Seq. No.
                  403486
Seq. ID
                  LIB3431-063-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  q871931
BLAST score
                  220
E value
                  8.0e-18
Match length
                  59
% identity
                  71
NCBI Description
                  (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  403487
Seq. ID
                  LIB3431-063-P1-N1-C4
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  144
E value
                  5.0e-09
Match length
                  36
% identity
                  81
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403488
Seq. ID
                  LIB3431-063-P1-N1-C9
Method
                  BLASTX
NCBI GI
                  g4098250
BLAST score
                  164
E value
                  3.0e-11
                  71
Match length
                  41
% identity
NCBI Description (U76611) similar to Solanum tuberosum ci21A gene product
```

E value

Match length

3.0e-26

182

```
encoded by the sequence presented in GenBank Accession Number U76610 [Solanum tuberosum]
```

```
403489
Seq. No.
Seq. ID
                  LIB3431-063-P1-N1-D11
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  473
                  2.0e-47
E value
Match length
                  86
% identity
                  100
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  403490
Seq. ID
                  LIB3431-063-P1-N1-D12
Method
                  BLASTN
NCBI GI
                  q2950394
BLAST score
                  35
E value
                  5.0e-10
                  51
Match length
                  92
% identity
NCBI Description
                  Zea mays me gene, exons 1 to
                  403491
Seq. No.
Seq. ID
                  LIB3431-063-P1-N1-D2
Method
                  BLASTX
NCBI GI
                  g5734636
BLAST score
                  173
E value
                  3.0e-12
Match length
                  53
                  58
% identity
NCBI Description
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
                  sativa]
Seq. No.
                  403492
Seq. ID
                  LIB3431-063-P1-N1-D6
Method
                  BLASTX
NCBI GI
                  q6014934
BLAST score
                  381
E value
                  1.0e-36
Match length
                  84
% identity
                  76
NCBI Description
                  DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS
                  AND LEAVES PROTEIN) >gi_1305531 (U55219) defective
                  chloroplasts and leaves; required for chloroplast
                  development and palisade cell differentiation in leaves
                  [Lycopersicon esculentum] >gi 1323698 (U55278) DCL [Solanum
                  lycopersicum]
Seq. No.
                  403493
Seq. ID
                  LIB3431-063-P1-N1-D7
Method
                  BLASTN
NCBI GI
                  g902200
BLAST score
                  62
```

```
% identity
NCBI Description Z.mays complete chloroplast genome
                  403494
Seq. No.
                  LIB3431-063-P1-N1-E4
Seq. ID
Method
                  BLASTX
                  g451193
NCBI GI
BLAST score
                  314
                  2.0e-33
E value
Match length
                  120
% identity
                  68
                  (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
                  403495
                  LIB3431-063-P1-N1-E5
Seq. ID
Method
                  BLASTX
                  g1835731
NCBI GI
BLAST score
                  438
                  2.0e-43
E value
                  102
Match length
% identity
                  85
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  403496
                  LIB3431-063-P1-N1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2182028
BLAST score
                  324
                  0.0e + 00
E value
Match length
                  324
                  100
% identity
NCBI Description Oryza sativa mRNA for shaggy-like kinase etha
Seq. No.
                  403497
                  LIB3431-063-P1-N1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  226
E value
                  1.0e-124
Match length
                  226
                  100
% identity
NCBI Description Oryza sativa qlycine-rich protein (OSGRP1) mRNA, complete
                  403498
Seq. No.
                  LIB3431-063-P1-N1-F10
Seq. ID
Method
                  BLASTX
                  g1705624
NCBI GI
BLAST score
                  180
E value
                  4.0e-13
Match length
                  41
% identity
                  88
NCBI Description CATALASE ISOZYME A (CAT-A)
Seq. No.
                  403499
Seq. ID
                  LIB3431-063-P1-N1-F12
```

```
Method
                  BLASTX
NCBI GI
                  g2570515
BLAST score
                  159
                  9.0e-11
E value
                  34
Match length
                  97
% identity
                  (AF022740) glycolate oxidase [Oryza sativa]
NCBI Description
Seq. No.
                  403500
                  LIB3431-063-P1-N1-F2
Seq. ID
Method
                  BLASTX
                  g3953471
NCBI GI
BLAST score
                  207
E value
                  3.0e-16
Match length
                  62
                  61
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                  403501
Seq. No.
                  LIB3431-063-P1-N1-F3
Seq. ID
Method
                  BLASTX
                  g3075488
NCBI GI
BLAST score
                  227
                  2.0e-18
E value
Match length
                  44
                  98
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  403502
Seq. No.
                  LIB3431-063-P1-N1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3036946
BLAST score
                  307
E value
                   4.0e-28
Match length
                   60
                   98
% identity
                   (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
Seq. No.
                   403503
                  LIB3431-063-P1-N1-F6
Seq. ID
Method
                  BLASTX
                  q1076724
NCBI GI
                   278
BLAST score
E value
                   1.0e-24
Match length
                   56
                   93
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
```

Seq. No. 403504

Seq. ID LIB3431-063-P1-N1-F7

Method BLASTX
NCBI GI g2407279
BLAST score 469
E value 6.0e-47

```
Match length
                  95
% identity
NCBI Description
                  (AF017362) aldolase [Oryza sativa]
                  403505
Seq. No.
                  LIB3431-063-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115802
BLAST score
                  189
E value
                  3.0e-14
Match length
                  36
                  97
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                  CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
Seq. No.
                  403506
                  LIB3431-063-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120668
BLAST score
                   469
E value
                  7.0e-47
Match length
                  102
% identity
                  88
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_82399_pir__A24159 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                  >gi 167044 (M36650) glyceraldehyde-3-phosphate
                  dehydrogenase [Hordeum vulgare] >gi 225347 prf 1301218A
                  dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                  distichum]
Seq. No.
                   403507
Seq. ID
                  LIB3431-063-P1-N1-G10
Method
                  BLASTX
NCBI GI
                  q21839
BLAST score
                   595
E value
                   7.0e-62
Match length
                  118
% identity
                   94
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
Seq. No.
                   403508
Seq. ID
                  LIB3431-063-P1-N1-G11
Method
                  BLASTX
NCBI GI
                   q517500
BLAST score
                   273
E value
                   3.0e-24
Match length
                   68
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi_444338_prf_ 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                   403509
Seq. No.
```

```
LIB3431-063-P1-N1-G12
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2407279
 BLAST score
                    398
 E value
                    1.0e-38
 Match length
                    75
                    100
 % identity
 NCBI Description (AF017362) aldolase [Oryza sativa]
                    403510
 Seq. No.
                    LIB3431-063-P1-N1-G2
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g4138290
 BLAST score
                    283
                    3.0e-25
 E value
 Match length
                    55
                    100
 % identity
 NCBI Description (AJ005841) thioredoxin M [Oryza sativa]
 Seq. No.
                    403511
                    LIB3431-063-P1-N1-G7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g2191138
 BLAST score
                    275
 E value
                    3.0e-24
 Match length
                    84
                    64
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
 NCBI Description
                    thaliana]
                    403512
 Seq. No.
                    LIB3431-063-P1-N1-G8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g132105
 BLAST score
                    429
 E value
                    3.0e-42
 Match length
                    79
                    99
 % identity
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
 Seq. No.
                    403513
 Seq. ID
                    LIB3431-063-P1-N1-H1
 Method
                    BLASTX
 NCBI GI
                    q693920
 BLAST score
                    419
 E value
                    5.0e-41
 Match length
                    80
 % identity
                    97
```

NCBI Description (U21113) chlorophyll a/b binding protein [Solanum

tuberosum]

```
Seq. No.
                  403514
Seq. ID
                  LIB3431-063-P1-N1-H10
Method
                  BLASTX
NCBI GI
                  q121291
BLAST score
                  295
E value
                  2.0e-30
Match length
                  79
% identity
                  90
NCBI Description
                  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT
                   (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)
                   (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE)
                  >gi_82596_pir__S05079 glucose-1-phosphate
                  adenylyltransferase (EC 2.7.7.27) (clone AGA.1) - wheat
                   (fragment) >gi_21677 emb_CAA32531_ (X14348) ADP-glucose
                  pyrophosophorylase [Triticum aestivum]
                  >gi_226873_prf__1609236A ADP glucose pyrophosphatase AGA.1
                  [Triticum aestivum]
Seq. No.
                  403515
Seq. ID
                  LIB3431-063-P1-N1-H12
Method
                  BLASTX
NCBI GI
                  q1777375
BLAST score
                  152
                  6.0e-10
E value
Match length
                  31
                  97
% identity
                  (D78573) aspartate kinase-homoserine dehydrogenase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  403516
Seq. ID
                  LIB3431-063-P1-N1-H3
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  709
E value
                  5.0e-75
Match length
                  130
% identity
                  99
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  403517
Seq. No.
Seq. ID
                  LIB3431-063-P1-N1-H5
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  216
                  2.0e-17
E value
Match length
                  56
                  73
% identity
```

```
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  403518
Seq. No.
Seq. ID
                  LIB3431-063-P1-N1-H6
Method
                  BLASTX
                  g2462750
NCBI GI
                  154
BLAST score
E value
                  4.0e-10
Match length
                  52
% identity
                  62
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family) [Arabidopsis thaliana]
                  403519
Seq. No.
Seq. ID
                  LIB3432-001-P1-K1-H6
Method
                  BLASTX
                  g600771
NCBI GI
BLAST score
                  198
                  1.0e-15
E value
Match length
                  63
% identity
                  68
NCBI Description (L35844) G protein alpha subunit [Oryza sativa]
Seq. No.
                  403520
                  LIB3432-002-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5002357
BLAST score
                  156
E value
                  6.0e-11
Match length
                  56
% identity
                  59
                  (AF150957) heat-shock protein ClpP [Azospirillum
NCBI Description
                  brasilense]
Seq. No.
                  403521
Seq. ID
                  LIB3432-002-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q2739382
BLAST score
                  215
E value
                  3.0e-17
Match length
                  141
% identity
NCBI Description
                  (AC002505) myosin heavy chain-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  403522
Seq. ID
                  LIB3432-003-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g5263320
BLAST score
                  677
E value
                  3.0e-71
Match length
                  147
                  91
% identity
NCBI Description (AC007727) Similar to gb M87339 replication factor C,
```

Seq. No.

403528

37-kDa subunit from Homo sapiens and is a member of PF_00004 ATPases associated with various cellular activities. [Arabidopsis thaliana]

```
Seq. No.
                  403523
Seq. ID
                  LIB3432-005-P1-K1-A3
Method
                  BLASTX
                  g5912299
NCBI GI
BLAST score
                  587
                  7.0e-61
E value
Match length
                  123
                  93
% identity
NCBI Description
                  (AJ133787) gigantea homologue [Oryza sativa]
                  403524
Seq. No.
                  LIB3432-006-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g871931
BLAST score
                   492
                  8.0e-50
E value
Match length
                  116
                  88
% identity
NCBI Description
                  (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  403525
                  LIB3432-006-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827524
BLAST score
                   215
                  2.0e-17
E value
                   44
Match length
                   77
% identity
                  (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                   403526
Seq. No.
Seq. ID
                  LIB3432-007-P1-K1-B6
Method
                  BLASTX
NCBI GI
                   q1244566
BLAST score
                  719
E value
                   3.0e-76
Match length
                   145
                   92
% identity
NCBI Description
                   (U39321) acetyl-CoA carboxylase [Triticum aestivum]
                   >gi 1588584_prf 2208491A Ac-CoA carboxylase [Triticum
                   aestivum]
Seq. No.
                   403527
Seq. ID
                  LIB3432-007-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   g577352
BLAST score
                   55
                   6.0e-22
E value
Match length
                   148
% identity
                   38
NCBI Description
                  Streptococcus equi M protein (emmSzW60) gene, complete cds
```

Method

BLASTX

```
LIB3432-007-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  a5230785
                  214
BLAST score
                  5.0e-17
E value
Match length
                  63
% identity
                   65
                  (AF107024) histone H1 WH1B.1 [Triticum aestivum]
NCBI Description
                  403529
Seq. No.
Seq. ID
                  LIB3432-007-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q3417451
                  155
BLAST score
                   3.0e-10
E value
Match length
                   39
                  74
% identity
                  (AB013728) light-harvesting chlorophyll a/b-binding protein
NCBI Description
                  of photosystem II [Cryptomeria japonica]
                  403530
Seq. No.
                  LIB3432-007-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3980378
BLAST score
                   373
E value
                   1.0e-35
                   140
Match length
                   55
% identity
                   (AC004561) putative RNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   403531
Seq. No.
                  LIB3432-007-P1-K1-H12
Seq. ID
Method
                  BLASTX
                   q166835
NCBI GI
BLAST score
                   623
E value
                   4.0e-65
Match length
                   135
% identity
                   89
NCBI Description
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
                   activase [Arabidopsis thaliana] >qi 2642170 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
Seq. No.
                   403532
Seq. ID
                   LIB3432-007-P1-K1-H4
Method
                   BLASTX
                   q3789952
NCBI GI
BLAST score
                   562
E value
                   5.0e-58
Match length
                   112
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403533
Seq. ID
                   LIB3432-007-P1-K1-H6
```

```
q3914603
 NCBI GI
 BLAST score
                    317
                    4.0e-29
 E value
Match length
                    145
 % identity
                    50
 NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                    CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                    (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                    activase [Oryza sativa]
 Seq. No.
                    403534
 Seq. ID
                   LIB3432-009-P1-K1-A2
 Method
                   BLASTX
 NCBI GI
                    q3367594
 BLAST score
                    194
 E value
                    1.0e-14
 Match length
                    70
 % identity
                    53
 NCBI Description
                   (AL031135) putative protein [Arabidopsis thaliana]
 Seq. No.
                   403535
 Seq. ID
                   LIB3432-009-P1-K1-A7
 Method
                   BLASTX
 NCBI GI
                   q4574139
 BLAST score
                   159
 E value
                   2.0e-17
 Match length
                   83
 % identity
                   64
 NCBI Description
                   (AF073697) cysteine synthase [Oryza sativa]
 Seq. No.
                   403536
 Seq. ID
                   LIB3432-010-P1-K1-B11
 Method
                   BLASTX
 NCBI GI
                   q940288
 BLAST score
                   381
 E value
                   1.0e-36
 Match length
                   137
% identity
                   57
 NCBI Description
                   (L43510) protein localized in the nucleoli of pea nuclei;
                   ORF; putative [Pisum sativum]
 Seq. No.
                   403537
 Seq. ID
                   LIB3432-010-P1-K1-G11
 Method
                   BLASTX
                   g606817
 NCBI GI
 BLAST score
                   329
 E value
                   2.0e-30
 Match length
                   78
 % identity
                   82
NCBI Description
                   (U08404) carbonic anhydrase [Oryza sativa]
```

>gi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic

anhydrase 3 [Oryza sativa]

Seq. No. 403538

Seq. ID LIB3432-010-P1-K1-G2

Method BLASTX NCBI GI g2072555

```
BLAST score
E value
                   4.0e-17
Match length
                   44
                   91
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   403539
                   LIB3432-010-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g6041833
BLAST score
                   180
E value
                   5.0e-13
Match length
                   125
% identity
                   36
NCBI Description
                  (AC009853) unknown protein [Arabidopsis thaliana]
Seq. No.
                   403540
                  LIB3432-010-P1-K1-G9
Seq. ID
Method
                  BLASTX
                   g1353352
NCBI GI
BLAST score
                   190
E value
                   1.0e-14
Match length
                   61
% identity
                   67
NCBI Description
                   (U31975) alanine aminotransferase [Chlamydomonas
                   reinhardtii]
Seq. No.
                   403541
                  LIB3432-011-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2407281
BLAST score
                   680
E value
                   1.0e-71
Match length
                   139
% identity
                   91
NCBI Description
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
                   subunit [Oryza sativa]
Seq. No.
                   403542
Seq. ID
                  LIB3432-011-P1-K1-G7
Method
                  BLASTX
NCBI GI
                   q733458
BLAST score
                   340
E value
                   6.0e-32
Match length
                   90
% identity
                  77
NCBI Description
                   (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
                   [Zea mays]
Seq. No.
                   403543
Seq. ID
                  LIB3432-012-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1632822
BLAST score
                  214
E value
                  1.0e-17
```

Seq. ID

```
Match length
% identity
                   95
NCBI Description
                  (Y08962) transmembrane protein [Oryza sativa] >gi 1667594
                   (U77297) transmembrane protein [Oryza sativa]
Seq. No.
                  403544
Seq. ID
                  LIB3432-012-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g4056490
BLAST score
                  189
E value
                  2.0e-14
Match length
                  90
% identity
                  42
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  403545
                  LIB3432-012-P1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20155 · ·
BLAST score
                  65
E value
                  3.0e-28
Match length
                  85
                  94
% identity
NCBI Description O.sativa random single-copy DNA fragment 12RG214R
Seq. No.
                  403546
Seq. ID
                  LIB3432-012-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g4662632
BLAST score
                  230
                  6.0e-19
E value
Match length
                  71
% identity
                  68
NCBI Description
                  (AC007267) unknown protein [Arabidopsis thaliana]
Seq. No.
                  403547
Seq. ID
                  LIB3432-012-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  q5257255
BLAST score
                  83
E value
                  1.0e-38
Match length
                  168
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
Seq. No.
                  403548
Seq. ID
                  LIB3432-012-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g3885892
BLAST score
                  262
E value
                  1.0e-22
Match length
                  67
% identity
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                  403549
```

LIB3432-012-P1-K1-H7

```
Method
                  BLASTX
NCBI GI
                  q4455680
BLAST score
                  150
                  4.0e-10
E value
Match length
                  66
                  47
% identity
                  (AL035472) putative prolyl tRNA synthetase [Mycobacterium
NCBI Description
                  403550
Seq. No.
                  LIB3432-013-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2373403
BLAST score
                  157
                  5.0e-11
E value
Match length
                  42
                  67
% identity
                  (D85193) similar to the membrane protein RD28 [Arabidopsis
NCBI Description
                  thaliana]
                  403551
Seq. No.
                  LIB3432-014-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006855
BLAST score
                  215
                  2.0e-17
E value
Match length
                  76
                  57
% identity
                  (Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  403552
Seq. No.
                  LIB3432-015-P1-K1-D5
Seq. ID
Method
                  BLASTX
                  g1173347
NCBI GI
BLAST score
                  618
E value
                  1.0e-64
Match length
                  120
                  94
% identity
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  403553
                  LIB3432-015-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2281115
BLAST score
                  631
                  6.0e-66
E value
Match length
                  154
% identity
                  (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
```

thaliana]

```
403554
Seq. No.
                  LIB3432-016-P1-K1-D2
Seq. ID
Method
                  BLASTX
                  g1617197
NCBI GI
                  275
BLAST score
                  3.0e-24
E value
Match length
                  71
                  75
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  403555
Seq. No.
                  LIB3432-016-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  192
                  1.0e-14
E value
Match length
                  82
% identity
                  56
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146 pir__ S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
                  403556
Seq. No.
                  LIB3432-016-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  233
                  2.0e-19
E value
Match length
                  44
% identity
                  98
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  403557
Seq. No.
                  LIB3432-017-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2253092
BLAST score
                  196
E value
                  3.0e-20
Match length
                  68
                  66
% identity
                  (Y14198) hypothetical protein [Spinacia oleracea]
NCBI Description
Seq. No.
                  403558
                  LIB3432-018-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587524
BLAST score
                  159
```

E value 1.0e-10 Match length 42 69 % identity

(AC007060) T5I8.13 [Arabidopsis thaliana] NCBI Description

Seq. No. 403559

Seq. ID LIB3432-018-P1-K1-D2

```
Method
                  BLASTX
NCBI GI
                  q4567273
BLAST score
                  433
                  9.0e-43
E value
Match length
                  140
% identity
                  60
                  (AC006841) putative vacuolar proton ATPase subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  403560
                  LIB3432-019-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  479
E value
                  3.0e-48
Match length
                  109
                  85
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone posss1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_ 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403561
Seq. ID
                  LIB3432-019-P1-K1-H12
Method
                  BLASTX
                  g2570497
NCBI GI
BLAST score
                  206
E value
                  3.0e-16
Match length
                  123
% identity
                  42
                  (AF022731) H protein subunit of glycine decarboxylase
NCBI Description
                  [Oryza sativa]
Seq. No.
                  403562
Seq. ID
                  LIB3432-020-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q3281853
BLAST score
                  536
E value
                  7.0e-55
Match length
                  139
% identity
                  76
NCBI Description
                  (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                  403563
Seq. ID
                  LIB3432-020-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q4104056
BLAST score
                  279
                  1.0e-24
E value
Match length
                  62
% identity
                  81
```

NCBI Description (AF031194) S276 [Triticum aestivum]

% identity

76

```
Seq. No.
                  403564
Seq. ID
                  LIB3432-020-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  108
E value
                  7.0e-54
Match length
                  179
                  89
% identity
NCBI Description
                  Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone: t17804
Seq. No.
                  403565
                  LIB3432-020-P1-K1-D5
Seq. ID
Method
                  BLASTX
                  g1173347
NCBI GI
BLAST score
                  189
E value
                  1.0e-14
Match length
                  79
                  54
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                  403566
Seq. No.
Seq. ID
                  LIB3432-021-P1-K1-A2
Method
                  BLASTN
                  g6063530
NCBI GI
BLAST score
                  39
                  5.0e-13
E value
Match length
                  43
% identity
                  98
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
Seq. No.
                  403567
Seq. ID
                  LIB3432-021-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g6063542
BLAST score
                  273
E value
                  3.0e-24
Match length
                  61
% identity
                  85
                  (AP000615) EST C74302 (E30840) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
Seq. No.
                  403568
Seq. ID
                  LIB3432-021-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g115766
BLAST score
                  316
E value
                  1.0e-29
Match length
                  71
```